THE UNIVERSITY of ADELAIDE

Molecular Genetics and Genomics Approaches to Improve Phytophthora Root Rot Resistance in Chickpea

By

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Thesis submitted in fulfilment of the requirements for the degree of **Doctor of Philosophy** in the Faculty of Sciences at the University of Adelaide

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Abstract

Phytophthora root rot (PRR) caused by the oomycete *Phytophthora medicaginis* is a major soil-borne disease of chickpea in Australia. No economic in-crop control is available and breeding for PRR resistance is considered a sustainable management option. Moderate field resistance was identified in *Cicer arietinum* and incorporated into the cultivated variety Yorker. Also, a higher level of resistance identified from a wild relative of chickpea (*C. echinospermum*) was incorporated into a cultivated background. These genotypes were used to develop intra-specific and interspecific recombinant-inbred line (RIL) populations, respectively, to facilitate genetic studies. The genetic basis of PRR resistance in chickpea is unknown. The aim of this thesis is to identify quantitative trait loci (QTL) linked to PRR resistance in chickpea and determine underlying molecular mechanisms. RIL populations were genotyped using Genotype-by-Sequencing and phenotyped for PRR in three field environments inoculated with *P. medicaginis*. Multi-environment genetic analysis identified major QTL on chromosomes 3, 4 and 6 with resistance derived from wild *Cicer*. Two QTL were identified on chromosomes 5 and 6 with resistance derived from *C. arietinum*. Aligning these QTL to the chickpea reference genome indicated that *C. arietinum* and *C. echinospermum* sources of PRR resistance are different. A PRR phenotyping method was developed in hydroponics using *P. medicaginis* zoospores as inoculum. Efficiency of the system was validated both qualitatively by observations of PRR symptom development, and quantitatively by measuring the amounts of pathogen DNA in roots. Large-scale screening with two RIL populations was performed. QTL were identified that associated with two measures of PRR resistance, canker length and Kaplan-Meier estimates of plant survival. PRR resistance traits from field and hydroponics experiments were combined in model-based correlation analysis, showing strong genetic correlations between them.

A QTL region identified in hydroponics on chromosome 4 corresponds to the same region identified for PRR resistance in field screening. These analyses substantiated the hydroponics PRR phenotyping method as a suitable alternative to screening in field conditions. RNA-sequencing study identified changes in gene expression linked to PRR infection responses in roots of resistant chickpea genotypes derived from *C. arietinum* and *C. echinospermum* sources, and in a PRR-susceptible variety. Redox processes were regulated, signifying successful pathogen recognition in all genotypes. Differences in signalling events between Yorker and wild *Cicer* derivative indicated a difference in their resistance response to *P. medicaginis*. Several differentially expressed genes mapped to PRR resistance QTL identified from genetic studies. The gene Ca_24447, encoding aquaporin SIP1-2, is located within the QTL region on chromosome 6 and was up-regulated in both PRR-resistant genotypes compared to the susceptible variety following PRR infection.

The QTL identified in this thesis will enable the implementation of marker-assisted selection in breeding for PRR resistance. The hydroponics PRR phenotyping method could be scaled up for screening of PRR resistance in a breeding program, and to provide plant tissue suitable for molecular studies to further knowledge of the host-pathogen interaction. The RNA-sequencing study provides a basis for future research to decipher the genetic factors underlying PRR resistance in wild *Cicer* and cultivated sources.

Declaration

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in my name in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint award of this degree.

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Structure of the thesis

This doctoral thesis is presented in six chapters, preceded with an Abstract which gives an overview of the research undertaken. Chapter 1 is a General Introduction which provides a broad overview of the research field and the overall aim of this thesis. Chapter 2 is a Literature Review that presents a comprehensive review of literature which establishes the field of knowledge in Phytophthora root rot (PRR) in chickpea, the available disease management strategies and the need for an integrated genetic and genomic approach to improve PRR resistance in crop resistance breeding. The specific aim of this thesis will also be briefly discussed. Chapter 3, 4 and 5 are experimental papers of which two have been published in peer reviewed journals and one is an unpublished work written in manuscript format shortly to be submitted for publication. Each of the experimental papers contains an Abstract, Introduction, Materials and Methods, Results, Discussion and References. In addition, they are prefaced by a statement of authorship that describes the contribution of each author and a link page to the publications included in this thesis. Chapter 6 presents the General Discussion and future research directions. It describes how the findings reported in this thesis contribute to the field of managing PRR resistance in chickpea through pre-breeding and breeding research and provides strategies for future research direction. References included in Chapter 1, 2 and 6 are presented in the list of references (Bibliography) at the end. This thesis contains two appendices: Appendix 1 includes the supplementary tables and figures presented in Amalraj et al., 2018; Appendix 2 contains the supplementary tables and figures presented in Chapter 5. This thesis is in agreement with the specification of "thesis by publication" format of the Adelaide Graduate Centre Higher Degree by Research, the University of Adelaide, South Australia.

List of publications

1. Amalraj A., Taylor J., Bithell S., Li Y., Moore K., Hobson K., Sutton T., Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (*Cicer arietinum* L.) and wild (*Cicer echinospermum* P.H. Davis) chickpea, Theoretical and Applied Genetics, 132: 1017 (2018)
2. Amalraj, A., Taylor, J., Sutton, T. A hydroponics based high throughput screening system for Phytophthora root rot resistance in chickpea (*Cicer arietinum* L.). Plant Methods 15, 82 (2019) doi:10.1186/s13007-019-0463-3

List of abbreviations

AB	Ascochyta blight
ABA	Abscisic acid
Avr	avirulence
BAK1	BRI1-associated receptor kinase 1
BC	backcrosses
BGM	Botrytis grey mould
BLAST	Basic Local Alignment Search Tool
BRI1	brassinosteroid insensitive 1
BSR-seq	Bulked segregant RNA-seq
bZIP	basic leucine zipper domain
Cas9	CRISPR associated protein 9
cDNA	complementary DNA
CGIAR	Consultative Group for International Agricultural Research
CPM	counts per million
CRISPR	clusters of regularly interspaced short palindromic repeats
DArT	Diversity Arrays Technology
DEG	Differential expression of genes
DH	double haploid
DNA	deoxyribonucleic acid
EF1-α	Elongation factor 1-alpha
ET	ethylene
ETI	effector-triggered immunity
F_6	Filial generation 6
FW	Fusarium wilts

GBS	Genotype-By-Sequencing
GFF	General Feature Format
GO	Gene Ontology
goi	gene of interest
GS	genomic selection
GSTs	glutathione-S-transferases
GWAS	Genome Wide Association Mapping
H2O2	Hydrogen per oxide
InDels	insertion or deletion of bases
JA	Jasmonic acid
KASP	Kompetitive allele specific PCR
KME-survival	Kaplan-Meier estimates of plant survival
LRR	leucine rich repeat
MAPK	mitogen-activated protein kinase
MAS	marker-assisted selection
Mbp	millions of base pairs
MDS	multi-dimensional scaling
MGB	minor groove binder
MIP	major intrinsic protein
mL	milli litre
mRNA	Messenger RNA
NES	not elsewhere specified
NGS	Next Generation Sequencing
NIL	near isogenic lines
NRQ	Normalised relative quantities

PAMPs	pathogen-associated molecular patterns
PCR	Polymerase chain reaction
PIP	Plasma membrane Intrinsic Proteins
PR	pathogenesis related
PRR	Phytophthora root rot
PRRs	pattern recognition receptors
PTI	PAMP-triggered immunity
QDR	quantitative disease resistance
qRT-PCR	Quantitative real-time PCR
QTL	quantitative trait loci
r^2	R-squared
RIL	recombinant inbred lines
RIN	RNA Integrity Number
RNA	Ribonucleic acid
ROS	reactive oxygen species
SA	salicylic acid
SAM	Sequence Alignment/Map
SCAR	sequence-characterized DNA marker
SI	Survival index
SIP	small and basic intrinsic proteins
SNPs	Single Nucleotide Polymorphisms
TaqMan	Taq Polymerase PacMan
w/v	weight per volume
w/w	weight per weight

Chapter 1

Introduction:

An increasing human population together with the challenge of a changing climate threatens food security worldwide. Farming systems need to become simultaneously more sustainable and more productive. Food legumes such as soybean, peanut, pulses, fresh peas and fresh beans play a major role in the sustainability and profitability of farming systems and are a major protein component of the human diet, especially in developing countries. Legumes have become an important alternate protein source for dietary intake as meat consumption significantly contributes to global warming (Sadler, 2004; Wild et al, 2014). Pulses are a type of leguminous plant where the dried seed from the pod is edible. Globally, the harvested area under pulse crops is 11.5% of the harvested area under cereal crops (FAOSTAT 2017). In 2017, average global yields of pulse crops were about one-fourth the average yields of cereal crops (FAOSTAT 2017). There are eleven types of pulses, these being dry beans, dry broad beans, dry peas, chickpeas, cow peas, pigeon peas, lentils, Bambara beans, vetches, lupins and pulses NES (not elsewhere specified: minor pulses that don't fall into one of the other categories), recognised by the United Nations Food and Agriculture Organization (FAO).

Chickpea (*Cicer arietinum*) is a nutritious pulse crop which serves as a good and cheap source of protein for people in developing countries. It is also rich in other essential minerals such as phosphorus, calcium, magnesium, iron and zinc (Gaur & Gowda, 2005). The genus *Cicer* belongs to the *Leguminosae* family and to the sub-family *Papilionoideae* (Arumaganthan & Earle, 1991). There are two different types of chickpea based on seed size, shape and colour: desi and kabuli. The desi type is small-seeded, angular-shaped with a wide range of colours from brown, yellow, orange, black to green,

while the kabuli type is generally large-seeded, cream-coloured and 'ram's head' shaped (Varshney et al, 2017). Chickpea is a protein-rich pulse crop that ranks third among the pulses in terms of global annual production, accounting for 14.77 million tons (FAOSTAT 2017) after beans (31.4 million tons) and peas (16.2 million tons). It is grown in more than 50 countries around the world with 90% of the area sown being in developing countries such as India, Pakistan, Turkey, Ethiopia, Myanmar and Mexico (Knights, 2007). Other major chickpea producing countries include Australia, Iran and Canada. India is the largest producer of chickpea in the world, accounting for 61.4% of the world's total production in 2017 according to FAOSTAT. In addition to the nutritional benefits of chickpea, the presence of root nodules supports biological nitrogen fixation through symbiosis with Rhizobium (*Mesorhizobium ciceri*) bacteria, fixing atmospheric nitrogen and providing up to 80% of the plant's nitrogen requirement (Sharma et al, 2013b). This helps to improve soil fertility and chickpea is often grown as a rotation crop with cereals to contribute nitrogen into the system (Saraf et al, 1998). Thus, chickpea plays an important role in crop diversification and the long term sustainability of farming systems.

In Australia, chickpea was first grown as a commercial crop in southern Queensland in the early 1970's. With continued efforts of nationwide programs of germplasm introduction as well as investment in public plant breeding programs, the Australian chickpea industry has now become established in all mainland states of Australia, including New South Wales, Queensland, Victoria, South Australia and Western Australia (Knights, 2007). Of the total pulse production in Australia, chickpea ranks second after lupin (Fig. 1.1). 90% of the chickpea grown in Australia belongs to the desi type and the other 10% is of kabuli type (Knights, 2007). There is an increasing trend in the production value of chickpea in Australia (Fig. 1.2). Only 10% of production is retained for domestic consumption while the remainder is exported, mainly to the

Indian subcontinent where demand often exceeds local supply. Thus, there is an increased interest among Australian growers to cultivate chickpea, primarily driven by the crop's high economic value, but also for added benefits such as human nutrition, crop diversification and sustainable agriculture.

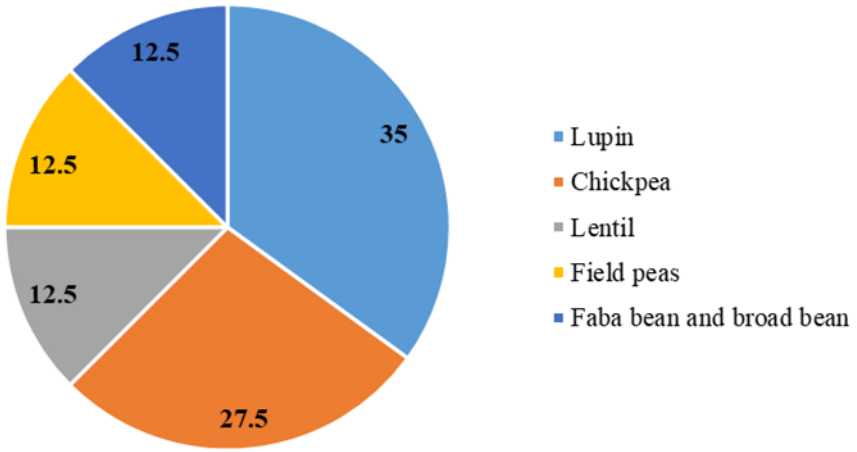

Fig. 1.1. Percentage of pulse production in Australia (2013–14 to 2017–18) (GRDC, 2018).

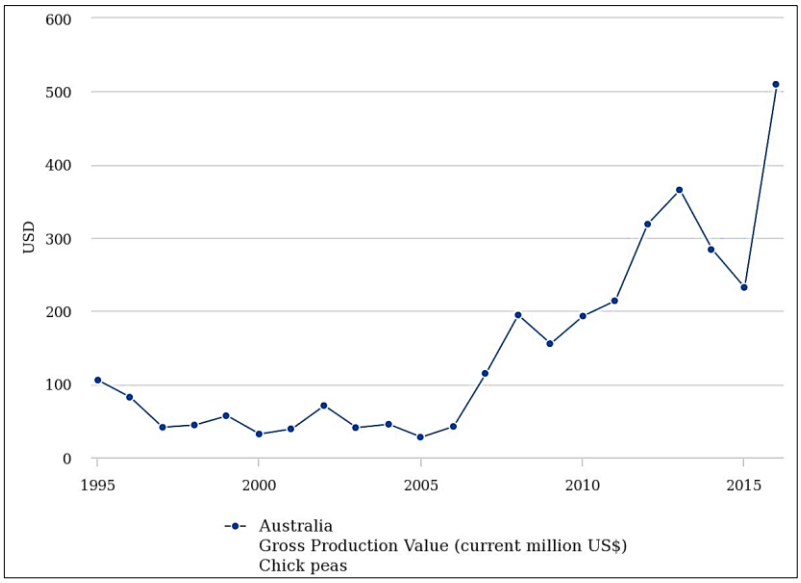

Fig. 1.2. Graph showing the growth in production value of chickpea in Australia. Source (FAOSTAT 2017)

The developing Australian chickpea industry has encountered a number of challenges including the need for specialised cultivation and harvesting machinery, adaptation to diverse regional environments, changing climate, major disease threats and the demands of a volatile export market. Major crop disease threats arising from Ascochyta blight (AB), Phytophthora root rot (PRR), Fusarium wilts (FW), Botrytis grey mould (BGM), sclerotinia and other seedling root diseases are persisting problems and continue to limit chickpea production in Australia. While AB and FW affect chickpea production across wide geographical areas, PRR is sporadic in occurrence (wet, warm conditions) and endemic in distribution (Northern growing regions) but is still an economically important disease in Australia (Schwinghamer, 2011).

The incidence of plant disease requires (1) the presence of the pathogen, (2) suitable environmental conditions for the pathogen to survive and (3) a susceptible host plant, as illustrated in the classic 'disease triangle' shown in Fig. 1.3. Plant disease management requires a focus on one or more of these three points to protect the crop. Spread of a pathogen and the development of disease in crops can be restricted by the use of chemicals (fungicides), or by controlling the environment to reduce pathogen viability (e.g. pre-sowing decision to avoid high risk paddocks specific to the pathogen). However, the use of chemicals is harmful to the environment and to human health (Dormann et al, 2007). Policymakers strive for low-fungicide use in agricultural production systems, articulating strict chemical regulations (Lamichhane et al, 2016). Moreover, the use of in-crop chemicals and subsequent residue detection in end products can potentially impact trade and the immediate potential export value of a crop. Alternatively, the use of resistant or tolerant crop varieties can reduce direct yield losses by increasing the adaptability of the crop in areas that were earlier limited by high disease risks. Genetic improvement of resistance is an environmentally-safe way to protect the crop by reducing the dependence on chemicals, and is considered a valuable investment,

especially to low-income farmers where the high input costs required to manage disease are not viable. Also, pathogens continually show resistance to fungicides (Lucas et al, 2015). Therefore, crop disease management using disease-resistant varieties plays a major role in ensuring global food security.

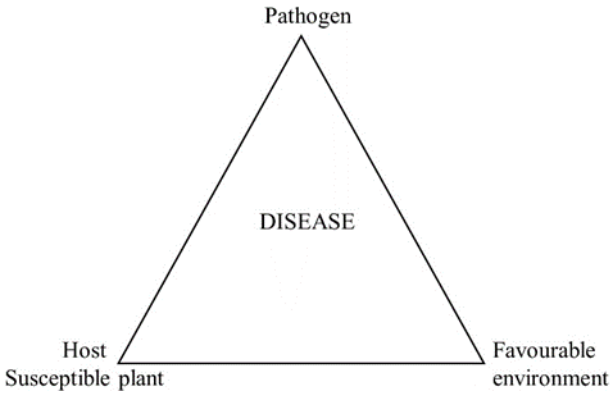

Fig. 1.3. Disease triangle (Scholthof, 2006)

In the near future, there is potential for significant gains for the Australian chickpea industry from local breeding programs releasing new resistant varieties, combining sources of resistance for the major crop diseases such as AB and PRR, along with other adaptive features (e.g. early flowering combined with chilling tolerance) (T. Knights, 2005). To achieve this, plant breeders use natural sources of genetic variation from landraces, obsolete varieties and crop wild relatives for trait introduction and selection in the breeding cycle (from crossing to variety release) (Singh & Ocampo, 1997). Outcomes and progress from an extensive range of Australian pre-breeding research projects aligned with the national breeding programs will support local chickpea breeders to respond to major industry threats.

This Doctoral dissertation is focussed on research to improve Phytophthora root rot (PRR) resistance in chickpea using molecular genetics and genomics approaches, utilising genetic resources developed by the Australian chickpea breeding program. PRR is a major soil-borne disease in northern New South Wales and southern Queensland,

where chickpea is predominantly grown in Australia. It is a fatal disease that results in significant yield loss and currently there is no practical in-crop control available to prevent the disease and protect the crop. A resistance source from a cultivated chickpea variety (*Cicer arietinum*) and another higher level of resistance from a wild relative of cultivated chickpea (*Cicer echinospermum*) were identified and incorporated into adapted backgrounds to generate interspecific hybrids. These are intended for introduction of PRR resistance into Australian chickpea germplasm. However, the genetic basis and molecular mechanism of PRR resistance in chickpea is not yet understood and tools are now needed to support the genetic breeding strategy for improved resistance. Thus, the overall aim of this dissertation is to identify genomic regions associated with PRR resistance in chickpea and determine the molecular mechanism underlying the expression of this trait.

Chapter 2

Literature Review:

2.1 Phytophthora root rot (PRR):

PRR is a major soil-borne disease in chickpea caused by a fungus-like oomycete *Phytophthora medicaginis* E. M. Hansen and D. P. Maxwell (Hansen & Maxwell, 1991) (Vock et al, 1980). It is also referred to as root rot, stem and root rot, foot blight or foliar blight, but PRR mainly applies to the post-emergence root disease of chickpea and lucerne.

2.1.1 Causal organism of PRR and its host range:

Phytophthora isolates were originally identified as *P. megasperma* var. *sojae* and *P. megasperma* f. sp. *medicaginis* (Kuan & Erwin, 1980). Later, according to Hansen and Maxwell, these have both been re-classified as *P. medicaginis*. Extensive field surveys, taxonomic studies and pathogenicity tests have determined that PRR in chickpea in Australia is caused by *P. medicaginis*. The pathogen has also been shown to cause disease in a small number of genera species within the *Fabaceae* family including lucerne (*Medicago* sp.,) (Hansen & Maxwell 1991), sainfoin (*Onobrychis viciifolia L.*), sulla (*Hedysarum* sp.,) (Southwell & Crocker, 2005) and sesbania (*Sesbania* sp.,) (Schwinghamer, 2011). Prior to this study researchers had identified *P. medicaginis* isolates similar to *P. crytogea* (Erwin, 1965) and *P. citrophthora* (Frezzi, 1950) in Argentina as the cause of PRR in cultivated crops including chickpea, but their economic importance remains unclear (Knights et al, 2008). There are about 43 isolates of *P. medicaginis* that have appeared to be aggressive on chickpea irrespective of their primary host of isolation (APPD, 2019), although there is some selection in aggressiveness towards lucerne genotypes (Schwinghamer, 2011). There is no evidence for the existence of distinct pathogenic races of *P. medicaginis* on chickpea as has been shown to occur in

other phytophthora pathosystems such as *P. sojae* that causes PRR in soybean (Sugimoto et al, 2012), or *P. capsici* that causes PRR and foliar blight in pepper (Barchenger et al, 2018).

2.1.2 Life cycle of *P. medicaginis* causing PRR in chickpea:

P. medicaginis is homothallic (self-fertile) and lives as thick-walled oospores in soil or root tissues (El-Hamalawi & Erwin, 1986). Mating types A1 and A2 (as seen in Fig. 2.1) occur in some of the heterothallic (self-sterile) *Phytophthora* species while in homothallic species such as *P. medicaginis*, oospores survives as propagules in infected plant material (Slusher & Sinclair, 1973). Oospores are formed by the fusion of oogonia and antheridia, produced by hyphae in roots. Early researchers recorded that oospores can survive in soil for up to three years in the absence of chickpea (Schwinghamer, 2011). The primary source of inoculum is infested plant debris and /or soil containing oospores. During favourable conditions, oospores produce lemon-shaped sporangia which develop into motile zoospores (Fig. 2.1) that are released into the soil. Zoospores swim towards the root and collar of the plant chemotactically. They accumulate at the elongation zone of the root tip, junction of the tap root and lateral roots and around subterranean stomata. On reaching the root surface, zoospores germinate to produce a germ tube (Miller & Maxwell, 1984) to penetrate the plant tissue. Following penetration into root tissue, zoospores produce hyphae which develops into new sporangia, thus enabling further cycles of infection to occur. Zoospores are capable of swimming only a few millimetres and thus long-distance travel is a result of physical movement of soil and/or water contaminated with oospores during flooding or irrigation, or by agricultural machinery (Schwinghamer, 2011).

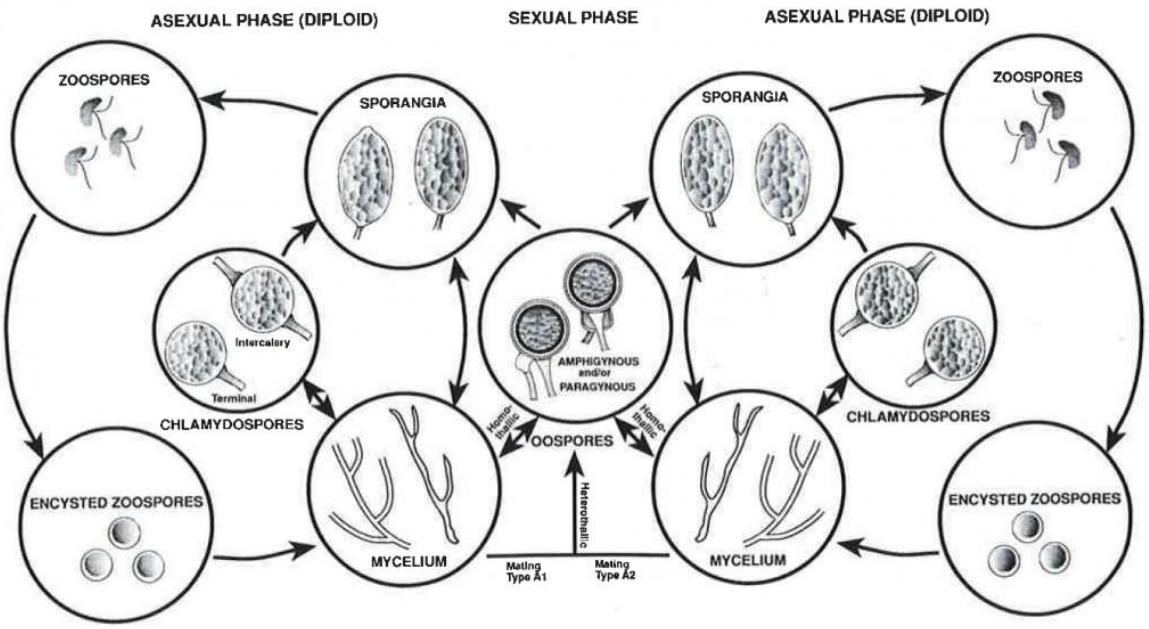

Fig. 2.1. Life cycle of *Phytophthora* (in general). Reproduced from (Davison, 1998).

2.1.3 Symptoms of PRR in chickpea:

PRR is multicyclic and is commonly a lethal disease, affecting chickpea crops at any stage of development. The symptoms observed in infected chickpea plants include decay of lateral and tap roots, seed decay, defoliation from the ground up, chlorosis, wilting of entire plants and death of older plants. When PRR disease pressure is high, severe damage to the plant root system results, with dark brown to black lesions girdling the taproot and lateral roots (Fig. 2.2), which can lead to the infected plant being easily dislodged from the soil. In chickpea seedlings, the lesions extend up the stem above ground level. PRR can be sub-lethal under cool temperatures and when the soil is moist causing mild infection and delayed symptoms. In this case, lesions are restricted to lateral roots and/ or the lower taproot with reduced defoliation and foliar-stress symptoms. The affected plant recovers by producing new roots from the upper part of the taproot but with reduced or no seed yield (Vock et al, 1980).

Fig. 2.2. Chickpea infected with *P. medicaginis.* Severely affected plants (left) have no lateral roots and defoliation below tips of stems. An uninfected plant is shown on the right for comparison (Kevin Moore, 2011).

2.1.4 PRR disease distribution and economic cost:

PRR has a field distribution commonly affecting winter crops such as chickpea cultivated in heavy rainfall regions. It is more intense in watercourses, depressions, areas of soil with heavy texture, high clay content and soils prone to saturation as shown in Fig. 2.3 (Schwinghamer, 2011). The disease is induced by prolonged soil saturation and surface water following a heavy rainfall event and is therefore a major concern in low-lying areas of paddocks where water stagnates (Kevin Moore, 2011).

Fig. 2.3. Chickpea field trials exhibiting symptoms of PRR (left panel) (Sean Bithell, 2018); Chickpea crops affected by PRR along a watercourse (right panel) (Schwinghamer 2011).

During the 1980's, PRR caused significant damage to chickpea crops grown in New South Wales and Queensland. Although there are no crop loss assessment data available, on the basis of aerial and ground inspections it was estimated that 20% of the area of chickpea production in New South Wales and Queensland was affected (Schwinghamer, 2011). Up to 50% yield losses were reported in individual crops (Knights et al, 2008). Overall, PRR is estimated to cost up to $8.2 million per year to chickpea growers in Australia (Murray. GM 2012), indicating the need to develop solutions to manage the disease.

2.1.5 Diagnostic techniques for PRR in chickpea:

PRR in chickpea is mainly diagnosed based on characteristic symptoms observed in host plants, field history and distribution, soil type, morphology of the pathogen and by baiting from an infected plant tissue (Schwinghamer, 2011). A nucleic acid-based testing technique using a real time fluorescent PCR assay has been developed using specific sets of primers and fluorochrome-labelled probes (TaqMan) to quantify the amount of *P. medicaginis* DNA in infected tissues of alfalfa and chickpea (Vandemark & Barker, 2003). The primers used in the assay were developed from a sequence-characterized DNA marker (SCAR) that is specific only for *P. medicaginis*. The specificity of the primer used in the TaqMan assay to detect *P. medicaginis* was confirmed by testing several oomycete plant pathogens and fungal species known to cause root rot in alfalfa and other legumes. Recently, this molecular diagnostic technique was developed into a soil DNA test by the South Australian Research and Development Institute (SARDI) (Alan McKay, 2018), and is commercially available to growers to determine the soil-borne disease risk within a paddock, assisting growers with pre-sowing decisions related to variety choice and management practices to minimise losses.

2.1.6 Effective management options for PRR in chickpea:

Once the crop is infected with phytophthora there is nothing that a grower can do to halt progression of the disease. Metalaxyl based seed dressings can be used before infection to control pre-emergence or early post-emergence of PRR (Kevin Moore 2011). However, this treatment is expensive and provides protection only for the first 6 to 8 weeks post germination. The crop remains at risk of development of the disease later in the season, and so it is not a preferred management option for growers. There is no economically viable in-crop control for PRR in chickpea and current management of the disease is purely through pre-sowing decisions. These include avoiding fields with a history of PRR of chickpea or alfalfa and fields that are poorly drained or prone to flooding (Knights, EJ et al. 2008). However, despite these preventative measures, major yield losses cannot be eliminated under prolonged soil saturation following a heavy rainfall event. There is a clear industry need for the development of chickpea varieties with improved PRR resistance that will help to minimise losses from this disease.

2.2 Plant defence response to pathogen in roots:

The rhizosphere contains a variety of micro-organisms such as bacteria, fungi and nematodes in soil (Watt et al, 2006). Some of them, such as Rhizobia, may be essential for the growth and development of leguminous plants including chickpea, while others such as *Phytophthora* and *Fusarium* spp., cause disease resulting in yield loss affecting crop production and food security (Mendes et al, 2013). Thus, root is a main entry point for soil-borne pathogens. Pathogens penetrate mostly through natural apertures present on the extracellular side of roots, at the intersection of the main and lateral roots, and/or through developing root tissues which lack secondary cell wall (Okubara & Paulitz, 2005). They derive nutrients from host plant cells. Therefore, it is essential for plants to detect and initiate defence responses to inhibit pathogen infection and disease progression. Plants are able to protect themselves from harmful pathogens through a

combination of preformed and/ or induced responses (Thatcher et al, 2005). Preformed defence responses in plants include antimicrobial compounds and structural barriers that are non-specific in nature, and can protect plants from a wide range of pathogens. Pathogens that are capable of overcoming these preformed barriers activate an induced response in the plant. These are based on pathogen recognition followed by a series of signalling cascades that activate the expression of various defence related molecular pathways in the host plant. The early defence response in plants occurs soon after the pathogen makes contact with the infection site. This involves a combination of distinct biochemical processes that lead to immediate activation of enzymes, structural changes in the host cell membrane and the synthesis of intra- and intercellular signals. The late defence response includes transcription and translation dependent responses that aid in reducing the long-term effects of infection and also in preventing further infections from occurring (Talarczyk & Hennig, 2001). An effective resistance response in plants relies on the timely detection of the invading pathogen and effective activation of the corresponding defence mechanisms. Thus, it is presumed that the defence response in plants is time-based, comprising a network of signalling events aimed at eliminating the pathogen spread and limiting infection. This suggests that an approach to identify the expression of genes associated with early and /or late defence responses in resistant and susceptible plants will enable the characterisation of specific molecular mechanisms associated with crop disease.

Plant breeders routinely rely on resistance genes to control crop diseases. This has initiated many genetic studies to determine the relationship between host resistance genes (R) and their corresponding pathogen virulence factors, commonly, referred to as ‘gene-for-gene’ (Flor, 1971). However, recent molecular research studies have revealed that host resistance genes are also associated with the plant immune system involved in pathogen recognition and in generating specific responses to pathogens. The former type

of resistance is known as host-specific and the latter is referred as non-host resistance which can confer resistance against all members of a pathogen species. Although less is known about non-host resistance mechanisms, these are a preferred type of resistance in the context of plant breeding because they are considered to provide more durable and stable protection. The simplest model of plant-pathogen recognition is the interaction between pathogen elicitors, referred to as pathogen-associated molecular patterns (PAMPs), and plant receptors known as pattern recognition receptors (PRRs). This subsequently leads to an array of signal transduction events for the induction of defence related genes encoding pathogenesis related (PR) proteins, glutathione-S-transferases (GSTs), peroxidases, proteinase inhibitors and those involved in the production of secondary metabolites (Chisholm et al, 2006; Dangl & Jones, 2001). This type of plant defence response is termed PAMP-triggered immunity (PTI) (Boller & Felix, 2009). Another type of pathogen recognition involves the intracellular receptors of pathogen virulence molecules called effectors, and the generated plant defence response is referred to as effector-triggered immunity (ETI). The PTI and ETI types of plant defence response have an overlap of signalling molecules but varies in expression levels (Dodds & Rathjen, 2010). Moreover, the defence signalling system in leguminous plants is believed to be more complex than in other plant families because of these plant's capability to form root nodules for nitrogen fixation through a symbiotic relationship with rhizobia. For this reason, it is essential that the host plant cells be able to distinguish between the microbial 'friend' and 'foe'. Signalling molecules such as salicylic acid (SA), ethylene (ET) and reactive oxygen species (ROS) are known to be associated with the establishment of root nodulation as well as in the early defence responses against pathogens in legume species such as *M. trunculata* (Martinez-Abarca et al, 1998; Mithöfer, 2002). Studies of the defence response in roots of legumes will help to clarify if any differences in specific

aspects of signalling are likely to occur during pathogen attack compared to when forming symbioses.

In the *P. sojae* phytophthora pathosystem of soybean, genetic studies have revealed the existence of a gene-for-gene resistance mechanism (Tooley & Grau, 1984). More than 20 different major phytophthora resistance (*Rps*) genes have been identified, but only a few of these have been deployed in soybean varieties. Phytophthora-resistant soybean varieties deployed with the *Rps1k* gene carry high to moderate levels of partial resistance that have shown to be effective over a long period of time (Schmitthenner, 1985). Owing to the ability of the *P. sojae* pathogen to overcome the qualitative resistance in existing soybean resistant varieties (co-evolution of pathogen and host), current disease management efforts are aiming at developing quantitative disease resistance (QDR) for durability. In chickpea, there is currently no information available relating to the type of signalling and defence response mechanism(s) that are associated with PRR. Therefore, current research efforts should focus on the identification of PRR resistance genes for the development of molecular markers and in determining the molecular mechanism associated with the expression of resistance. Furthermore, research into the pathogen population structure and variability in avirulence (Avr) genes in *P. medicaginis* will greatly compliment efforts in breeding for PRR resistance to manage this disease.

2.3 Breeding for improved PRR resistance in chickpea:

Given that host/ in-crop resistance is currently the most effective control option, the Australian chickpea breeding program has been pursuing the following approaches in an integrated manner to develop varieties with improved PRR resistance: (1) introduction and evaluation of resistant germplasm; (2) screening of existing breeding lines for PRR resistance; and (3) local crossing programs seeking to combine PRR resistance with other key traits such as AB resistance and early flowering and chilling

tolerance. The efficient use of available plant genetic resources and the application of molecular genetics tools to this end are considered important, and will be discussed in the following sections.

2.3.1 Chickpea genetic resources for crop improvement:

Chickpea and its immediate wild relatives are predominantly self-pollinated diploids, with eight chromosomes and a genome size of about 740 Mbp (Varshney et al, 2013). The *Cicer* genera includes one annual cultivated species (*C. arietinum*), eight annual wild species (*C. reticulatum, C. echinospermum, C. judaicum, C. bijugcum, C. pinnatifidum, C. cuneatum, C. yamashitae* and *C. chorassanicum*), and 35 wild perennials (Kazan et al, 1993). Chickpea germplasm is maintained predominantly at two Consultative Group for International Agricultural Research (CGIAR) centres: The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in India, and the International Centre for Agricultural Research in the Dry Areas (ICARDA) in Morocco. ICRISAT maintains 20,602 *Cicer* accessions and ICARDA 13,818 accessions. Using a concept proposed by Frankel & Brown, (1984), small subsets representing the diversity of the entire germplasm collections were made available to researchers for evaluation and to facilitate greater use of these extensive genetic resources in crop improvement. This includes a core collection of 1,956 accessions, a mini core collection set consisting of 211 accessions (Upadhyaya & Ortiz, 2001; Upadhyaya et al, 2001) and a genotype-based reference set of 300 lines developed by ICRISAT and ICARDA under the Generation Challenge Program (GCP) in CGIAR to denote the genetic variability in the broader germplasm pool. In Australia, access to germplasm collections has been facilitated by the Australian Temperate Field Crops Collection (ATFCC) now known as the Australian Grains Genebank (AGG) in Horsham, Victoria, which has established a collection of more than 6,000 landrace accessions and breeding lines (Knights & Hobson, 2015). These resources represent significant value for research to dissect population

structure, mine for allelic variation and conduct genetic mapping to identify genomic regions associated with biotic and abiotic stress resistance/ tolerance, or agronomic and nutritional attributes that are of value in breeding.

Focussing on PRR, early researchers in Australia screened approximately 200 chickpea breeding lines and germplasm accessions in the field for PRR resistance and identified a useful field resistance source in a *C. arietinum* accession (CPI 56564 = ICC11870) to *P. medicaginis* (Brinsmead et al, 1985). This resistance source was later incorporated into Australian chickpea varieties such as Barwon, Norwin, Moti, Yorker, Jimbour and Kyabra. However, despite an improved level of resistance, under heavy rainfall and high inoculum load these moderately resistant varieties are still highly susceptible to the disease, resulting in significant yield loss. The apparent absence of a stronger source of PRR resistance in *C. arietinum*, despite presumed co-evolution of the pathogen (Irwin et al, 1995), was attributed to the reduction in genetic variation as a result of domestication and selective breeding of cultivated chickpea (Abbo et al, 2003). Repeated selection and breeding practices within *C. arietinum* has led to genetic drift, has decreased diversity and reduced the frequency of rare alleles.

2.3.1.1 Use of wild *Cicer* species to improve cultigen gene pool:

Crop wild relatives are the principal reservoir of a crop's genetic variation (Dempewolf et al, 2014; McCouch et al, 2013). Significant genetic diversity exists among the *Cicer* species. According to the Harlan & de Wet, (1971) gene pool concept, the *Cicer* species are classified into three gene pools based on their cross-ability with cultivated chickpea. The primary gene pool includes the cultivated chickpea species *C. arietinum* and its wild annual progenitor species, *C. reticulatum*. These two species are readily crossable with systematic gene exchange. The wild annual species *C. echinospermum* in the secondary gene pool is freely crossable with *C. arietinum* but with relatively reduced fertility in resulting progeny. The remaining six wild *Cicer* annual and

35 wild perennial *Cicer* species are grouped into the tertiary gene pool and require specialized techniques for the transfer of genes into the cultivated chickpea background. Croser et al, (2003) reported that genetic diversity within wild *Cicer* species can be used as a source of resistance to various abiotic and biotic stresses. Singh et al, (2005) demonstrated the use of a *C. reticulatum* accession, the immediate progenitor of chickpea as an improved source of resistance to four fungal root pathogens in crosses with chickpea. Furthermore, accessions of *C. reticulatum* and *C. echinospermum* crossed with Australian chickpea varieties were reported to be better sources of resistance to endemic root- lesion nematodes than cultivated chickpea (Reen et al, 2019; Thompson et al, 2011).

Despite the potential of wild *Cicer* to improve the challenges presented by modern agriculture, their use in chickpea improvement has been hampered for several reasons. There is a lack of information on many of the accessions, particularly for economically important traits such as yield and resistance/tolerance to biotic/abiotic stresses that are highly influenced by genotype x environment interactions. There are ineffective database management systems for information on phenotypes and genotypes and restrictive regulations governing the exchange of germplasm between researchers and breeders (Sharma et al, 2013a). Further, the use of wild germplasm in breeding programs requires relatively more effort and time to generate useful material of value to growers. Recently, an extensive collection of wild *Cicer* relatives belonging to *C. reticulatum* and *C. echinospermum* was assembled using ecological principles to guide collection across a wide range of wild chickpea habitats. Population genomics and phenotyping for some key traits have been performed to begin characterising the collection (von Wettberg et al, 2018). Genetic crosses from selections out of the collection have also been carried out to generate pre-breeding populations. Analysis of the ecological and genomic data revealed that the wild *Cicer* collection holds potential sources of genetic variation for phenology (early flowering), drought, heat and cold

tolerance and resistance to pod borer and root-lesion nematode (Reen et al, 2019; von Wettberg et al, 2018). This collection is expected to broaden the extent of genetic diversity presently available to breeders by providing novel allelic variation to existing traits of potential agronomic importance.

2.3.1.2 The role of wild *Cicer* in improving PRR resistance in chickpea:

A superior source of resistance to *P. medicaginis* was identified in *C. echinospermum* by Singh et al, (1993) when screening a small set of *C. echinospermum* accessions in both field and greenhouse. More recently, Knights and Southwell included five annual wild *Cicer* species in testing for resistance against *P. medicaginis* (Knights et al, 2008). Field and greenhouse experiments were conducted on 182 genotypes originating from both Australia and overseas which included 7 commercial varieties, 101 breeding lines and 8 bulk populations (F_3 or F_4). The wild *Cicer* entries included 29 accessions from *C. reticulatum*, 21 from *C. bijugum*, 9 from *C. echinospermum*, 4 from *C. judaicum* and 3 from *C. pinnatifidum*. The accessions were provided by ICARDA and ICRISAT. Field and glasshouse experiments were conducted at the Tamworth Agricultural Institute in north-eastern New South Wales. The study reported that *C. echinospermum* showed high resistance to *P. medicaginis* (as shown in Fig. 2.4) in both field and greenhouse experiments, with relatively reduced disease scores (field experiment) and increased survival time (greenhouse experiment).

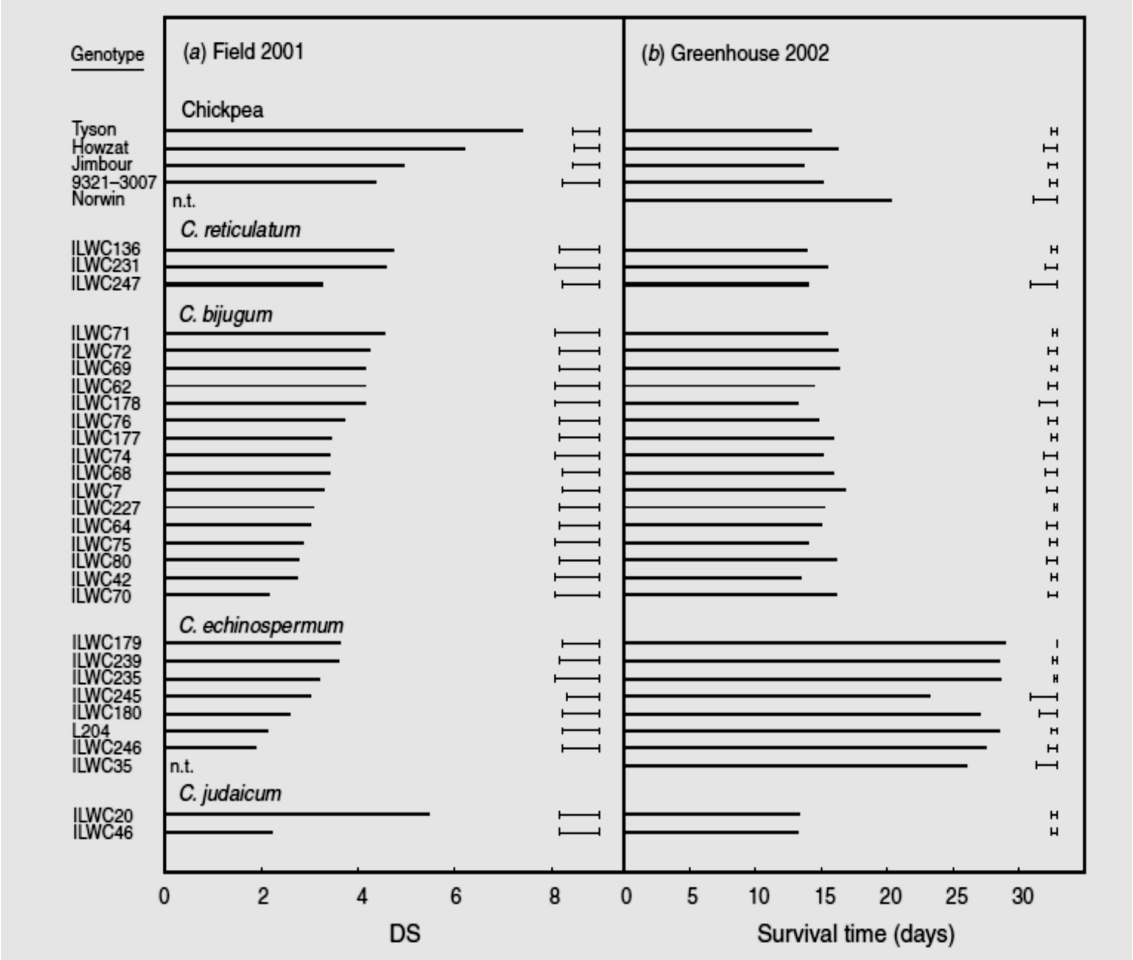

Fig. 2.4. Source of PRR resistance in wild chickpea species

Comparison of resistance between (a) a field experiment (2001) and (b) a greenhouse experiment (2002). Left-hand bars in each panel indicate (a) disease scores (DS) and (b) survival time for 32 representative genotypes. Right-hand bars denote standard errors. Reproduced from (Knights et al, 2008).

These findings were supported by later field screening in a 2012 trial at Hermitage research station (Warwick, Queensland) which included five released Australian chickpea varieties (Yorker, PBA HatTrick, Jimbour, Kyabra and PBA Boundary), three advanced breeding lines (CICA0912, CICA0709 and CICA1007) and three elite hybrid lines (D06318, D06344 and D06321) generated by crossing cultivated chickpea *C. arietinum* with a *C. echinospermum* line (Kevin Moore MR, 2013). In this trial, the yield

loss following PRR infection was found to be lowest in the three hybrid lines that were progeny of crosses *C. echinospermum*. Moderate resistance was found in one of the commercial varieties, Yorker and the advanced breeding line CICA0912 (Table 2.1).

Table 2.1. Yield loss in the presence and absence of PRR

Variety / Line[A]	Yield (t/ha) without PRR	% yield loss due to PRR
D06318	2.40	14
D06344	2.47	22
D06321	2.41	26
CICA0912	2.49	34
Yorker[Φ]	2.52	35
CICA0709	2.42	59
CICA1007	2.87	60
PBA HatTrick[Φ]	2.56	64
Jimbour	2.70	66
Kyabra[Φ]	2.83	78
PBA Boundary[Φ]	2.58	85

[A] D lines are hybrid crosses between chickpea and a wild *Cicer* species.

Yield of commercial chickpea varieties and breeding lines in the absence of PRR and % yield losses due to PRR from a 2012 trial at Warwick QLD (P Yield<0.014; lsd Yield = 0.31; P %yield loss<0.001, lsd Yield loss = 24) Reproduced from (Kevin Moore MR, 2013).

This higher level of resistance identified in *C. echinospermum* from the secondary gene pool has been incorporated into the cultivated chickpea background to form interspecific hybrids (Knights et al, 2008). In subsequent years, these interspecific hybrids have been used as parental genotypes to develop bi-parental mapping populations by Ted Knights and his team with an aim to identify the genetic basis of PRR resistance in chickpea.

2.3.2 Genetic analysis approaches for crop improvement:

Until recently, conventional plant breeding practices have been purely based on selection following phenotypic evaluation wherein the information on gene or genes underlying the breeding trait is unknown. This can become challenging when screening germplasm for quantitative traits such as partial resistance to plant pathogens, drought, heat and cold tolerance, and other agronomically important traits that are often controlled by many interacting genes with small effects. Expression of these quantitative traits are influenced by environmental conditions, effect of more than one gene controlling the trait and genotype x environment interactions.

In order to identify the genomic regions associated with a particular trait, two main approaches have been widely adopted; (i) bi-parental population based linkage mapping, and (ii) diversity-based Genome Wide Association Mapping (GWAS). Linkage mapping combined with candidate gene approaches have shown to be effective in identifying candidate genomic regions/genes associated with resistance to FW (Cobos et al, 2005; Gowda et al, 2009; Sabbavarapu et al, 2013; Sharma et al, 2004), rust (Madrid et al, 2008), BGM (Anuradha et al, 2011) and AB (Lichtenzveig et al, 2006; Millan et al, 2003; Rakshit et al, 2003), salinity tolerance (Vadez et al, 2012) and traits associated with drought tolerance (Chandra et al, 2004; Rehman et al, 2011; Rehman, 2009), phenology (Aryamanesh et al, 2010; Ortega et al, 2019), and seed characteristics (Gowda et al, 2009) in chickpea. An alternative approach to linkage mapping is the GWAS approach which is based on historical recombination events occurring in a diverse population/germplasm set. More than two alleles associated with the trait of interest can be identified by GWAS as opposed to only two alleles in bi-parental mapping approach. GWAS approaches have shown to be used to identify candidate genes associated with yield related traits (Gowda et al, 2016; Tripathi et al, 2019) and for resistance to AB (Li et al, 2017) in chickpea. The steps involved in genetic mapping include the development

of a segregating, bi-parental mapping population, generation of molecular markers and construction of a genetic map, and phenotyping for the trait of interest.

Different mapping populations such as filial generation (F_2), F_2 derived F_3 progeny, backcrosses (BC), double haploid (DH), recombinant inbred lines (RIL) and near isogenic lines (NIL) (Burr et al, 1988; Doerge, 2002) can be used for genetic studies. F_2 and BC populations are considered to be temporary as they cannot be propagated indefinitely through subsequent generations. RILs, NILs and DH populations are immortal and phenotyping can be replicated over locations and years. In general, the size of a mapping population varies from 50 to 250 individuals, and even greater numbers are used for high-resolution mapping (Collard et al, 2005). Recently, the improvements in Next Generation Sequencing (NGS) technologies at an affordable cost have facilitated the development of large number of molecular markers from plant genomes. Polymorphic DNA markers based on Single Nucleotide Polymorphisms (SNPs) have now become the marker platform of choice in molecular breeding for the measurement of variation in specific DNA targets. The advancements in technology to develop SNPs has enabled better detection and scoring of polymorphism. In recent years, there has been rapid development in SNPs because of their abundance and amenability to high-throughput approaches. There are a variety of different protocols available for SNP genotyping and it is necessary to consider different aspects of SNP technology such as sensitivity, accuracy, reproducibility and cost effectiveness (Li, 2011). One recent and now common application of NGS in crop improvement is Genotype-By-Sequencing (GBS) (Poland & Rife, 2012). The GBS approach is based on the principle of enzyme-based complexity reduction (using restriction endonucleases to target a small portion of the genome) coupled with DNA-barcoded adapters to produce multiplex libraries of samples ready for NGS sequencing (Poland & Rife, 2012). Huang et al. (2014) first developed GBS in maize. More recently, the method has been applied to other crops,

including chickpea where Jaganathan et al, (2015) used a GBS approach to identify and genotype SNPs in an intra-specific mapping population, ICC 4958 × ICC 1882, in which genomic regions for drought tolerance traits were identified. GBS is an ideal platform for studies ranging from single gene markers to whole genome profiling (Poland & Rife, 2012). In the GBS method, SNP discovery and genotyping are completed together in one step and knowledge of the species reference genome is usually not required. GBS can generate a large number of SNPs for use in genetic analyses and breeding (Beissinger et al, 2013). It is a rapid and low-cost tool to genotype breeding populations, allowing plant breeders to implement Genome Wide Association Studies (GWAS), genomic diversity studies, genetic linkage analysis, molecular marker discovery, and genomic selection (GS) in large-scale breeding programs (Narum et al, 2013; Poland et al, 2012).

Given that a *C. echinospermum* source of PRR resistance was used to develop bi-parental RIL mapping populations, these could be used as a starting point to determine genomic regions associated with PRR resistance. Linkage mapping is based on the principle of systematically scanning the plant genome of either intraspecific or interspecific bi-parental mapping populations segregating for the trait of interest, using polymorphic DNA markers as the variable to identify quantitative trait loci (QTL) linked to the trait (Collard et al, 2005). These QTL or genomic regions can then be prioritised for fine mapping and map-based cloning to identify the genetic factors underlying the trait.

2.3.3 Phenotyping for PRR resistance in chickpea:

In order to identify consistent and stable QTL through genetic mapping, it is important to be able to accurately phenotype the trait of interest using a well-designed experimental set-up, which includes check varieties, sufficient numbers of biological replicates and good control over the specific treatment. Rational evaluation of crop disease resistance depends on several important factors, including the choice of

appropriate isolate(s) for screening, methodology and comparable standard check varieties and pathotypes. The most critical aspect is developing an appropriate level of disease for an appropriate expression of resistance (and susceptibility). Based on the epidemiology of PRR, the development of the disease requires both presence of the pathogen and a prolonged soil saturation event with surface water (Schwinghamer, 2011).

Field-based experiments screening for PRR resistance using chickpea breeding lines were originally developed by Ted Knights and his team as a part of the chickpea breeding program based at the Tamworth Agricultural Institute in northern New South Wales, Department of Primary Industries (NSW DPI) and at Hermitage Research Station, at Warwick in southern Queensland (Knights et al, 2008). Both rainfed and irrigated trials were performed with *P. medicaginis* oospore inoculum being drenched into the field sites. This PRR phenotyping method was reported to be reproducible (Knights et al, 2008). However, a glasshouse PRR phenotyping method used to screen for PRR resistance in chickpea showed significant discrepancy with the field PRR phenotyping experiments (Knights et al, 2008). This soil-based cup method involves the growth of chickpea seedlings individually in plastic cups containing 10% (w/w) soil-sand and inoculated with *P. medicaginis* oospores. The seedlings were subjected to repeated cycles of flooding with water (40 hours) and draining (56 hours), to induce the development of zoospores from an oospore inoculum and to initiate PRR infection. The flooding and draining cycles have been reported to introduce significant variation in disease development, eventually altering the expression of host-plant resistance (Dale & Irwin, 1991a; Knights et al, 2008). This indicates the need to develop a more robust PRR phenotyping method in a controlled environment, both for large scale screening of breeding populations and also to progress molecular studies to identify the genetic factors underlying PRR resistance in chickpea and understand the biological processes involved

in plant response to PRR infection. Also, attempts to classify virulence in *P. medicaginis* have been inconclusive and could also be progressed if disease phenotypes could be replicated in a controlled environment. In other phytophthora pathosystems, such as for soybean, PRR resistance is studied using tests that can cause localized infection in wounded and non-wounded cotyledons or roots (McBlain et al, 1991; Tooley & Grau, 1982; Wagner et al, 1993), layer tests (Dorrance et al, 2003; Ferro et al, 2006; Thomison et al, 1991) and rice screen tests (Stewart & Robertson, 2012). The use of these methods is restricted to screening a small number of genotypes and therefore may not be very efficient within the breeding program. Thus, there is a need for the development of an efficient, reproducible, and high-throughput screening system to study PRR reaction in chickpea in a controlled environment, with good control over the disease pressure and infection rate.

2.3.4 Chickpea genomic resources for candidate gene mapping and crop improvement:

Once a QTL for a particular trait is identified, the next step is to use this knowledge in crop improvement through genomics-assisted breeding for developing elite varieties with better response to abiotic and or biotic stress and other adaptive traits. Although there are a large number of cultivated and wild accessions available, use of these accessions in breeding is limited because of a lack of information on major quantitative and economic traits such as yield, durable resistance to crop diseases and tolerance to abiotic stress. Chickpea was considered as an ‘orphan crop’ until recently, because of the limited availability of genomic resources. With the availability of molecular markers and advancements in NGS, trait-associated molecular markers can be used for phenotype prediction and selection of progenies for next-generation breeding (Varshney et al, 2012). The availability of draft genome sequences of both kabuli (Varshney et al, 2013) and desi (Jain et al, 2013) chickpea types has significantly

advanced geneticists' understanding of chickpea genome architecture and provided new opportunities for improvements in seed quality and disease resistance.

One now commonly used NGS application is the study of the transcriptome. Expression levels of RNA sequences in given samples can be examined (Chu & Corey, 2012; Wang et al, 2009). Computational analysis of the sequence reads generates gene expression profiles for comparison between genotypes, tissue types and/or treatments, which could assist in identifying the molecular mechanisms underlying a particular trait. Transcriptome analysis is being widely used in other crops and recently in chickpea to determine candidate genes associated with drought tolerance in kabuli chickpea varieties (Mashaki et al, 2018).

The availability of sequencing and genome assembly data will help to accelerate the identification of candidate genes underlying traits of interest and help chickpea breeders to understand the genetic variation between different genotypes. This knowledge can be applied in breeding programs for the selection of parental genotypes for crossing, screening early generation progenies for favourable alleles and for the integration of desired traits into chickpea varieties for crop improvement.

2.4 Research Aims:

The existence of a novel source of PRR resistance in wild *Cicer* species, and the subsequent development of recombinant inbred line (RIL) mapping populations provides an opportunity to undertake genetic analysis to provide molecular tools such as markers to assist breeding for this trait. To date, there has been no research reported on the genetic analysis of PRR resistance in chickpea. There is also a need for the development of a phenotyping method in controlled environment conditions for use as a routine screening tool for PRR resistance selection in chickpea breeding and to facilitate molecular studies associated with resistance responses in host chickpea plants during phytophthora infection.

This research aims to identify genomic regions associated with PRR resistance in chickpea and determine the molecular mechanism underlying the trait using molecular genetics and genomic approaches. To address the overall research aim, the following specific objectives were developed:

I. Identify genomic regions associated with PRR resistance using genetic mapping and QTL analysis in biparental mapping populations specifically developed to study PRR resistance in chickpea.

II. Develop an *in planta* PRR infection system that can be used as a high-throughput screening method to study PRR in chickpea under controlled environments.

III. Determine the molecular mechanisms associated with defence response in chickpea following phytophthora infection using RNA sequencing for differential expression of genes.

Link to Chapter 3

Early research in Australia identified moderate field-based PRR resistance in *C. arietinum* accessions, which was subsequently incorporated in chickpea varieties such as Yorker. Another high level of PRR resistance was identified in a wild relative of chickpea (*C. echinospermum*) and incorporated into adapted cultivated backgrounds to form interspecific hybrids. These PRR resistant genotypes along with PRR susceptible varieties Rupali and Genesis114 were used to develop one intra-specific and two interspecific bi-parental RIL mapping populations referred as YG, RB and YB, respectively, to facilitate genetic studies. Until recently, there has been no research reported on the genetic basis of PRR resistance in chickpea. This study identified genomic regions associated with PRR resistance from field-based phenotyping, with independent resistance sources derived from *C. arietinum* and *C. echinospermum*. This work was published in Theoretical and Applied Genetics during my PhD research candidature as follows: Amritha Amalraj, Julian Taylor, Sean Bithell, Yongle Li, Kevin Moore, Kristy Hobson, Tim Sutton, Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (*Cicer arietinum* L.) and wild (*Cicer echinospermum* P.H. Davis) chickpea, Theoretical and Applied Genetics (2018), 132: 1017. Supplementary material included within this publication is provided in the appendix section of the thesis.

Statement of Authorship

Title of Paper	Mapping of Phytophthora root rot identifies independent loci from cultivated (Cicer arietinum L.) and wild (Cicer echinospermum P.H. Davis) chickpea
Publication Status	☑ Published ☐ Accepted for Publication ☐ Submitted for Publication ☐ Unpublished and Unsubmitted work written in manuscript style
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Principal Author

Name of Principal Author (Candidate)	Amritha Amalraj		
Contribution to the Paper	Involved in the design of phenotyping experiments and assisted with phenotyping. Performed genotyping experiments and analysis of phenotypic data, construction of linkage maps and QTL analysis. Interpreted the results and drafted the manuscript.		
Overall percentage (%)	80%		
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.		
Signature		Date	03/05/2019

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);
ii. permission is granted for the candidate to include the publication in the thesis; and
iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Julian Taylor		
Contribution to the Paper	Involved in data analysis and manuscript drafting.		
Signature		Date	10/05/2019

Name of Co-Author	Sean Bithell		
Contribution to the Paper	Involved in the design of phenotyping experiments, development of field disease assessment method, carried out phenotyping.		
Signature		Date	23/5/19

Please cut and paste additional co-author panels here as required.

Name of Co-Author	Yongle li
Contribution to the Paper	Contributed to the design of phenotyping experiments and genotyping.
Signature	Date 13/05/19

Name of Co-Author	Kevin Moore
Contribution to the Paper	Contributed to the design of phenotyping experiment and developed the oospore inoculation method.
Signature	Date 13 May 19

Name of Co-Author	Kristy Hobson
Contribution to the Paper	Involved in the design of phenotyping experiments and project supervision.
Signature	Date 23/5/19

Name of Co-Author	Tim Sutton
Contribution to the Paper	Involved in the design of phenotyping experiments, project supervision and acted as the corresponding author.
Signature	Date 8/5/19

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ORIGINAL ARTICLE

Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (*Cicer arietinum* L.) and wild (*Cicer echinospermum* P.H. Davis) chickpea

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Abstract

Key message **Major QTL for Phytophthora root rot resistance have been identified in three mapping populations with independent sources of resistance contributed by *C. echinospermum* and *C. arietinum*.**

Abstract Phytophthora root rot (PRR) caused by the oomycete *Phytophthora medicaginis* is a major soil-borne disease of chickpea in Australia. With no economic in-crop control of PRR, a genetic approach to improve resistance is the most practical management option. Moderate field resistance has been incorporated in the cultivated *C. arietinum* variety, Yorker, and a higher level of resistance has been identified in a derivative of wild chickpea (*C. echinospermum*, interspecific breeding line 04067-81-2-1-1). These genotypes and two other released varieties were used to develop one intra-specific and two interspecific F_6-derived recombinant inbred line mapping populations for genetic analysis of resistance. The Yorker × Genesis114 (YG), Rupali × 04067-81-2-1-1 (RB) and Yorker × 04067-81-2-1-1 (YB) populations were genotyped using genotyping-by-sequencing and phenotyped for PRR under three field environments with a mixture of 10 *P. medicaginis* isolates. Whole-genome QTL analysis identified major QTL *QRBprrsi01*, *QYBprrsi01*, *QRBprrsi03* and *QYBprrsi02* for PRR resistance on chromosomes 3 and 6, in RB and YB populations, respectively, with the resistance source derived from the wild *Cicer* species. QTL *QYGprrsi02* and *QYGprrsi03* were also identified on chromosomes 5 and 6 in YG population from *C. arietinum*. Aligning QTL regions to the corresponding chickpea reference genome suggested that the resistance source from *C. arietinum* and *C. echinospermum* may be different. The findings from this study provide tools for marker-assisted selection in chickpea breeding and information to assist the development of populations suitable for fine-mapping of resistance loci to determine the molecular basis for PRR resistance in chickpea.

Introduction

Chickpea (*Cicer arietinum* L.) is grown for its high nutritional value and provides a cheap source of protein to people in developing countries. It is also widely grown as a rotation crop for its ability to fix up to 80% of the plant's nitrogen requirement through nitrogen fixation (Schwenke et al. 1998). Global chickpea production is 12.09 million tonnes from 12.65 million ha (FAOSTAT 2016). Australia is the second largest producer of chickpea in the world, grown predominantly in the low-rainfall tropical region of central Queensland and the low- and medium-rainfall subtropical regions of northern New South Wales and southern Queensland (Knights et al. 2007).

Phytophthora root rot (PRR), caused by the fungus-like oomycete *Phytophthora medicaginis* E. M. Hansen and D. P. Maxwell, is a major chickpea disease in the northern chickpea-growing regions of Australia, causing significant yield

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losses that can account for about 20% of the area of chickpea crops on a regional basis in years with above-average rainfall (Schwinghamer et al. 2011). The symptoms of PRR in chickpea include defoliation from the ground up and dark brown to black lesions on tap and lateral roots, which can extend above ground level on the stem; infected plants usually die (Schwinghamer et al. 2011; Vock et al. 1980). The pathogen can infect the plant at any stage of development; however, the incidence of the disease is most severe during periods of soil saturation following heavy rainfall. Yield losses are higher during wet seasons than in normal growing seasons (Schwinghamer et al. 2011). PRR costs up to $8.2 million per year to chickpea growers in Australia (Murray and Brennan 2012).

PRR is currently managed through paddock rotation, variety selection and avoiding high-risk paddocks. Since there is no economic in-crop control for PRR, a genetic approach to improve resistance is the most practical management option. Very little is known about the genetics and inheritance of PRR in chickpea, and no molecular tools are available to assist with breeding for resistance. Partial resistance has been identified in the chickpea accessions ICC11870 (Dale and Irwin 1991), and breeders have used this as a source of resistance in breeding, resulting in levels of resistance observed in varieties such as Kyabra, Jimbour, Moti and Yorker. However, under high disease pressure, i.e. poorly drained soils and/or following saturating rainfall events, even moderately resistant varieties can sustain high yield loss. There exists a significant genetic diversity in wild *Cicer* species (*C. echinospermum* P.H. Davis and *C. reticulatum* Ladizinsky) in response to various biotic and abiotic stresses (Croser et al. 2003; Li et al. 2015) with *C. arietinum* × *C. reticulatum* crosses demonstrating improved resistance to a number of important fungal root pathogens (Singh et al. 2005). In a field experiment that was conducted to screen for PRR resistance, five different wild *Cicer* species such as *C. echinospermum*, *C. reticulatum*, *C. bijugum* Rech.f., *C. judaicum* Boissier, and *C. pinnatifidum* Jaub. and Spach were compared to cultivated chickpea varieties (*C. arietinum*) with known improved resistance to PRR. It was found that *C. echinospermum* accessions generally have superior resistance to PRR, showing lower field disease scores and significantly longer survival times in controlled environments (Knights et al. 2008). Despite undesirable features like prostrate growth habitat and dehiscent pods, researchers have observed that fertile interspecific progeny can be obtained relatively easily from crossing wild chickpea species in the secondary gene pool with cultivated chickpea (Knights et al. 2008). Singh and Ocampo 1997, for example, have demonstrated the transfer of genes associated with seed yield from *C. echinospermum* into cultivated varieties.

In chickpea, there is no evidence for race-based resistance, but *P. medicaginis* can affect other hosts such as lucerne and annual medics (Knights et al. 2008; Southwell and Crocker 2005). Many of the described Phytophthora pathosystems are characterised by both partial and race-specific resistance for PRR; for example in soybean (*Glycine max* L.), PRR is caused by specific races of *P. sojae* A. A. Hildebrand (Sugimoto et al. 2012); in pepper (*Capsicum annuum* L.), PRR and foliar blight in pepper are caused by specific races of *P. capsici* Leonian (Barchenger et al. 2018). The ephemeral nature of R-gene-mediated qualitative resistance which is predominantly controlled by single major genes is usually of short durability and hence not the preferred strategy of a given breeding programme. Quantitative resistance, however, is generally contributed by several genes associated with genomic regions or quantitative trait loci (QTL) with relatively small effect that function in the resistance phenotype by extending beyond the process of pathogen recognition and contribute variably towards to the resistance phenotype. Although quantitative, or partial resistance does typically not block or inhibit pathogen multiplication, it is preferred for its increased durability by conferring a broad spectrum of resistance to the ongoing challenge presented by the emergence of new races of pathogen isolates.

The identification of molecular markers linked to complex quantitative traits such as PRR resistance requires the rigorous construction of high-density genetic linkage maps and a statistically robust approach to QTL analysis. Recent QTL and genome-wide analysis approaches used in chickpea studies (Daba et al. 2016; Jaganathan et al. 2015; Kujur et al. 2015; Verma et al. 2015) have focussed on composite interval mapping (CIM) techniques originally derived in Jansen 1994; Zeng 1994. Although implementation of CIM is readily available in many stand-alone software packages such as WinQTL Cartographer (Wang et al. 2012) and ICIMapping (Meng et al. 2015), more robust whole-genome analysis approaches have also become available (Verbyla et al. 2007). More specifically, methods described by Verbyla et al. (2007, 2012) simultaneously model all sources of genetic and non-genetic variation using an extended linear mixed model that incorporates the whole-genome marker set. These approaches provide an attractive computational resource for efficient high-dimensional genome-wide analysis of disease resistance traits in comparative experiments involving chickpea.

In plant breeding experiments multiple-environment trials are commonly used to study the differential expression of marker loci across environments (Hackett et al. 2001; Tinker and Mather 1995; Verbyla et al. 2003), but there is limited use of these techniques in chickpea research. In research where it has been applied, the multi-environment models have had reduced statistical rigour (Daba et al. 2016; Hamwieh et al. 2013) due to the absence of highly structured genotype by environment interaction terms now commonly

used in plant breeding experiments (Smith et al. 2001; Smith et al. 2005). The objective of this research was to use robust statistical approaches to identify genomic regions linked to PRR resistance in chickpea using three biparental RIL mapping populations specifically developed for PRR resistance analysis.

Materials and methods

Plant material

One intra-specific and two interspecific F_6-derived recombinant inbred line (RIL) mapping populations were used in this study. The intra-specific F_6-derived RIL population referred to as YG consisted of 192 genotyped lines derived from a cross between the moderately PRR-resistant Australian chickpea variety Yorker (pedigree: 8507-28H/946-31) and the PRR-susceptible kabuli variety Genesis114 (pedigree: FLIP91-150C/FLIP90-124C//S9231). One of the interspecific F_6-derived populations referred to as RB consisted of 212 genotyped RIL individuals derived from a cross between a highly PRR-resistant breeding line 04067-81-2-1-1 (a backcross derivative from *C. echinospermum*: Howzat/ILWC 245//99039-1013) and a PRR-susceptible Australian chickpea variety Rupali (pedigree: AMETHYST-1-17_WA_COLD_TOL_CROSS). The second interspecific F_6-derived population referred to as YB consists of 196 genotyped recombinant inbred lines derived from a cross between Yorker and 04067-81-2-1-1. All populations were developed by the National Chickpea Breeding Program based at the Department of Primary Industries, Tamworth, New South Wales, Australia.

Phenotyping

In 2014 and 2015, the three RIL mapping populations were phenotyped for PRR in field experiments inoculated by applying an oospore-mycelial suspension consisting of equal concentrations of oospores from ten isolates (Table 1), in-furrow during planting in 1.2-m-long single-row plots at Hermitage Research Station, Warwick, Queensland, Australia (latitude: 28.21°S). Each plot contained 20 seeds. Rainfed field experiments were conducted in 2014 and in 2015 (Online Resource 1). In 2015, an irrigated (provided by dripper tape delivering 2–4 L/m^2/h) experiment was also established to increase disease pressure. Each field experiment included four replicates of each RIL, parental genotypes (Online Resource 1), chickpea breeding lines and Australian desi varieties such as PBA Slasher, PBA HatTrick, PBA Boundary and PBA Seamer that have a known range of resistance to PRR as checks. All field experiments followed a randomised complete block design. The number of emerged dead plants with PRR symptoms was recorded at three time points (*t1*, *t2* and *t3*), and the number of surviving plants per plot was determined. For each experiment, the survival index for plot *i* was calculated as follows: $SI_i = [$(the number of plants surviving in plot *i* at time point *t*)/(the number of plants in plot *i* at time point *t*)$] \times 100$. For each population by environment combination, the genotypes were found to have the greatest allelic segregation for PRR disease at the third time point. For this reason the survival index at *t3*, defined as *SI-t3*, was used for subsequent analysis. Based on the phenotype data the field experiments in 2014 (rainfed), 2015 (rainfed) and 2015 (irrigated) were classified as low, moderate and high disease levels.

DNA extraction and genotyping

Genomic DNA was isolated from RIL and parental genotypes using a modified CTAB method. DNA quality was determined on 0.8% agarose gel and quantified using a spectrophotometer (Nanodrop® ND-100- BIOLAB). This high-quality DNA was used for genotyping. All individuals from three RIL mapping populations including the parental genotypes were genotyped based on genotyping-by-sequencing

Table 1 Details of 10 *P. medicaginis* isolates used to inoculate field trials in a mixture

Isolate name	Host	Source	Collection site
4019	Chickpea	Irwin UQ5750, *Medicago. sativa* L.	Gatton, Queensland
4021	Chickpea	O'Dea UQ5751, *M. sativa*	Gatton, Queensland
4026	Chickpea	Hawley UQ5618, *M. sativa*	Gatton, Queensland
4027	Chickpea	Hawley UQ5617, *M. sativa*	Gatton, Queensland
4046	Chickpea	Moore, *C. arietinum*	Moree, New South Wales
4065	Chickpea	DTM05 Paddock 24	Tamworth, New South Wales
4091	Chickpea	Moore, *C. arietinum*	Trangie, New South Wales
1129-1	Chickpea	Southwell, *C. arietinum*	Yetman, New South Wales
943c-1	Chickpea	Southwell, *C. arietinum*	Tamworth, New South Wales
5601	Chickpea	Rhode, *C. arietinum*	Pallamallawa, New South Wales

All isolates were collected in Australia

(GBS) methods by Diversity Arrays Technology Pty. Ltd. (University of Canberra, Bruce, ACT, Australia) using chickpea DArT-Seq, version 1.0.

Linkage map construction

For each population, genetic linkage maps were constructed and analysed using a synergistic combination of the R package qtl (Broman et al. 2003) and R package ASMap (Taylor and Butler 2017), available in the R statistical computing environment (Team 2017). For RB and YB populations, initial attempts at linkage map construction revealed that the presence of silico-DArT markers in the linkage map increased noise dramatically. Consequently, for RB and YB populations, only co-dominant SNP markers were used for map construction. A similar process for linkage map construction was then followed for all populations. Prior to linkage map construction, genetic marker sets were analysed diagnostically. This included the removal of individual lines with greater than 50% missing allele scores. Markers were also refined for quality and retained only if they had less than 15% missing allele scores. If any pairs of individuals shared more than 98% of their alleles across the marker set, they were classified as genetic clones and their allelic data were merged to form consensus lines. Markers were then assessed for segregation distortion using a Chi-square test of the observed frequencies of the parental homozygotes against an expected 50:50 ratio. Markers considered significantly distorted (family-wise adjusted p value $<$ 1e$-$10) were removed from the map construction process. The markers remaining in each population set were then clustered into linkage groups and ordered within each linkage group using the MSTmap (Wu et al. 2008) functionality available in ASMap. For these initial linkage maps, the suite of visual diagnostic tools available in ASMap was used to assess the accuracy of marker clustering and ordering. A heat map displaying the pair-wise recombination fractions and LOD scores between markers was used to infer weak linkages between separate marker clusters. Recombination rates of lines were also visually assessed, and lines were removed from further construction if their recombination rate significantly exceeded the median recombination rate of the linkage map being constructed. For each population, markers within linkage groups were then reordered and the linkage maps were graphically reassessed. Included in this assessment was a simultaneous visual profiling of marker and interval statistics. Markers exhibiting excessive numbers of double recombination, given the number of recombination defined in their adjacent intervals, were also removed. Markers within linkage groups were then ordered a final time. For each constructed linkage map, identification and orientation of linkage groups was achieved through direct comparison of marker sequences against known physical sequences for chickpea.

Each linkage map was then prepared for genetic analysis. Initially, the homozygotic parental alleles within each marker were numerically encoded with AA = 1 and BB = − 1. Markers co-locating at the same position on any given linkage group were then condensed to form unique consensus markers, and missing allele scores in the unique markers were imputed using the flanking marker rules of (Martinez and Curnow 1994). Pseudo-markers were calculated at the mid-point between adjacent markers (called interval markers from herein) using the methods of Verbyla et al. 2007.

Single-environment linear mixed model

Preceding analysis, *SI-t3* traits for each experiment required an appropriate transformation. If the survival index for plot i is SI_i with initial plant counts n_i then an adjusted logit transformation was used, namely

$$y_i = \log \frac{\left(SI_i/100 + 1/2n_i\right)}{\left(1 - SI_i/100 + 1/2n_i\right)}$$

The correction used in the numerator and denominator of the odds ratio ensures plants with high survival rates (near 100%) and plant with low survival rates are adjusted away from the boundary constraints of the logit transformation.

The transformed traits were then analysed using a linear mixed model that appropriately partitioned and accounted for genetic and non-genetic sources of variation. The linear mixed model had the form

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Zu} + \boldsymbol{Z}_g\boldsymbol{g} + \boldsymbol{e} \quad (1)$$

where $\boldsymbol{y}$ is a vector of transformed trait observations and $\boldsymbol{X\beta}$ is the fixed component of the model containing a term that captured the mean effects of the progeny of the population, their parents and control lines planted in the field. Non-genetic variation associated with the experimental design such as replicates was modelled through the random component term $\boldsymbol{Zu}$. The underlying genetic variation of the progeny population was captured by the random component term $\boldsymbol{Z}_g\boldsymbol{g}$. The model error, $\boldsymbol{e}$, consisted of a variance to account for the residual field plot variation as well as a separable AR1 × AR1 (AR1 = auto-regressive process of order 1) correlation structure to model the co-dependency of the observations due to the proximity of neighbouring plots in the rows and columns of the field experiments. The set of effects $(\boldsymbol{u}, \boldsymbol{g}, \boldsymbol{e})$ were considered to be mutually independent. For each of the fitted trait models, the best linear unbiased predictors (BLUPs) of the progeny lines were extracted and broad-sense heritabilities were determined using the formula derived by Cullis et al. (2006).

Multiple-environment linear mixed model

For each of the populations, transformed trait data across environments were analysed in a multi-environment trial (MET) linear mixed model of the form described in (1). All terms accounting for non-genetic variation in the single-environment models were used in the MET model. The MET model also contained a term to parsimoniously model the genotype by environment interaction (Smith et al. 2001, 2005), consisting of a genetic variance for the set of recombinant inbred lines in each of the trials as well as a genetic correlation to capture the connectivity of the recombinant inbred lines between trials. Estimates of the genetic correlation were extracted from the fitted MET models and summarised.

Single-environment QTL analyses

A QTL analysis was then conducted on each of the transformed traits using the whole-genome average interval mapping (WGAIM) approach of Verbyla et al. (2007, 2012). The approach initially extends the baseline linear mixed model defined in (1) by incorporating the whole genome of interval markers as a contiguous block of random covariates with a single variance parameter. This variance parameter is then tested for significance by comparing the extended model to the baseline model through a likelihood ratio test. If the test infers significance, outlier statistics are calculated for each interval marker and the interval marker with the maximum outlier statistic is selected as a set of flanking markers linked to a QTL. This interval marker is then removed from the contiguous block of interval markers and placed in the model as a separate random covariate. This forward selection process was repeated until the variance parameter associated with the remaining random interval marker effects was not significant. The selected interval markers were then summarised with the sizes of their effects, their LOD scores of significance and their percentage contribution of the total genetic variance.

Multiple-environment QTL analysis

To determine potential differential expression of interval markers linked to QTL across different environments for each population, a MET linear mixed model QTL analysis was conducted using the complete set of pseudo-intervals of the genome. Individual interval markers as a fixed main effect and an interval marker by environment interaction effect were incorporated in the baseline MET linear mixed model. Each interval marker was considered individually, and a separate MET linear mixed model was fitted for all interval markers spanning the genome of the population (Bonneau et al. 2013; Malosetti et al. 2014). A Wald statistic was then calculated for the interval marker main effect as well as the interval marker by environment interaction effect, and separate genome-wide profiles were developed. To allow for the simultaneous examination of multiple marker effects, a profile-independent family-wise error rate was initially calculated from a Bonferroni-adjusted p-value at an alpha level of 0.05 using the techniques of Li and Ji (2005). The Wald statistic threshold for the main effect profile (THM) was then determined by using the family-wise error rate to calculate the appropriate quantile of the Chi-square distribution with one degree of freedom. In a similar fashion, the Wald statistic threshold for the interaction effects profile (THI) was calculated using the quantile of the Chi-square distribution with two degrees of freedom. An interval marker was considered to be linked to a QTL and exhibiting differential expression across environments if the Wald statistic profile for the interval marker by environment interaction effect contained a peak greater than the defined threshold. An interval marker was considered to be linked to a QTL with similar expression across environments if the main effect Wald statistic profile contained a peak greater than the defined threshold and simultaneously the Wald statistic profile for the interval marker by environment interaction was lower than the defined threshold. The latter of these two requirements ensured the statistical principle of marginality was imposed when determining significant main effect QTL. All interval markers potentially linked to a QTL were simultaneously added to the fixed effects of the baseline multi-environment linear mixed model to determine their individual significance and summarised, including their flanking markers, effect sizes and their LOD scores across environments.

Computations

All models were analysed using the flexible linear mixed modelling software ASReml-R (Butler et al. 2009). For all single-experiment QTL analyses, the R package wgaim (Taylor and Verbyla 2011) was used. The package uses the linear mixed model functions in ASReml-R for fitting QTL models as well as summarising and visualising results. For the MET QTL analysis unpackaged R code was used to implement the marker scanning algorithm.

Results

Genetic maps

DArT GBS generated a total of 420 SNP markers (co-dominant) and 552 silico-DArT markers (dominant) for the YG population, with 3163 SNP markers and 6166 silico-DArT markers identified for the RB population. Similarly, 3132

SNP markers and 3515 silico-DArT markers were obtained for the YB mapping population. The genetic linkage map for the intra-specific RIL population YG (Online Resource 2) contained a total of 573 SNP and silico-DArT markers with an overall length 993.8 cM. High-density genetic maps for the two interspecific RIL populations RB (Online Resource 2) and YB (Online Resource 2) contained a total of 1940 SNP markers with overall length 949.7 cM and 2061 SNP markers with overall length 1334.7 cM, respectively. A strong linkage between markers was observed, as shown in the respective heat map corresponding to each population (Online Resource 3 Fig. S1, Fig. S2 and Fig. S3). The average spacing of markers within the linkage groups for the maps YG, RB and YB was 1.8 cM, 0.5 cM and 0.7 cM, respectively, and the overall length of these maps were similar to linkage maps in previous chickpea mapping studies (Thudi et al. 2011; Verma et al. 2015). To prepare the linkage maps for analysis, consensus markers were calculated for each set of co-locating markers and the genetic maps for YG, RB and YB populations reduced to 273, 373 and 314 unique marker loci, respectively. In most chromosomes of the genetic maps, an uneven distribution of markers was observed, indicating regions of increased recombination (hot spots) as well as regions of suppressed recombination (dead-spots). On all three genetic maps, chromosome 6 was found to have recombination hot spots with the highest number of markers very tightly linked.

Reaction to *P. medicaginis*, disease distribution and trait association

The PRR phenotype trait *SI-t3* data obtained from three field experiments 2014 rainfed, 2015 rainfed and 2015 irrigated were used to understand the reaction of *P. medicaginis* on the three RIL mapping populations as well as the disease distribution across the populations and environments. The moderately resistant parent Yorker had a higher *SI* in low-to-moderate environments compared to Genesis114, the PRR-susceptible genotype. Although it has previously been reported that Genesis114 is classified as a PRR-susceptible variety (Online resource 1) the results obtained from this field phenotyping across three different disease environments indicate that under these conditions Genesis114 is classified as more moderately PRR susceptible (Table 2). It was interesting that Yorker showed a low *SI* under high disease pressure (2015 irrigated) in both YG and YB populations, indicating that a moderately PRR-resistant variety like Yorker had become more susceptible when exposed to increased PRR disease pressure. The breeding line 04067-81-2-1-1 is known to exhibit high resistance to PRR and showed higher *SI* consistently in all environments, whilst Rupali, the PRR-susceptible genotype, had a relatively low *SI*. The population mean values for the trait *SI* in YG, RB and YB populations dropped with increasing PRR disease pressure across the 2014 rainfed, 2015 rainfed and 2015 irrigated experiments (Table 2). The broad-sense heritability values (H^2) differed with the mapping population and the intensity of disease. The heritability values were consistent in moderate-to-high disease pressure environments in each of the three populations (~ 0.57 in YG; ~ 0.83 in RB; ~ 0.8 in YB), but were very low under conditions where disease pressure was low (0.36 in YG; 0.574 in RB; 0.28 in YB). This suggests that there is a need to increase disease pressure to enhance the segregation for PRR in the populations phenotyped.

Table 2 Parental means and mapping population means for the trait *SI-t3* in each RIL population screened for PRR resistance in three experiments

Experiment	Parental mean			RIL population		
	Yorker (A)	Genesis114 (A)	PRR disease level	Mean	Range	Heritability H^2
2014 Rainfed	74.02	–	Low	76.20	0–100	0.362
2015 Rainfed	69.41	63.22	Moderate	50.37	0–100	0.576
2015 Irrigated	20.33	38.65	High	31.74	0–100	0.575
	Rupali (A)	04067-81-2-1-1 (B)	PRR disease level	Mean	Range	Heritability H^2
2014 Rainfed	56.72	93.49	Low	85.78	0–100	0.574
2015 Rainfed	17.46	96.06	Moderate	59.80	0–100	0.828
2015 Irrigated	6.87	96.95	High	21.81	0–100	0.847
	Yorker (A)	04067-81-2-1-1 (B)	PRR disease level	Mean	Range	Heritability H^2
2014 Rainfed	85.01	96.56	Low	93.35	25–100	0.280
2015 Rainfed	40.64	96.85	Moderate	82.97	0–100	0.700
2015 Irrigated	9.21	95.88	High	38.50	0–100	0.873

– Not available due to no germination of the genotype. (A) and (B) identify seeds derived from the plant used as a parental RIL genotype

Heat maps were plotted to indicate the survival index from PRR disease at time point *t3* in each population across the three environments (Fig. 1). In all populations, higher survival index (redder areas in Fig. 1) was more pronounced under rainfed conditions in 2014 and 2015, where the severity of the disease was classified as low (2014 rainfed) to moderate (2015 rainfed). In contrast, under 2015 irrigated conditions, disease pressure was higher than for 2014 and 2015 rainfed environments, which resulted in an overall decrease in plant survival for all three RIL populations.

From each of the fitted MET models for survival index, the estimated genetic correlation matrix was extracted

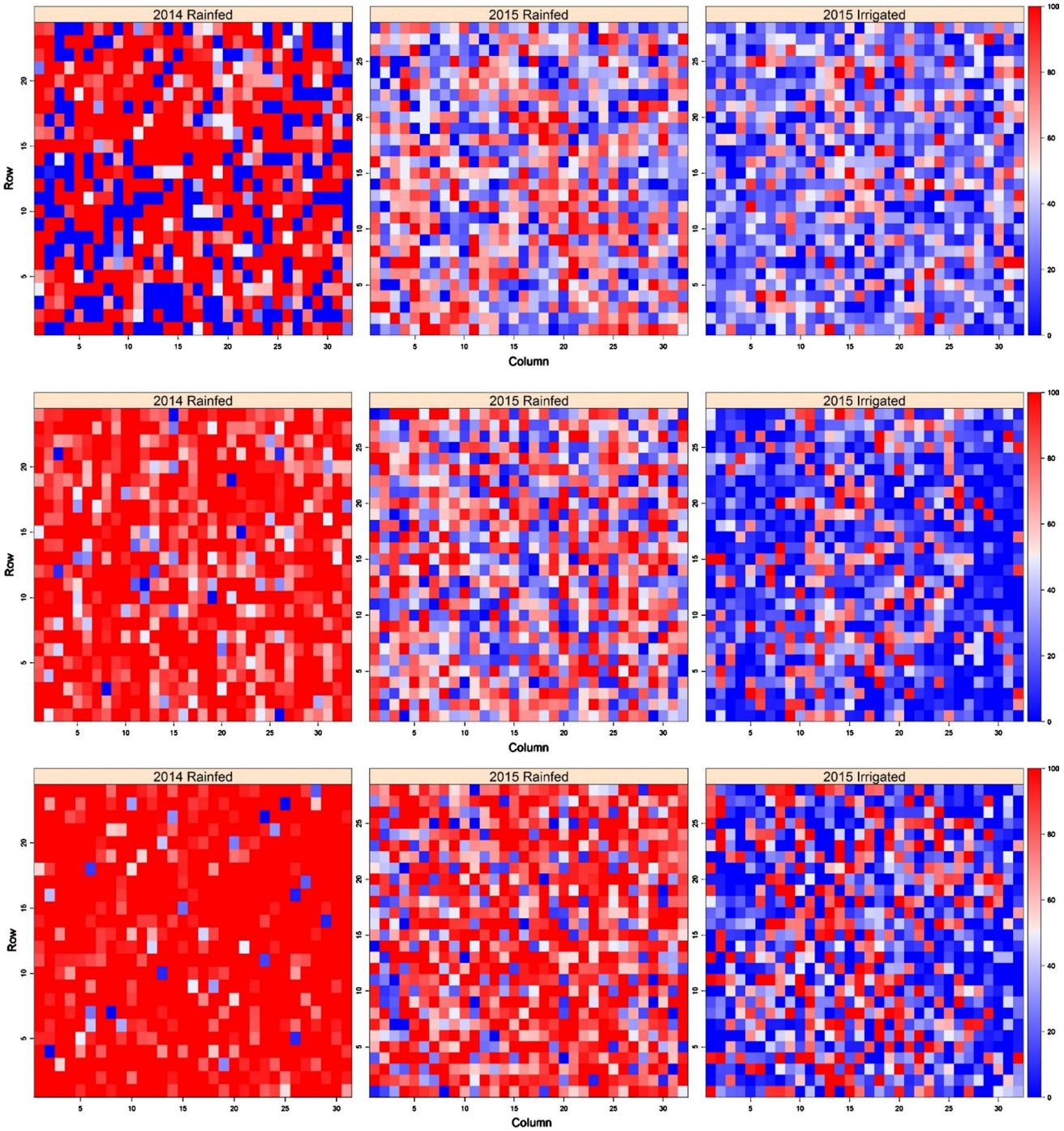

Fig. 1 Heat map plots showing the prevalence of PRR disease across the three field environments 2014 rainfed, 2015 rainfed and 2015 irrigated in the YG, RB and YB populations (from top to bottom) at time point t3. Blue areas indicate 0% survival (*SI-t3*), and red areas indicate 100% survival

(Table 3) and used to assess the genetic performance of the progeny lines in an environment as well as the genetic similarity of the lines between environments with differing disease pressure. For each population, there were consistent moderate genetic correlations between the 2014 rainfed and 2015 rainfed environments, suggesting a similar genetic expression of plant survival across the progeny lines in environments with low-to-moderate infection of PRR. Additionally, the high genetic correlation between the 2015 rainfed and 2015 irrigated environments observed for all RIL populations indicates the underlying genetic basis for plant survival may be linked to the presence of adequate disease pressure in the environment.

Table 3 Estimated genetic correlation from the fitted multi-environment model for the survival index *SI-t3* in each RIL mapping population

	2014 Rainfed	2015 Rainfed	2015 Irrigated
YG			
SI-t3			
2014 Rainfed	0.283		
2015 Rainfed	0.444	0.443	
2015 Irrigated	0.389	0.818	0.454
RB			
SI-t3			
2014 Rainfed	0.888		
2015 Rainfed	0.890	1.980	
2015 Irrigated	0.829	0.921	2.321
YB			
SI-t3			
2014 Rainfed	0.653		
2015 Rainfed	0.702	1.883	
2015 Irrigated	0.551	0.918	3.818

QTL analyses for YG population

Single-environment QTL analyses for the YG population identified genomic regions associated with PRR resistance (Table 4). The identified QTL varied between each field experiment, suggesting the role of genotype by environmental effects in the expression of resistance. Under low disease pressure (2014 rainfed), three QTL on chromosomes 4 and 5 were identified, accounting for 16.9%, 23.0% and 18.3% of genetic variation, respectively. Under moderate disease pressure (2015 rainfed), one major QTL and one minor QTL were identified on chromosomes 6 and 4, explaining 25.0% and 8.7% of the genetic variation, respectively. Under high disease pressure (2015 irrigated), one major QTL on chromosome 4 and a minor QTL on chromosome 3 were found to be significant and accounted for 15.5% and 8.5% of the genetic variation, respectively. The exact genetic positions of the identified QTL on chromosome 4 differed across the environments, indicating the dependence of environment on expression of the resistance QTL.

QTL analyses for RB population

In the interspecific mapping population RB, single-environment QTL analyses identified genomic regions associated with PRR resistance under environments where there was low, moderate and high disease conditions (Table 5). A few co-locating QTL were identified across the three environments; however, many were specific to a single environment which again implies the presence of genotype by environment effects. Under low disease pressure conditions (2014 rainfed), four major QTL were identified on chromosomes 3, 4, 5 and 6 accounting for 17.5%, 10.8%, 18.5% and 11.3% of the genetic variation, respectively. Two minor QTL on chromosomes 3 and 4 were also identified. Under moderate disease condition (2015 rainfed), three major QTL were identified on chromosomes 4, 5 and 6 associated with 20.7%, 9.3% and 25.9% of the genetic variation, respectively. The QTL on

Table 4 QTL associated with *SI-t3* in YG population in field experiments (2014 rainfed, 2015 rainfed and 2015 irrigated)

Experiment	Chr.	Interval	Distance cM	Size[a]	Prob.	%Var.	LOD
2014 Rainfed	C4	*9001SD4-2:9001SNP4-1(C)*	0.00–1.06	−0.239	0.000	16.9	3.187
	C4	*9001SD4-74:9001SD4-75(C)*	109.05–118.25	0.279	0.000	23.0	3.828
	C5	*9001SNP5-15(C): 9001SNP6-6*	85.79–99.48	−0.249	0.001	18.3	2.559
2015 Rainfed	C4	*9001SD4-58(C):9001SD4-56*	88.57–90.15	0.212	0.002	8.7	2.172
	C6	*9001SD6-30(C): 9001SD6-44*	70.94–76.40	−0.360	0.000	25.0	5.415
2015 Irrigated	C3	*9001SNP3-8: 9001SNP3-9(C)*	83.30–90.05	0.218	0.001	8.5	2.394
	C4	*9001SD4-21(C): 9001SNP4-13*	12.51–20.44	0.295	0.000	15.5	4.025

Field experiments 2014 rainfed, 2015 rainfed and 2015 irrigated were classified as low-to-moderate and high PRR disease pressure, respectively. QTL interval names with (C) indicate several co-locating markers at the loci

[a]Positive and negative values indicate that Genesis114 and Yorker alleles increased the phenotypic values, respectively

Table 5 QTL associated with *SI-t3* in RB population in field experiments (2014 rainfed, 2015 rainfed and 2015 irrigated)

Experiment	Chr.	Interval	Distance cM	Size[a]	Prob.	%Var.	LOD
2014 Rainfed	C3	*RB-SNP-scf33(C): RB-SNP3-4(C)*	0.00–2.28	0.227	0.000	4.9	3.038
	C3	*RB-SNP3-165(C):RB-SNP3-160(C)*	78.03–79.67	−0.428	0.000	17.5	9.551
	C4	*RB-SNP-79(C): RB-SNP-72(C)*	80.53–81.70	−0.335	0.000	10.8	4.400
	C4	*RB-SNP-scf69: RB-SNP4-506*	126.37–128.8	−0.212	0.002	4.3	2.151
	C5	*RB-SNP5-3: RB-SNP-173*	85.85–106.10	−0.440	0.000	18.5	6.045
	C6	*RB-SNP6-377: RB-SNP-16(C)*	104.22–105.17	−0.343	0.000	11.3	4.595
	C8	*RB-SNP8-36(C): RB-SNP-136*	10.85–12.57	−0.272	0.000	7.1	3.402
2015 Rainfed	C4	*RB-SNP-131(C): RB-SNP4-475*	88.86–89.91	−0.643	0.000	20.7	11.043
	C5	*RB-SNP5-3: RB-SNP-173*	85.85–106.10	−0.431	0.000	9.3	4.146
	C6	*RB-SNP6-211: RB-SNP-scf117(C)*	86.04–87.46	−0.719	0.000	25.9	14.931
	C8	*RB-SNP-162(C): RB-SNP8-144(C)*	34.89–36.16	−0.344	0.000	5.9	4.293
2015 Irrigated	C3	*RB-SNP3-67(C): RB-SNP3-69(C)*	68.55–69.98	−0.523	0.000	11.4	10.240
	C4	*RB-SNP4-140(C): RB-SNP4-36(C)*	28.84–39.62	0.286	0.002	3.4	2.175
	C4	*RB-SNP-114(C): RB-SNP-12(C)*	92.46–93.99	−0.783	0.000	25.6	18.698
	C6	*RB-SNP-scf117(C): RB-SNP-scf61*	87.46–88.33	−0.648	0.000	17.5	11.772
	C6	*RB-SNP6-335: RB-SNP6-46*	124.58–25.44	−0.387	0.000	6.3	4.267
	C8	*RB-SNP-scf221: RB-SNP8-76*	53.40–61.15	−0.319	0.000	4.2	3.401

Field experiments 2014 rainfed, 2015 rainfed and 2015 irrigated were classified as low-to-moderate and high PRR disease pressure, respectively. QTL interval names with (C) indicate several co-locating markers at the loci

[a]Positive and negative values indicate that Rupali and 04067-81-2-1-1 alleles increased the phenotypic values, respectively

chromosome 5 was identified under both low and moderate disease conditions in a comparative genetic interval. Under high disease pressure conditions (2015 irrigated), three QTL were found to be significant on chromosomes 3, 4 and 6, explaining 11.4%, 25.6% and 17.5% of the genetic variation, respectively. Two minor QTL on chromosomes 6 and 8 were also identified. Interestingly, the QTL identified on chromosome 4 across all three environments in RB population are located at comparative genetic locations, suggesting the presence of a major locus on chromosome 4 associated with PRR resistance, contributed by the highly resistant parental genotype 04067-81-2-1-1 derived from *C. echinospermum*. The major QTL identified on chromosome 6 was found to co-locate under both moderate and high disease conditions, suggesting the identification of an additional locus derived from *C. echinospermum* with a potential role in resistance to PRR in chickpea that could be targeted through marker-assisted selection.

QTL analyses for YB population

Single-environment QTL analyses on the trait *SI-t3* in low, moderate and high disease conditions for the interspecific population YB derived from a cross between moderately PRR-resistant and highly PRR-resistant parental genotypes identified genomic regions associated with PRR resistance (Table 6). Under low disease pressure conditions in the 2014 rainfed environment, no QTL were identified, possibly indicating that there was insufficient phenotypic discrimination in the response of RIL individuals to the level of PRR disease. Under moderate (2015 rainfed) and high disease pressure (2015 irrigated) conditions two major

Table 6 QTL associated with *SI-t3* in YB population in field experiments (2014 rainfed, 2015 rainfed and 2015 irrigated)

Experiment	Chr.	Interval	Distance cM	Size[a]	Prob.	%Var.	LOD
2015 Rainfed	C3	*9024SNP3-4(C):9024SNP3-189(C)*	112.50–123.20	−0.476	0.000	14.6	3.955
	C6	*9024SNP6-127(C):9024SNP6-146(C)*	106.95–108.11	−0.532	0.000	18.3	5.355
2015 Irrigated	C3	*9024SNP3-4(C):9024SNP3-189(C)*	112.50–123.20	−0.734	0.000	14.5	5.191
	C6	*9024SNP6-146(C):9024SNP6-150(C)*	108.11–109.16	−0.946	0.000	24.0	8.808

Field experiments 2014 rainfed, 2015 rainfed and 2015 irrigated were classified as low-to-moderate and high PRR disease pressure, respectively. QTL interval names with (C) indicate several co-locating markers at the loci

[a]Positive and negative values indicate that Yorker and 04067-81-2-1-1 alleles increased the phenotypic values, respectively

QTL were identified on chromosomes 3 and 6 with resistance alleles derived from the high PRR-resistant parental genotype 04067-81-2-1-1 derived from *C. echinospermum*. These two major QTL were found to co-locate in both 2015 rainfed and 2015 irrigated environments, suggesting there may be negligible environmental influence on the expression of resistance.

Multiple-environment QTL analysis

In order to identify QTL by environment interaction effects, a MET linear mixed model QTL analysis was conducted and Wald statistic profiles spanning the genome were calculated for the interval marker main effect and marker by environment interaction effects (Fig. 2). Interval markers were considered significantly linked to QTL with differential expression across environments if the estimated Wald statistic for the interaction effects exceeded THI at any given peak in the profile. Interval markers were only reported as significantly linked to main effect QTL if the estimated Wald statistics for the main effect exceeded THM and, simultaneously, were below THI (Table 7). The QTL linked to main effect in all three RIL mapping populations were named referring to Varshney et al. 2014. In the YG population, all identified QTL had a significant main effect, suggesting the expression of the QTL is similar across environments that differ in disease pressure. The results indicate two major QTL *QYGprrsi02* and *QYGprrsi03* on chromosomes 5 and 6, respectively, were associated with PRR resistance with the resistant allele contributed by the moderately PRR-resistant genotype Yorker. In the RB population, the QTL *QRBprrsi01* and *QRBprrsi02* on chromosomes 3 and 4, respectively, and a minor QTL *QRBprrsi03* on chromosome 8 exhibited significant main effects. The QTL *QRBprrsi04* on chromosome 6 had a strong significant QTL by environment interaction effect due to the reduced expression of the interval marker in the low disease pressure environment, 2014 rainfed. In the YB population, the major QTL *QYBprrsi01* and *QYBprrsi02* on chromosomes 3 and 6, respectively, exhibited significant QTL by environment effects. In both cases individual environmental QTL effects indicated

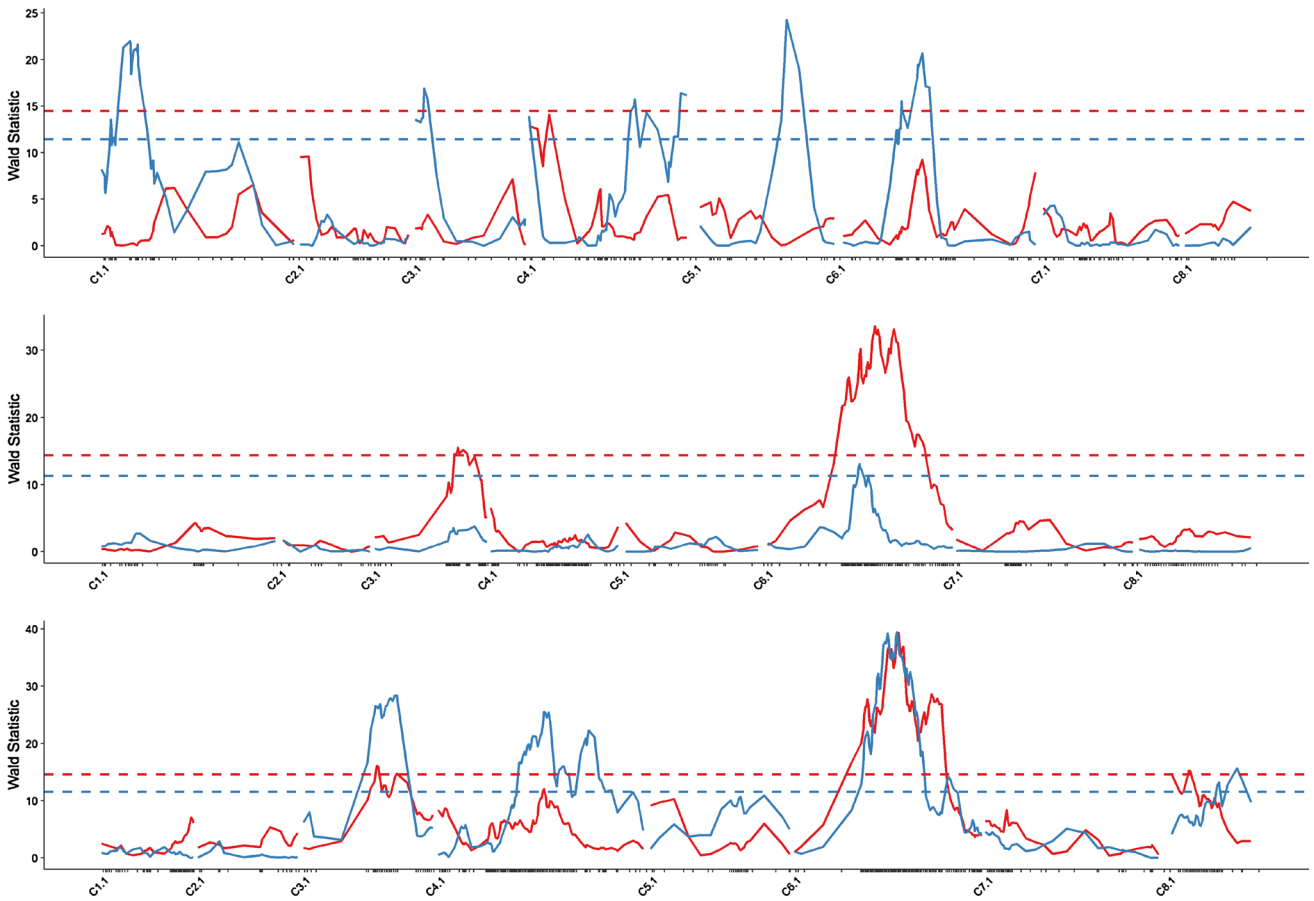

Fig. 2 QTL main effect (blue) and QTL by environment effect (red) Wald statistic profile plots obtained from the multi-environment QTL analysis of *SI-t3* for YG, YB and RB populations (top to bottom). Horizontal lines represent significance thresholds for the main effect (THM) and interaction effect (THI)

Table 7 QTL associated with *SI-t3* in YG, RB and YB RIL mapping populations in field environments (2014 rainfed, 2015 rainfed and 2015 irrigated) detected using the fitted multi-environment model

RIL population	Chr.	QTL name	Interval	Genetic map distance (cM)	Physical position (bp)	Experiment	Size[a]	*p* Value	LOD	%Var.
YG	C4	*QYGprrsi01*	*9001SNP4-42(C): 9001SNP4-43*	92.87–93.44	35,233,539–36,456,096	2014 Rainfed	0.1815	3.83E−05	3.681	2.687
	C4	*QYGprrsi01*	*9001SNP4-42(C): 9001SNP4-43*	92.87–93.44	35,233,539–36,456,096	2015 Rainfed	0.1815	3.83E−05	3.681	1.748
	C4	*QYGprrsi01*	*9001SNP4-42(C): 9001SNP4-43*	92.87–93.44	35,233,539–36,456,096	2015 Irrigated	0.1815	3.83E−05	3.681	1.495
	C5	*QYGprrsi02*	*9001SNP5-19: 9001SNP5-15(C)*	76.95–85.79	38,106,599–46,569,019	2014 Rainfed	−0.1678	0.000542	2.599	3.381
	C5	*QYGprrsi02*	*9001SNP5-19: 9001SNP5-15(C)*	76.95–85.79	38,106,599–46,569,019	2015 Rainfed	−0.1678	0.000542	2.599	2.200
	C5	*QYGprrsi02*	*9001SNP5-19: 9001SNP5-15(C)*	76.95–85.79	38,106,599–46,569,019	2015 Irrigated	−0.1678	0.000542	2.599	1.881
	C6	*QYGprrsi03*	*9001SD6-30(C): 9001SD6-44*	70.94–76.40	17,366,266–18,853,960	2014 Rainfed	−0.1374	0.003579	1.843	1.111
	C6	*QYGprrsi03*	*9001SD6-30(C): 9001SD6-44*	70.94–76.40	17,366,266–18,853,960	2015 Rainfed	−0.1374	0.003579	1.843	0.723
	C6	*QYGprrsi03*	*9001SD6-30(C): 9001SD6-44*	70.94–76.40	17,366,266–18,853,960	2015 Irrigated	−0.1374	0.003579	1.843	0.619
RB	C3	*QRBprrsi01*	*RB-SNP3-165(C): RB-SNP3-160(C)*	78.03–79.67	34,523,347–34,911,684	2014 Rainfed	−0.3691	1.71E−09	7.878	14.04
	C3	*QRBprrsi01*	*RB-SNP3-165(C): RB-SNP3-160(C)*	78.03–79.67	34,523,347–34,911,684	2015 Rainfed	−0.3691	1.71E−09	7.878	7.077
	C3	*QRBprrsi01*	*RB-SNP3-165(C): RB-SNP3-160(C)*	78.03–79.67	34,523,347–34,911,684	2015 Irrigated	−0.3691	1.71E−09	7.878	6.673
	C4	*QRBprrsi02*	*RB-SNP-131(C): RB-SNP4-475*	88.86–89.91	15,542,584–15,752,261	2014 Rainfed	−0.3672	4.47E−07	5.533	13.90
	C4	*QRBprrsi02*	*RB-SNP-131(C): RB-SNP4-475*	88.86–89.91	15,542,584–15,752,261	2015 Rainfed	−0.3672	4.47E−07	5.533	7.005
	C4	*QRBprrsi02*	*RB-SNP-131(C): RB-SNP4-475*	88.86–89.91	15,542,584–15,752,261	2015 Irrigated	−0.3672	4.47E−07	5.533	6.605
	C8	*QRBprrsi03*	*RB-SNP-scf221: RB-SNP8-76*	53.40–61.15	72201[a]–15,860,254	2014 Rainfed	−0.2158	0.000835	2.424	4.803
	C8	*QRBprrsi03*	*RB-SNP-scf221: RB-SNP8-76*	53.40–61.15	72201[a]–15,860,254	2015 Rainfed	−0.2158	0.000835	2.424	2.420
	C8	*QRBprrsi03*	*RB-SNP-scf221: RB-SNP8-76*	53.40–61.15	72201[a]–15,860,254	2015 Irrigated	−0.2158	0.000835	2.424	2.282
	C6	*QRBprrsi04*	*RB-SNP-scf117(C): RB-SNP-scf61*	87.46–88.33	33,493,429–244686[a]	2014 Rainfed	−0.3833	5.33E−08	6.426	15.15
	C6	*QRBprrsi04*	*RB-SNP-scf117(C): RB-SNP-scf61*	87.46–88.33	33,493,429–244686[a]	2015 Rainfed	−0.7846	0.000	20.053	31.97
	C6	*QRBprrsi04*	*RB-SNP-scf117(C): RB-SNP-scf61*	87.46–88.33	33,493,429–244686[a]	2015 Irrigated	−0.8823	0.000	25.615	38.13
YB	C3	*QYBprrsi01*	*9024SNP3-1(C): 9024-SNP-108*	97.67–98.90	34,523,347–34,911,684	2015 Rainfed	−0.3532	0.00191	2.092	6.691
	C3	*QYBprrsi01*	*9024SNP3-1(C): 9024-SNP-108*	97.67–98.90	34,523,347–34,911,684	2015 Irrigated	−0.691	7.71E−07	5.305	12.58
	C6	*QYBprrsi02*	*9024SNP6-240(C): 9024SNP6-429(C)*	126.48–127.39	30,089,649–31,011,058	2015 Rainfed	−0.5363	2.25E−06	4.857	15.42
	C6	*QYBprrsi02*	*9024SNP6-240(C): 9024SNP6-429(C)*	126.48–127.39	30,089,649–31,011,058	2015 Irrigated	−0.9564	5.57E−12	10.309	24.10

QTL intervals with p values <0.01 are presented. QTL interval names with (C) indicate several co-locating markers at the loci

Physical locations are based on the chickpea kabuli v1.0 reference genome; [a] values indicate unplaced location of the scaffold marker

[a]Positive and negative values indicate that Genesis114 and Yorker alleles increased the phenotypic values in YG population; Rupali and 04067-81-2-1-1 alleles in RB population and Yorker and 04067-81-2-1-1 alleles in YB population, respectively

increased PRR resistance associated with the allele contributed by the resistant genotype 04067-81-2-1-1 derived from *C. echinospermum*.

Discussion

This study describes the mapping of QTL for the identification of genomic regions associated with partial PRR resistance in chickpea. Whole-genome QTL analysis utilising GBS genotype data and PRR survival trait data collected across different sites enabled the representation in the analysis of a range of target disease environments. The GBS platform DArT-Seq was used to genotype one intra-specific and two interspecific RIL mapping populations and allowed us to detect genomic regions associated with PRR resistance. This provides a new source of genetic variation which could be used for understanding the inheritance of PRR resistance in chickpea.

Cultivated chickpea is known to have a narrow genetic base (Yadav and Chen 2007). A need for higher levels of resistance in chickpea led to searches in more diverse species related to cultivated chickpea, such as *C. echinospermum* and *C. reticulatum*. In field and glasshouse experiments, significantly increased levels of resistance were found in accessions of *C. echinospermum* in contrast to the levels identified in *C. arietinum* (Knights et al. 2008). Subsequent to that study crossing strategies have been implemented to introgress desirable loci from *C. echinospermum* into agronomically adapted backgrounds. In addition to breeding, backcross derivatives such as 04067-81-2-1-1 have also been utilised as parental genotypes in the development of RIL populations, with an aim to characterise these favourable, stronger sources of resistance over those observed in cultivated species. In contrast to the relatively low level of polymorphism identified in the intra-specific population YG, the use of the interspecific populations RB and YB also enabled an increase in the level of polymorphism to facilitate the generation of genetic maps with improved resolution. Genetic maps for the YG, RB and YB mapping populations reported in this study contained a large number of co-locating markers within each linkage group. These markers may potentially be useful when selecting for a specific region across a broad set of germplasm and also of use to improve the resolution of interesting QTL in fine-mapping populations.

Qualitative resistance conferred typically by single major genes results in a narrow resistance spectrum, as opposed to quantitative resistance (Linde 2002) which although more genetically complex, can provide a more durable option for breeding. This is particularly true if knowledge relating to the genomic regions associated with resistance and tools to select resistance loci in combination are available. In the present study where all three RIL mapping populations were phenotyped for PRR trait, the levels of PRR resistance for the parental genotypes Rupali, Genesis114, Yorker and 04067-81-2-1-1 across the three field environments based on the *SI-t3* mean values were rated as susceptible, moderately susceptible, moderately resistant and highly resistant, respectively. The low heritability for the *SI-t3* trait across the populations in 2014 rainfed (low) suggested the presence of relatively lower disease pressure and potentially a greater influence from environmental variation. For the YB and RB populations grown in moderate and high disease conditions, there was a consistent increase in trait heritability, suggesting the higher disease pressure of these environments enabled the discrimination of distinct phenotypic responses amongst segregating RIL individuals. The low–moderate heritability of *SI-t3* in the YG population observed across the different environments is due to the reduced contrast in levels of PRR resistance for these parental genotypes used to develop this population. The high genetic correlation observed between 2015 rainfed and 2015 irrigated environments in both intra-specific (YG) and interspecific (RB and YB) mapping populations along with high heritability of the *SI-t3* PRR phenotype trait indicates that implementation of its selection should be an effective strategy in the chickpea breeding programme.

The QTL analysis adopted in this study applied an extended linear mixed model to appropriately account for non-genetic sources of environmental variation in field experiments, as well as incorporate markers across the whole genome to improve the accuracy of interval marker detection and selection (Verbyla et al. 2007; Verbyla et al. 2012). Single-environment QTL analyses of *SI-t3* identified QTL in all three RIL populations. In YG, RB and YB populations, most QTL identified were environment specific, strongly suggesting environmental influence on the expression of PRR resistance, which led us to conduct multi-environment QTL analyses to identify QTL associated with the main effect. In the YB population, no QTL were identified in the 2014 rainfed experiment, an observation most likely due to low disease pressure prevalent in that season.

Multiple-environment experiments are used in plant breeding to study the performance of genotypes across a range of conditions representing target environments (Berger et al. 2004). This study involved the analysis of genotypes across three environments, and subsequent multi-environment QTL analysis identified the differential expression of markers linked to the identified QTL across these environments. Two major QTL *QYGprrsi02* and *QYGprrsi03* were identified in the YG population with resistance contributed by the Yorker parent, and a minor QTL *QYGprrsi01* on chromosome 4 with resistance contributed by the moderately PRR-susceptible Genesis114 parent. Three major QTL *QRBprrsi01*, *QRBprrsi02* and

QRBprrsi04 on chromosomes 3, 4 and 6 accounting for genetic variance of 6.7–14%, 6.6–13.9% and 15.2–38.1%, respectively, were identified in the RB population with the resistance allele contributed by 04067-81-2-1-1 derived from *C. echinospermum*. Similarly, two major QTL *QYBprrsi01* and *QYBprrsi02* on chromosomes 3 and 6 accounting for 6.7–12.6%, 15.4–24.1% of genetic variation, respectively, were identified in the YB population derived from the same source. These genomic regions from all populations were found to have negligible environment interactions and should be targeted for developing molecular markers associated with PRR resistance in chickpea.

Mapping the physical location of the SNP markers flanking the major QTL *QRBprrsi01* (physical position on chromosome 3: 34,523,347–34,911,684 bp) in RB and *QYBprrsi01* (physical position on chromosome 3: 34,439,325–34,718,938 bp) on chromosome 3 in YB mapping populations indicates that they overlap. Similarly, the location of QTL *QRBprrsi04* (physical position of left marker on chromosome 6: 33,493,429 bp flanked on the right by an unlocalised scaffold marker) in RB and *QYBprrsi02* (physical position on chromosome 6: 30,089,649 bp–31,011,058 bp) in YB indicated the physical position of QTL to be proximate (Fig. 3). Additionally, these two major QTL on two chromosomes 3 and 6 co-locate

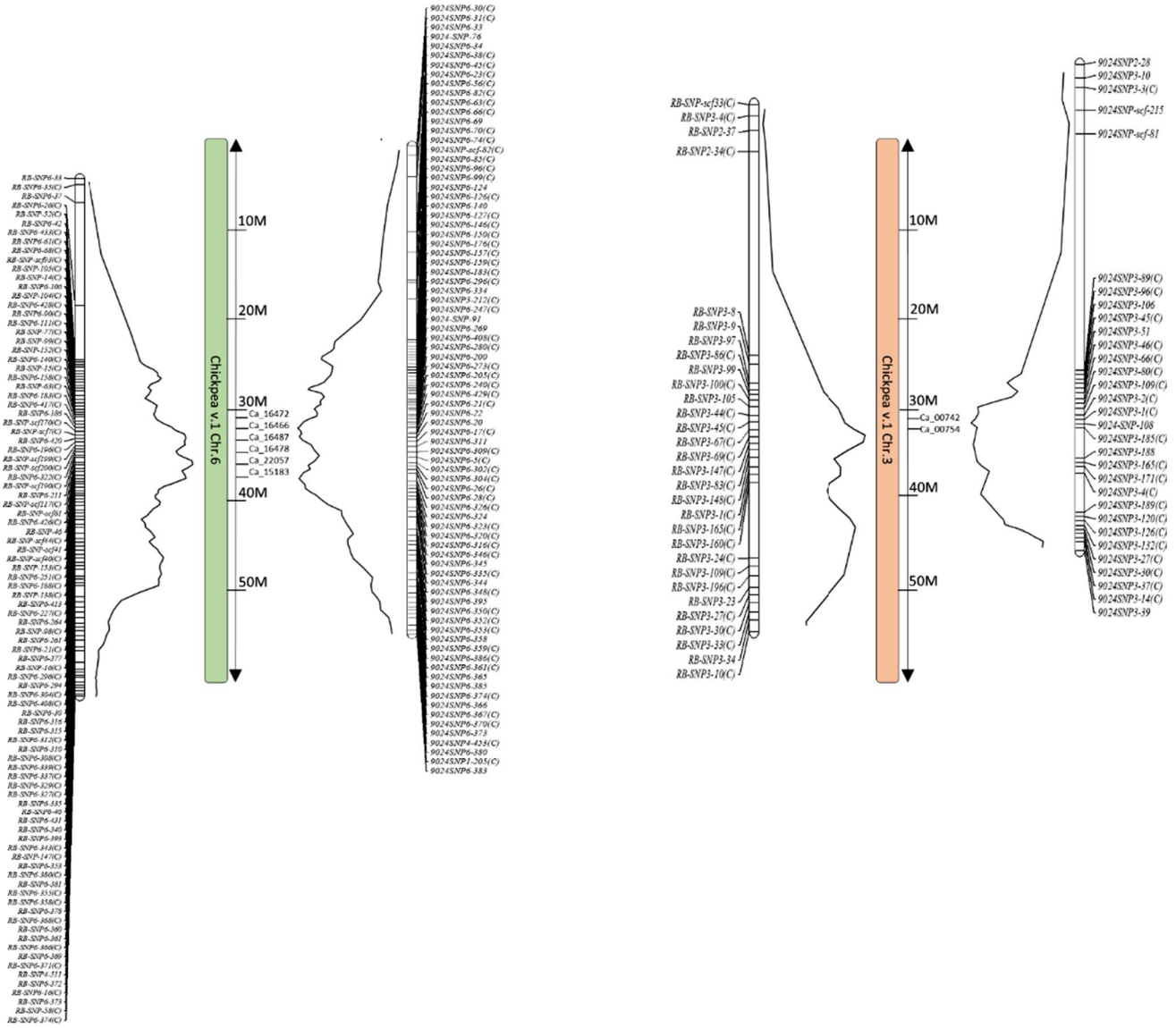

Fig. 3 Projected physical position of the PRR resistance QTL on chromosomes 3 and 6 in RB (on the left) and YB (on the right) populations across 2014 rainfed, 2015 rainfed and 2015 irrigated field environments. The genetic map images for RB and YB chromosomes 3 and 6 are plotted with unique markers, and those marker names ending with (*C*) indicate several co-locating markers at the loci

in two mapping populations across environments, validating these PRR resistance-associated genomic regions in chickpea. The major QTL *QYGprrsi02* (physical position on chromosome 5: 38,106,599–46,569,019 bp) on chromosome 5 and *QYGprrsi03* (physical position on chromosome 6: 17,366,266–18,853,960 bp) on chromosome 6 associated with PRR resistance contributed by Yorker (*C. arietinum*) are physically distinct from that identified in RB contributed by the wild *Cicer* species, suggesting the presence of independent sources of partial resistance in these populations. This finding is of significance in breeding as it allows the possibility to pyramid PRR resistance QTL in a marker-assisted breeding strategy to increase the level of durable resistance in elite varieties, thereby adapting to the possibility of genetic change in the Phytophthora pathogen.

With the availability of a chickpea reference genome sequence and a physical location identified for the major PRR partial resistance QTL, a search was conducted for candidate genes associated with plant pathogen resistance in chickpea. The kabuli v1.0 chickpea genome was chosen because of superior assembly and reduced fragmentation compared to the desi chickpea genome (Jain et al. 2013; Varshney et al. 2013). The kabuli v1.0 genome assembly contains approximately 187 disease resistance gene homologs, which has been reported to be relatively less than other legume species such as *M. truncatula* and soybean (Varshney et al. 2013). A subset of these disease resistance genes were found to be physically located within the identified major QTL *QRBprrsi01* and *QYBprrsi01* on chromosome 3 and the *QRBprrsi04* and *QYBprrsi02* region on chromosome 6, as shown in Table 8. Recently, candidate genes involved in R-gene-mediated PRR resistance in soybean have been identified based on a combination of fine-mapping of a known major QTL region and RNA-seq (Li et al. 2016). We performed an analysis with the predicted candidate genes listed in Table 8 using the Legume IP database (Li et al. 2012) to identify orthologous gene sequences in related legume species such as soybean. Amongst the chickpea candidates that have been identified to be located in QTL regions, Ca_00742 (annotated as a wall-associated receptor kinase, WAK) was found to be orthologous to the soybean gene *Glyma03g34600* which has been associated with R-gene-mediated PRR resistance in this species. WAK proteins belong to the group of receptor-like kinases and provide a linkage between the inner and outer surroundings of the plant cell wall (Wagner and Kohorn 2001). WAK proteins are known to be involved in regulating the cell wall–cytoskeleton interface during plant defence response following pathogen attack and thereby conferring resistance in the host plant (Nivedita and Upadhyaya 2017). The potential role of WAK proteins in resistance to PRR in chickpea needs to be explored to verify the role in this system.

It is known that quantitative or partial resistance in plants is contributed by genes associated with QTL regions with either major or minor effect, which can also be additive. Poland et al. 2009 proposed that partial resistance loci in plant pathosystems may be governed by genes functioning in the regulation of plant development, plant defence signalling pathways, R-gene clusters or indeed novel, presently uncharacterised genes. In this study a number of genes physically co-located with QTL *QRBprrsi01, QYBprrsi01, QRBprrsi04* and *QYBprrsi02* have been identified with functional roles consistent with the expression of partial resistance against PRR in chickpea. These include genes in the NBS-LRR class, leucine-rich repeat receptor-like protein kinases and zinc finger A20 and AN1 domain-containing stress-associated proteins (Table 8). Therefore, these genomic regions could be of importance for targeted introgression into elite chickpea breeding lines or released varieties to enhance PRR resistance. However, as this is the first detailed genetic

Table 8 Candidate genes predicted to be involved in plant defence responses located in the physical interval of the major PRR-resistant *SI-t3* QTL on chromosomes 3 and 6

Kabuli Gene ID[a]	Chromosome	Gene orthologs in soybean Gene Model Release 1.1	Predicted protein function[b]
Ca_00754	3	Glyma03g34750; Glyma10g07500; Glyma13g21380; Glyma19g37430	Leucine-rich repeat protein kinase family
Ca_00742	3	**Glyma03g34600**; Glyma19g37290	Wall-associated receptor kinase-like protein
Ca_16472	6	Glyma11g19110; Glyma12g09310	Serine/threonine-protein phosphatase 2A activator
Ca_16466	6	NA	NBS-LRR protein;
Ca_16487	6	Glyma11g19013; Glyma12g09445	F-box/LRR-repeat protein
Ca_16478	6	NA	Zinc finger A20 and AN1 domain-containing stress-associated protein
Ca_22057	6	Glyma12g00960	Leucine-rich repeat receptor-like protein kinase family
Ca_15183	6	Glyma11g18340; Glyma12g09910; Glyma12g31330; Glyma13g38980	Serine/Threonine-kinase Nek4

[a]Chickpea reference genome v.1. b according to chickpea genome annotation with UniRef90. The orthologous gene associated with PRR resistance in soybean is in bold. NA—not available

study of PRR resistance in chickpea, future ongoing research will involve the validation of molecular markers associated with PRR resistance QTL in a large collection of Australian chickpea breeding germplasm. The aim of this work will be to determine the degree of association of the SNP markers with plant resistance and therefore, the efficacy of approaches to adopt and implement a strategy for marker-assisted selection in the Australian breeding programme. The findings of this study can also be used to progress a fine-mapping approach to improve resolution around identified QTL and positionally clone the exact genetic factors associated with PRR resistance in chickpea. The evidence for distinct sources of resistance derived from *C. arietinum* and *C. echinospermum* will be further elucidated by ongoing molecular work, but does nonetheless now indicate that pyramiding these genomic regions will be an important strategy in breeding for improved PRR resistance.

Cultivated chickpea is a crop with limited genetic diversity (Berger et al. 2003), but the utilisation of related species to address adaptation to emerging disease threats, changing demands posed by domestic and export markets and the impact of climate change, has been challenging. This has in part been due to a lack of availability of systematic and documented collections of wild relatives that represent the full geographical range of these species. It has also been due to a lack of genomics resources and tools so that pre-breeders and breeders can make informed use of potentially advantageous variation in wild species to make step change improvements to key traits in varieties. The last few years have seen marked increase in the scale of related species collections and the development of pre-breeding populations and genomics resources to underpin their exploitation in breeding (von Wettberg et al. 2018). Whilst the challenges associated with the use of wild species in crop improvement are significant, these resources are providing detailed knowledge on the extent of phenotypic variation and thereby allowing the identification of rare alleles, the broad and fine-scale genome structural relationships that define the key species differences, and the overall differences in genetic complexity of traits identified between wild and cultivated species. Advancements in wide-crossing techniques such as embryo culture and the application of new methods to decrease generation time and therefore the breeding cycle in chickpea (Croser et al. 2018) will accelerate the introgression of multiple resistance QTL into single genotypes and facilitate the development of durable resistance to this significant pathogen of chickpea.

Author contribution statement SB, KM, KH, AA, YL and TS were involved in the design of phenotyping experiments. KM developed the oospore inoculation method. SB developed the disease assessment method and carried out phenotyping. AA assisted with phenotyping. AA and YL were involved in genotyping. AA and JT were involved in the analysis of phenotypic data, construction of linkage maps and QTL analysis. AA and JT drafted the manuscript. All authors reviewed and revised the manuscript. KH and TS supervised the project.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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Link to Chapter 4

Although sources of PRR resistance have been identified in chickpea, the molecular mechanism associated with the expression of resistance is not yet determined. In order to study the molecular aspects of PRR resistance in chickpea, a sensitive and a reliable phenotyping method under controlled environments is needed. Current PRR phenotyping methods in chickpea are field-based and rely on the application of mycelium slurries or oospore inoculum solutions. These methods can be challenging because of environmental variation and because of the need to mimic natural cycles of flooding and draining required for PRR disease development. Field treatments also lack the ability to specifically control the exact timing of infection which is critical when sampling plant tissues to study the early molecular response in chickpea to *P. medicaginis*. This study describes the development of an *in planta* PRR infection system that can be used as a high-throughput screening tool to phenotype chickpea genotypes, and also to provide clean, soil free plant tissue suitable for molecular analysis. Additionally, the study describes key traits such as KME-survival and canker length linked to PRR resistance that can be used for selection in breeding. Strong genetic correlation was observed between PRR resistance traits from both hydroponics and field-based experiments. This work was published in Plant Methods during my PhD research candidature as follows: Amritha Amalraj, Julian Taylor, Tim Sutton, A hydroponics based high throughput screening system for Phytophthora root rot resistance in chickpea (*Cicer arietinum* L.). Plant Methods volume 15, Article number: 82 (2019).

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Contribution to the Paper	Contributed to conceptualization, design and conduct of all experiments, data analysis, result interpretation and drafting of the manuscript.
Overall percentage (%)	85%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
Signature	Date 26/08/2019

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Julian Taylor
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A hydroponics based high throughput screening system for Phytophthora root rot resistance in chickpea (*Cicer arietinum* L.)

Amritha Amalraj[1], Julian Taylor[1] and Tim Sutton[1,2*]

Abstract

Background: Phytophthora root rot (PRR) caused by *P. medicaginis* is a major soil borne disease in chickpea growing regions of Australia. Sources of resistance have been identified in both cultivated and wild *Cicer* species. However, the molecular basis underlying PRR resistance is not known. Current phenotyping methods rely on mycelium slurry or oospore inoculum. Sensitive and reliable methods are desirable to study variation for PRR resistance in chickpea and allow for a controlled inoculation process to better capture early defence responses following PRR infection.

Results: In this study, a procedure for *P. medicaginis* zoospore production was standardized and used as the inoculum to develop a hydroponics based *in planta* infection method to screen chickpea genotypes with established levels of PRR resistance. The efficiency of the system was both qualitatively validated based on observation of characteristic PRR symptom development, and quantitatively validated based on the amount of pathogen DNA in roots. This system was scaled up to screen two biparental mapping populations previously developed for PRR studies. For each of the screenings, plant survival time was measured after inoculation and used to derive Kaplan–Meier estimates of plant survival (KME-survival). KME-survival and canker length were then selected as phenotypic traits associated with PRR resistance. Genetic analysis of these traits was conducted which identified quantitative trait loci (QTL). Additionally, these hydroponic traits and a set of previously published plant survival traits obtained from multiple PRR field experiments were combined in a model-based correlation analysis. The results suggest that the underlying genetic basis for plant survival during PRR infection within hydroponics and field disease environments is linked. The QTL *QRBprrkms03* and *QRBprrck03* on chromosome 4 identified for the traits KME-survival and canker length, respectively, correspond to the same region reported for PRR resistance in a field disease experiment.

Conclusion: A hydroponics based screening system will facilitate reliable and rapid screening in both small- and large-scale experiments to study PRR disease in chickpea. It can be applied in chickpea breeding programs to screen for PRR resistance and classify the virulence of new and existing *P. medicaginis* isolates.

Keywords: PRR resistance in chickpea, *P. medicaginis* zoospores production, PRR phenotyping method, Hydroponics screening system, Plant survival traits, Kaplan–Meier (KM) estimates of survival probability, Linear mixed model, Whole genome QTL analysis, Combined hydroponics and field trait model

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Background

Chickpea (*Cicer arietinum* L.) is an important legume crop with high nutritional value, mostly cultivated in arid and semi-arid regions of the world. Globally, Australia is the second largest chickpea producing country after India [1]. In Australia, chickpea is mainly grown in northern New South Wales and southern Queensland. Annually, in Australia approximately 90% of the chickpea produced is exported to developing countries like India and the subcontinent where demand exceeds the supply. Chickpea is grown as a rotational crop for its ability to fix atmospheric nitrogen through symbiotic fixation [2]. Susceptibility to soil borne pathogens is a major constraint to the expansion of chickpea production in Australia.

Phytophthora root rot (PRR) caused by an oomycete *Phytophthora medicaginis* E. M. Hansen and D. P. Maxwell is an economically important soil borne disease, causing significant yield loss in the major chickpea growing regions of Australia [3]. The occurrence of the disease is mainly reported in regions of high rainfall, poorly drained soils or following periods of prolonged soil saturation. PRR costs up to $8.2 million per year to chickpea growers in Australia, indicating the need to develop genetic or management solutions [4].

The pathogen *P. medicaginis,* survives as thick-walled oospores in soils of heavy texture, infected plant tissues over a long time period. During favourable conditions such as flooding from either irrigation or following a rainfall event, oospores develop into motile zoospores and are released into the soil. These zoospores swim towards the root of the susceptible host plant and on reaching the root surface, germinate to produce hyphae which invade the roots thus enabling further cycles of infection to occur in the host plant [5]. These zoospores are capable of swimming only a few millimetres and consequently long-distance dispersion of PRR infection is a result of physical movement of soil and water contaminated with oospores during flooding, irrigation or by machinery [6].

P. medicaginis has been reported to infect both lucerne and chickpea [7]. The pathogen can infect chickpea at any stage of plant development. The symptoms of PRR in chickpea include seed decay at germination, the decay of lateral and tap roots, defoliation from ground up, chlorosis, and wilting of the entire plant leading to plant death. Dark brown to black lesions (canker) often girdle the taproots of PRR-infected chickpea plants and result in plants being easily dislodged from the soil. In young plants, lesions can extend up the stem above ground level. When there is mild infection, the affected plant recovers by producing new roots from the upper part of the taproot [3].

Once the plant is infected there is nothing that a grower can do to manage the loss from PRR. Metalaxyl-based seed dressings are used before infection, but they are expensive and can only provide protection for 6 to 8 weeks. The only effective way to minimise the incidence of the disease is through pre-sowing decisions and assessment of disease risk for individual paddocks. Breeding for resistance is the desired option to control PRR in chickpea. Moderate field resistance has been identified in a chickpea landrace ICC11870 [3] and the Australian chickpea breeding program has incorporated this resistance into a range of cultivated *C. arietinum* varieties such as Yorker. Furthermore, a high level of resistance has been identified in a wild relative of chickpea (*C. echinospermum*) [3] and has been incorporated into a *C. arietinum* background to generate interspecific hybrids. These chickpea genotypes have been used as resistant parents to develop both intraspecific and interspecific recombinant inbred line (RIL) mapping populations within the Australian chickpea breeding program for the genetic analysis of PRR resistance in chickpea [8]. Genomic regions associated with PRR resistance were identified in a field-based study conducted in three target environments, classified as providing low, moderate and high disease pressure [8]. Additionally, the study reported independent sources of PRR resistance in cultivated and wild *Cicer* species. However, the molecular mechanisms underlying PRR resistance in chickpea are not yet clearly understood.

In order to study the molecular mechanisms underlying the plant response to PRR infection, there is a need to establish controlled environment methods that provide control over the precise timing of infection and consistent inoculum distribution across multiple genotypes. Knights et al. [3] developed a soil-based cup method to screen several wild *Cicer* species for PRR resistance in a greenhouse. Seedlings were grown individually in plastic cups containing 10% (w/w) soil-sand and inoculated with *P. medicaginis* oospores. The seedlings were subjected to repeated cycles of flooding with water (40 h) and draining (56 h), to induce the development of zoospores from the oospore inoculum and initiate PRR infection. Plants were scored for survival time after inoculation. The study compared findings from the cup method with field experiments and reported a significant discrepancy in PRR resistance rankings of genotypes [3]. These greenhouse experiments failed to reveal differences in PRR resistance in the chickpea genotypes used as check genotypes. The reasons for the variable results in the greenhouse experiment were explained in the context of the findings of Dale and Irwin [9]. They suggest resistance to *P. medicaginis* that is effective in chickpea roots may not be expressed if the infection occurred through stomata near the soil

Fig. 1 Phenotypic variation for PRR resistance in chickpea grown in hydroponics at 9 days after inoculation with *P. medicaginis* zoospores. **a** Wilting symptoms (04067-81-2-1-1 on left, Rupali on right) chickpea genotypes grown in hydroponics at 9 days after inoculation with *P. medicaginis* zoospores. **b** Root symptoms (04067-81-2-1-1 on left, Rupali on right). **c** Lateral and tap root death in Rupali

surface. Fundamentally, greenhouse seedling tests differ in many ways from the field disease experiments that typically cover more growth stages of chickpea and therefore may be less sensitive in resolving differences in resistance between genotypes [3]. This suggests that the choice of inoculum and the methodology used in these seedling tests has a major influence in disease distribution and in the expression of resistance in a given host plant. In other phytophthora pathosystems, such as for soybean, PRR resistance is studied using tests that can cause localized infection in wounded and non-wounded cotyledons or roots [10–12], layer tests [13–15] and rice screen tests [16]. The application of these methods is limited to a smaller number of genotypes and therefore not amenable to screening of breeding populations. Thus, there is a need for the development of an efficient, reproducible, higher throughput phenotyping approach to deriving a quantitative trait that is closely associated with the resistance phenotype expressing the same resistance observed in natural disease environment.

Given the epidemiology of the pathogen and specificity of the pathosystem, the main objective of this research was to develop a hydroponics based screening system using zoospore inoculation to control the timing and rate of infection that could be applied in breeding. An important specific objective was the derivation, quantification and analysis of PRR resistance related traits from the developed screening system. This included the individual and co-analysis of PRR traits using modern linear mixed modelling approaches that appropriately quantified environmental variation and accurately estimated the underlying genetic potential of PRR resistance across each genotype. Extended formulations of these models were then used to conduct QTL analysis and identify genomic regions associated with PRR resistance that were then compared to published results from recent PRR field trial research. A final objective was to conduct a multi-trait multi-environment analysis and directly assess the genetic connection between PRR traits derived from hydroponic screening and previous published plant survival traits obtained from field experiments.

Results

PRR symptom development in hydroponics based *in planta* infection system

Symptoms characteristic of PRR such as brown to black lesions and wilting were observed in the PRR susceptible chickpea variety Rupali at 9 days after inoculation (Fig. 1). The PRR resistant breeding line 04067-81-2-1-1 showed no symptoms and remained healthy following inoculation until the termination of the experiment. The presence of *P. medicaginis* in chickpea roots harvested from the varieties

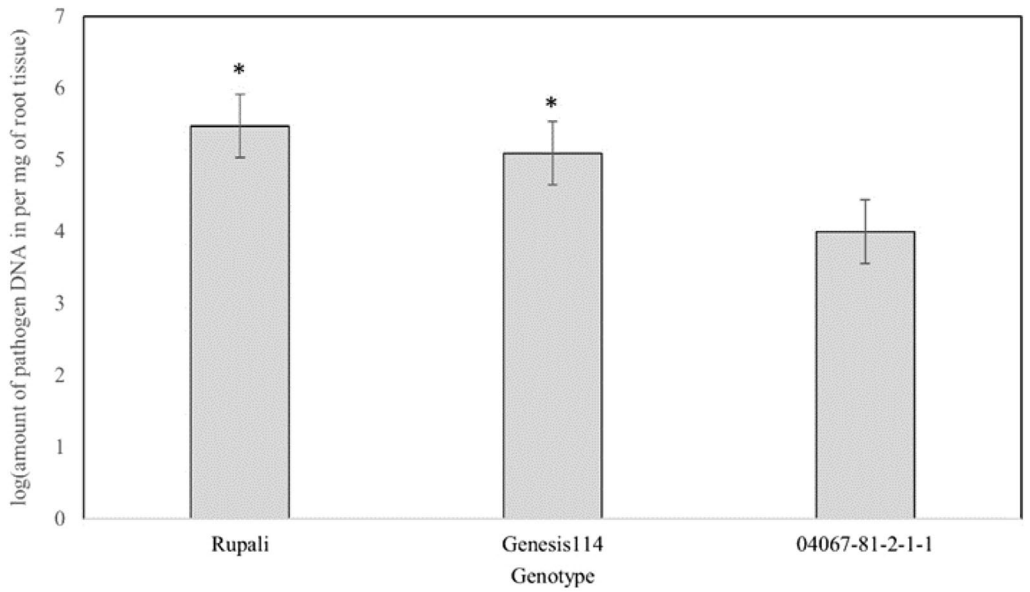

Fig. 2 Molecular quantification of PRR DNA in roots of chickpea genotypes with known levels of PRR resistance. The log-transformed values of the amounts of *P. medicaginis* DNA determined by a TaqMan MGB assay is presented. Error bars represent the standard error of the mean of six biological replicates. Asterisks indicate significant differences compared to PRR-resistant 04067-81-2-1-1 at the 5% ($P < 0.05$) significance level

Rupali, Genesis 114 and breeding line 04067-81-2-1-1 was confirmed and quantified using a TaqMan MGB assay specific for *P. medicaginis* DNA. The amount of *P. medicaginis* DNA was found to be relatively high in the PRR-susceptible variety Rupali and in the moderately susceptible variety Genesis 114 compared to the PRR-resistant breeding line 04067-81-2-1-1 (Fig. 2; $P < 0.05$). *P. medicaginis* DNA quantification in each chickpea genotype was in accordance with observations of PRR symptom development and with known levels of PRR resistance of these genotypes from field experiments and trials.

Response of RIL mapping populations to *P. medicaginis* and disease progression in hydroponics PRR screening system

To understand disease progression in the two RIL populations, the interval time of death and the canker length at the close of the experiment were recorded for each plant. From the known time of death, KME-survival probability was then derived for each plant to use for exploratory and quantitative analyses. The PRR moderately resistant parent of the YG population, Yorker, showed lower KME-survival values and short canker length while the PRR susceptible parent, Genesis 114, showed a slightly higher KME-survival value and a longer canker length (Table 1). Similarly, in the RB population,

Table 1 Parental and population means for the KME-survival and canker length in each RIL population screened for PRR resistance in hydroponics

Trait	Parental mean		RIL population		
	Yorker	Genesis 114	Mean	Range	Heritability H^2
KME-survival	0.334	0.457	0.475	0.058–0.995	0.427
Canker length (mm)	81.42	101.63	89.38	0–158.0	0.159
Trait	**Parental mean**		**RIL population**		
	Rupali	**04067-81-2-1-1**	**Mean**	**Range**	**Heritability H^2**
KME-survival	0.676	0.243	0.484	0.243–0.943	0.448
Canker length (mm)	23.437	4.559	8.300	0–50.0	0.421

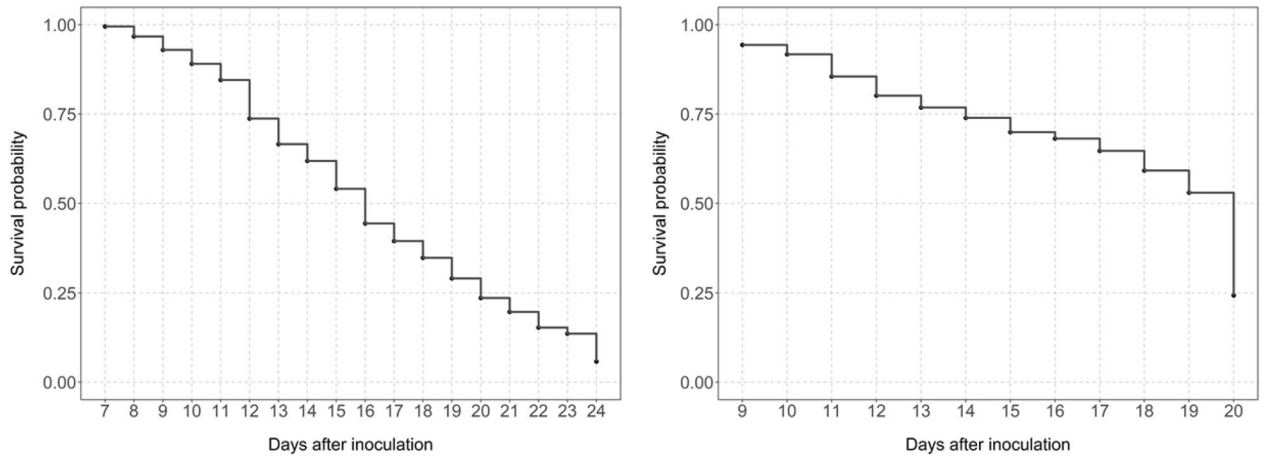

Fig. 3 KME-survival showing progress of PRR disease caused by *P. medicaginis* in YG (left) and RB (right) chickpea RIL mapping populations grown in hydroponics system

the breeding line 04067-81-2-1-1 which is known to exhibit higher PRR resistance showed a lower KME-survival value and a short canker length compared to the PRR susceptible parent Rupali. The population means for YG and RB for the KME-survival were 0.475 and 0.484, respectively, while the population mean and values for the canker length trait (Table 1) were found to be in general high for the YG population compared to that of the RB population.

To visualise the progression of PRR disease over the duration of the experiments the KME-survival were plotted, based on the initial observation of PRR symptoms after inoculation until the termination of the experiment (Fig. 3). The termination of the experiment was based on the death of the PRR susceptible parental genotype included in each of the RIL mapping population. In the YG population, it was marked by the death of the PRR susceptible variety, Genesis 114 and in the RB population it was marked by the death of PRR susceptible variety Rupali. For the YG population, there was a linear reduction in survival probability over time and survival approached zero at the termination of the experiment. In the RB population, this linear reduction in survival probability was less pronounced for most of the experiment i.e. 18 days post inoculation but then the survival probability sharply reduced from 0.5 to 0.25 in the final interval before the experiment terminated.

To visualise the spatial progression of PRR disease across the experiment, heat maps were plotted for each RIL population to graphically display the KME-survival and canker length at the termination of the experiment (Fig. 4 and Fig. 5). In the heat maps displaying KME-survival, blue areas indicate low KM estimate values and consequently higher resistance to disease while redder areas indicate high KME-survival and plants with increased susceptibility to the disease (Figs. 4 and 5). Similarly, in the heat map displaying the canker length of plants, blue areas indicate negligible lesion length suggesting high resistance to PRR and redder areas indicate longer lesion length and increased susceptibility to PRR (Figs. 4 and 5). In the RB population, lower KME-survival and shorter relative canker lengths (bluer areas in Fig. 5) were more pronounced compared to the YG population, using the same inoculum concentration.

Relationship between phenotypic traits measured in hydroponics

For each mapping population the BLUPs of the KME-survival and canker length were extracted from the BLMM. A strong linear genetic relationship exists between the traits (Fig. 6) in each population with model based genetic correlation estimates of 0.642 and 0.917 in YG and RB mapping populations (Table 3), respectively. The estimated broad sense heritability values (H^2) values for each trait (Table 1) were found to be adequate in the interspecific mapping population RB. Heritability for KME-survival was also found to be adequate in the YG population but reduced for canker length. Despite the varied heritability values, the high estimated genetic correlation between the two traits observed in both the intra and interspecific mapping populations indicates a similar genetic expression of the traits in the presence of PRR disease.

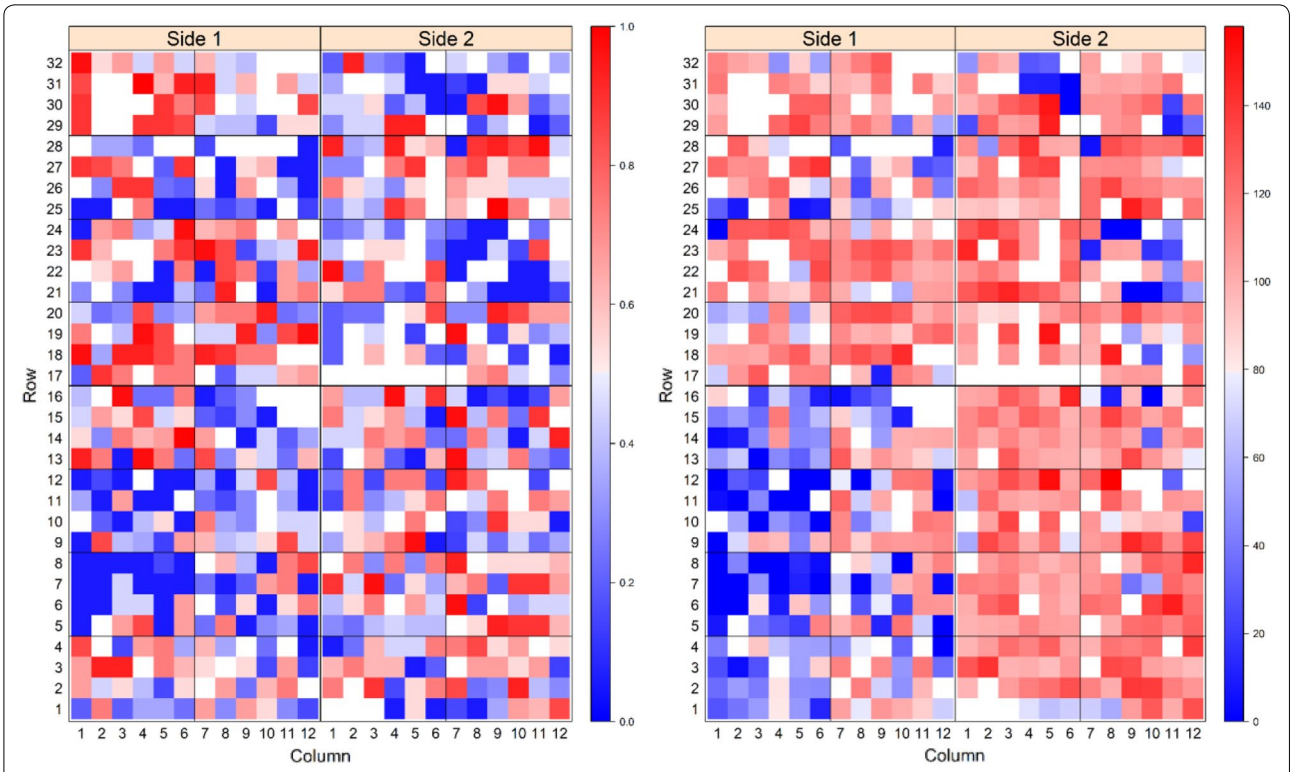

Fig. 4 Heat map plots showing prevalence of PRR disease at the close of the experiment in the YG population based on the traits KME-survival (left) and canker length (right) data. For the KME-survival heat map blue areas indicate longer time of survival and red areas indicate short survival time. Blue areas on the heat map plot for canker length indicate no or negligible canker and red areas indicate longer length of canker

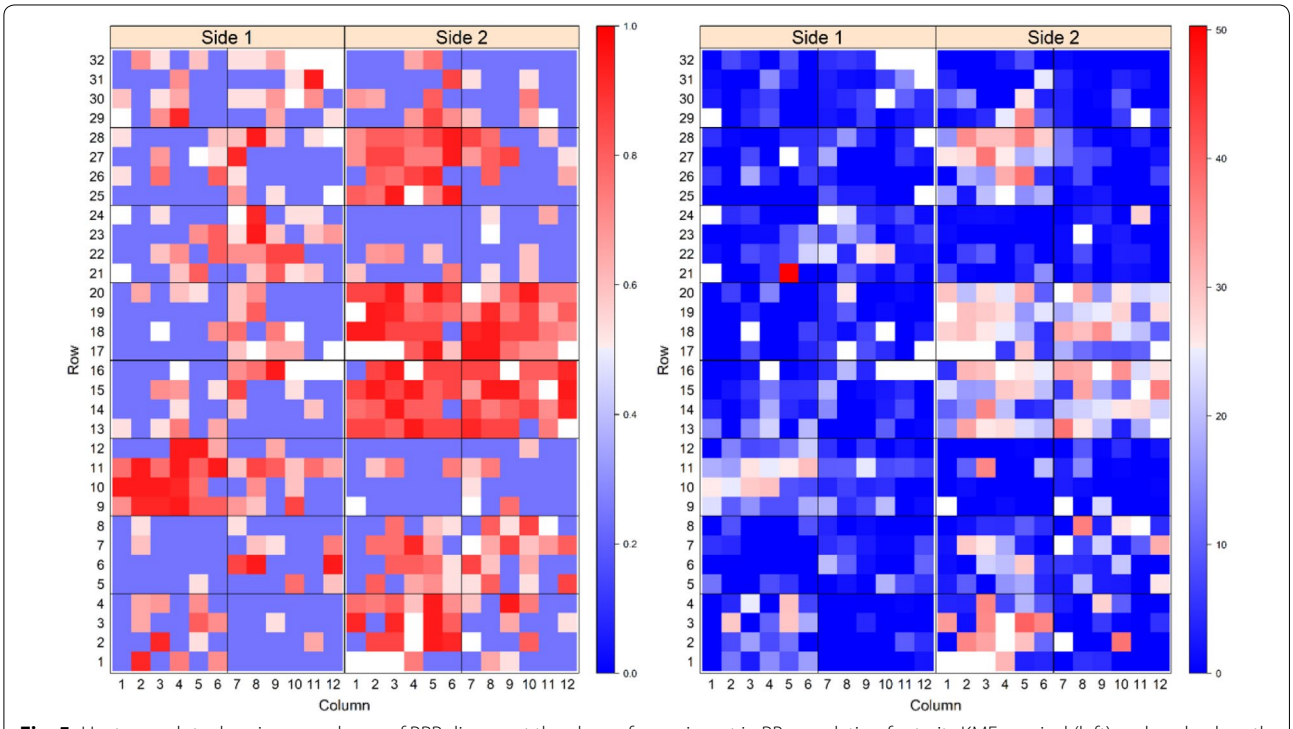

Fig. 5 Heatmap plots showing prevalence of PRR disease at the close of experiment in RB population for traits KME-survival (left) and canker length (right) data. For the KME-survival heat map blue areas indicate longer survival time and red areas indicate shorter survival time. Blue areas on the heat map plot for canker length indicate no or negligible canker and red areas indicate longer length of canker

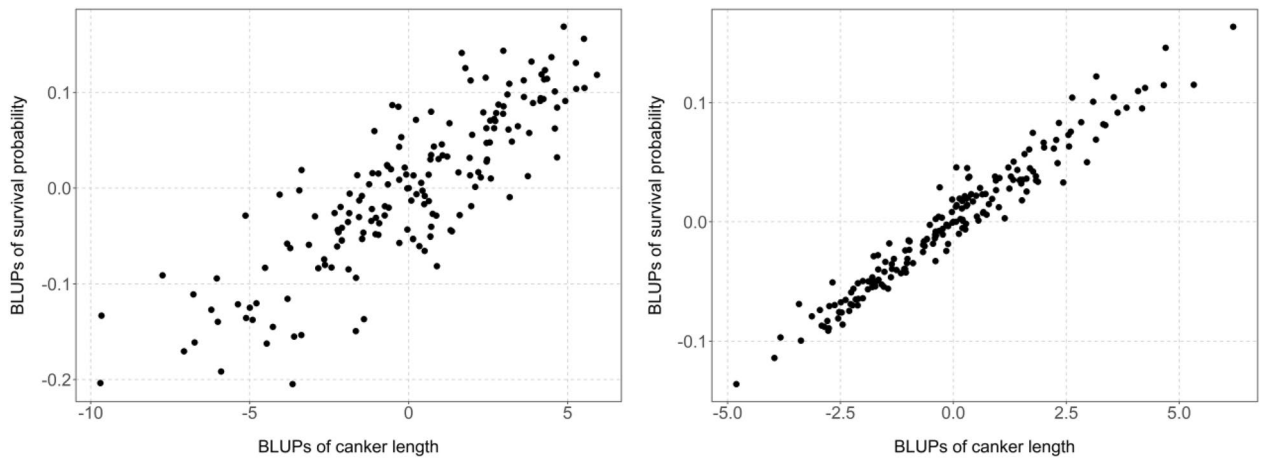

Fig. 6 Correlation plots of the BLUPs for KME-survival and canker length extracted from the bivariate linear mixed model. YG (left) and RB (right) RIL mapping populations

QTL analyses for YG population

QTL analysis conducted using whole genome average interval mapping (WGAIM) identified genomic regions associated with PRR resistance for KME-survival obtained from hydroponics phenotyping of the YG RIL population (Table 2). For the KME-survival, one major QTL *QYGprrkms01* on chromosome 7 explaining 16.3% of genetic variation was identified to be associated with PRR resistance. No QTL were identified for canker length in the YG population, suggesting inadequate genetic variation. This lack of genetic variation is also indicated by a reduced heritability value (H^2) of 0.159.

QTL analyses for RB population

In the interspecific mapping population RB, QTL analyses identified genomic regions associated with PRR resistance for both hydroponic traits (Table 2). For KME-survival, three major QTL on chromosomes 4, 6 and 7 associated with PRR resistance were found to be significant accounting for 12.6%, 27.5% and 14.6% of genetic variation, respectively. Two minor QTL on chromosomes 2 and 3 were also identified. Similarly, for canker length, four QTL on chromosomes 3, 4, 6 and 7 associated with PRR resistance were identified accounting for 21.2%, 14.9%, 12.9% and 13.6% of genetic variation, respectively. For the QTL identified on chromosomes 3, 4 and 6, the resistance source is contributed by the high PRR

Table 2 QTL associated with the traits KME-survival and canker length for PRR resistance in YG and RB RIL mapping populations screened in hydroponics experiment

Population	Trait	Chr.	QTL name	Interval	Distance (cM)	Size[a]	p.value	%Var	LOD
YG	KME-survival	C7	*QYGprrkms01*	*9001SNP7-31: 9001SNP7-32*	0.0–1.22	−0.271	0.000	16.3	2.668
RB	KME-survival	C2	*QRBprrkms01*	*RB-SNP2-32: RB-SNP2-31*	1.5–16.49	0.141	0.001	8.1	2.199
		C3	*QRBprrkms02*	*RB-SNP3-9: RB-SNP3-97*	54.66–58.84	0.153	0.001	9.6	2.627
		C4	*QRBprrkms03*	*RB-SNP-79(C): RB-SNP-72(C)*	80.53–81.7	0.176	0.000	12.6	2.881
		C6	*QRBprrkms04*	*RB-SNP6-183(C): RB-SNP6-417(C)*	74.66–75.82	0.259	0.000	27.5	7.366
		C7	*QRBprrkms05*	*RB-SNP7-30: RB-SNP-scf136(C)*	95.25–112.92	−0.188	0.000	14.5	3.634
	Canker length	C2	*QRBprrck01*	*RB-SNP2-6: RB-SNP2-7*	77.49–79.04	1.031	0.000	8.5	2.403
		C3	*QRBprrck02*	*RB-SNP3-100(C): RB-SNP3-105*	62.34–63.71	1.629	0.000	21.2	5.902
		C4	*QRBprrck03*	*RB-SNP-79(C): RB-SNP-72(C)*	80.53–81.70	1.366	0.000	14.9	4.378
		C6	*QRBprrck04*	*RB-SNP-scf200(C): RB-SNP6-322(C)*	83.31–84.35	1.274	0.000	12.9	3.505
		C7	*QRBprrck05*	*RB-SNP7-30: RB-SNP-scf136(C)*	95.25–112.92	−1.305	0.000	13.6	2.859

QTL interval names with (C) indicate several co-locating markers at the loci

[a] Positive and negative values indicate that Yorker and Genesis 114 alleles increased the phenotypic values in the YG population, and 04067-81-2-1-1 and Rupali alleles in the RB population, respectively

Table 3 Estimated genetic correlation from the fitted multi-environment model for KME-survival and canker length in each of the two RIL mapping population

	Experiment	2014 rainfed	2015 rainfed	2015 irrigated	KME-survival
YG					
Survival index	2014 rainfed	0.282			
	2015 rainfed	0.442	0.442		
	2015 irrigated	0.388	0.819	0.454	
KME-survival	Hydroponics	0.009	0.079	0.135	
Canker length	Hydroponics	−0.165	−0.221	−0.101	0.642
RB					
Survival index	2014 rainfed	0.883			
	2015 rainfed	0.890			
	2015 irrigated	0.833	0.921		
KME-survival	Hydroponics	−0.781	−0.557	−0.662	
Canker length	Hydroponics	−0.853	−0.597	−0.705	0.917

resistant parental genotype 04067-81-2-1-1 derived from *C. echinospermum*. The genomic regions *QRBprrkms03* and *QRBprrck03* on chromosome 4 and *QRBprrkms05* and *QRBprrck05* on chromosome 7 co-locate, confirming a genetic inter-relatedness between the hydroponic traits in association to PRR resistance. *QRBprrkms02* and *QRBprrck02* on chromosome 3 and *QRBprrkms04* and *QRBprrck04* on chromosome 6 identified for the traits KME-survival and canker length were found to be in similar genetic intervals.

Relationship between phenotypes in hydroponics experiment and field experiments

The estimated genetic correlation matrix was extracted from the fitted MVE-LMM and broadly shows a negative relationship between the hydroponics phenotypic traits and the plant survival traits collected from the multiple field environments (Table 3) of Amalraj et al. [8]. For the RB population, there were strong negative estimated genetic correlations between the plant survival trait from the 2014 rainfed field experiment and the two traits measured in hydroponics (−0.781 for the KME-survival trait and −0.853 for canker length trait. This indicates, that in the presence of PRR disease, the underlying genetic basis for plant survival in the controlled environment is linked to plant survival in the field. The strength of these negative correlations was reduced between the hydroponics traits and the plant survival trait measured in 2015 rainfed and 2015 irrigated field experiments (Table 3). In the intraspecific YG population, there were consistently lower estimated genetic correlations between hydroponics traits and plant survival traits measured in all field experiments. This may be due to reduced range in the levels of PRR resistance between the parental genotypes Yorker and Genesis 114 used to develop the YG mapping population [8].

Discussion

In this study, we have developed a scalable, hydroponics based phenotyping method for PRR disease screening, using zoospore inoculation. Results from the genetic analyses of the hydroponic phenotypic traits as well as combined hydroponic and field model-based correlation analysis, show there is an underlying genetic connection between hydroponic PRR survival traits derived using this newly developed screening method and field PRR survival traits from previously published field-based experiments. This method can overcome the limitations imposed by current PRR screening systems by reproducing the natural course of PRR infection, wherein zoospores can freely access the roots of the host chickpea plants. The use of zoospore as the inoculum is considered to be beneficial as it can immediately infect host plants in the system thereby eliminating the conditions such as flooding and draining needed for the development of phytophthora pathogen to cause PRR infection. The flooding and draining methodology can potentially introduce irregularity in the PRR disease development across a large number of genotypes that could ultimately lead to inappropriate expression of resistance in host chickpea plants. Thus, the zoospore inoculum is considered to be advantageous in maintaining the virulence pattern of the pathogen (as reported for, *P. sojae* isolates [17]), which is essential for the appropriate expression of host resistance.

An important factor to be considered when assessing PRR resistance in controlled systems is the choice of isolate used [18]. The chosen isolate should have compatible interaction with all chickpea genotypes included in the study, to generate an appropriate disease pressure. In an unpublished (Sean Bithell, personal communication) inoculated glasshouse experiment for the testing of

phytophthora isolates on the parental chickpea genotypes of the two RIL mapping populations, the isolate 1129-1 showed a pathogen–host interaction profile (in terms of plant mortality) similar to that of a mix of 10 *P. medicaginis* isolates used in field disease experiments and trials within the breeding program. For this reason, the isolate 1129-1 (DAR 66075) collected from Yetman, New South Wales, Australia [19], which has been reported to infect chickpea and *Hedysarum* spp., was used in this study. Initial pilot-scale testing confirmed the compatible interactions of the chickpea genotypes Rupali, Genesis 114 and breeding line 04067-81-2-1-1 with the *P. medicaginis* isolate 1129-1. These genotypes are the parents of two RIL mapping populations, RB and YG, developed for genetic studies of chickpea PRR responses as described in Amalraj et al. [8].

To test the efficiency of the hydroponics screening system to cause PRR infection in chickpea, qualitative and quantitative assessments were made of the responses of three genotypes with contrasting PRR disease resistance levels in the field. The hydroponics assay showed good discrimination between these genotypes (Table 1 and Fig. 2). Molecular quantification of the amounts of *P. medicaginis* DNA in chickpea roots using a previously developed TaqMan MGB assay [20] for *P. medicaginis* provided quantitative evidence of the phenotypic responses of the host plant genotypes to PRR infection (Fig. 2). The TaqMan MGB assay is a real-time fluorescent PCR assay using a set of specific primers and a fluorochrome-labelled probe. Primers used were developed from a sequence-characterized DNA marker (SCAR) that is specific only for *P. medicaginis* [21]. The assay demonstrated *P. medicaginis* infection in the zoospore-inoculated plants, and ranked disease severity in the chickpea genotypes similarly to visual assessments of plant survival and stem canker length. However, for practical reasons such as time involved and assay cost, it was determined that TaqMan DNA assay would not be the preferred choice to phenotype large number of breeding populations.

Scaling up of the hydroponics system allowed for high-throughput screening of a large number of genotypes to evaluate PRR resistance with an aim to identify linked quantitative traits that could potentially be used to assist selection in chickpea breeding. We screened the two RIL mapping populations, RB and YG, in consecutive experiments. Disease assessments were made during early stages of disease progression because older chickpea plants are able to survive by generating new roots from the upper main tap root [6].

Quantitative disease resistance (QDR) conditioned by a few to many genes is the preferred type of resistance in most crop breeding programs because of its increased durability [22]. However, phenotyping for quantitative resistance is challenging due to the polygenic nature of the phenotype and requires accurate methods for disease assessment with adequate replication. For some pathosystems, such as *P. medicaginis*-chickpea, where there is no conclusive evidence for race-based resistance, breeding for QDR is the only option to limit the impact of the disease and prevent yield loss. This involves identification of QTL associated with disease resistance, using accurate measurements of the disease to facilitate marker-assisted selection. The hydroponics phenotyping experiment in this study provided a basis for objectively measuring and deriving two quantitative traits linked to PRR resistance in chickpea: KME-survival and canker length. KME-survival and canker length data were then used in subsequent phenotypic and genetic analysis.

KME-survival and canker length were highly correlated in both the intraspecific (YG) and interspecific (RB) RIL mapping populations (Fig. 6). This is also evident from the co-location of QTL *QRBprrkms03*, *QRBprrck03* on chromosome 4 and *QRBprrkms05*, *QRBprrck05* on chromosome 7 in the RB population. The co-location of these QTL associated with PRR resistance suggests that the same genomic region(s) control the expression of two traits. In the RB population, the major QTL *QRBprrkms03 and QRBprrck03* on chromosome 4 (*RB-SNP-79(C): RB-SNP-72(C))* was also reported to be associated with PRR resistance in chickpea grown under rainfed field conditions [8]. Similarly, the major QTL *QRBprrck04* on chromosome 6 identified in this study is similar to a genetic interval *QRBprrsi04* reported across multiple field experiments from the field-based genetic study [8]. In both cases the resistance source is from the parental genotype 04067-81-2-1-1, a backcross derivative line from *C. echinospermum*.

The similarity of PRR QTL for the traits phenotyped in hydroponics and the field provides evidence of genetic similarity in the plant response to this disease across different environments. This was further supported by model-based correlation analyses, which for the RB RIL population showed a strong negative correlation between KME-survival and canker length from hydroponics and the plant survival trait (survival index) from the field-based genetic study described in Amalraj et al. [8] (Table 3). The genetic correlation between these traits indicates that genetic factors underlying the loci associated with PRR resistance in chickpea may be present in a similar location of the same chromosome. It also suggests that the host–pathogen interaction pattern of the *P. medicaginis* isolate 1129-1 used in this experiment is similar to that of the mix of *P. medicaginis* isolates used in the field based genetic study [8]. In YG population, the

correlation was weak, and this could be because the PRR disease pressure prevailing in the hydroponics experiment seemed to be high for this intraspecific population. Moreover, from the field-based experiment it was shown that Yorker, the resistant parent in the YG population was classified to be moderately resistant to PRR. These moderately resistant chickpea plants become highly susceptible under high inoculum loads and when conditions are favourable for the development of the disease. This is in agreement with YG field-based disease experiments described in Amalraj et al. [8], which showed consistently low to moderate broad sense heritability values across the conditions of low, moderate and high disease pressure. The similar performance of YG in the field and controlled environment experiments exhibiting moderate PRR resistance indicate that a stronger source of PRR resistance is present in RB, where the resistance source is derived from *C. echinospermum*. For PRR, the strategy of using resistance genes/alleles from wild chickpea relatives in breeding has shown it can provide better adaptation under high disease pressure than the currently available variants in the cultivated gene pool. This strategy of crop improvement has been broadly supported recently with a substantial increase in the development of genomic resources and the development of pre-breeding populations in wild relatives of *Cicer* for use in chickpea breeding [23]. In this study, the differences in heritability of the PRR related hydroponic traits obtained from screening RB and YG RIL populations further highlights the differences in genetic complexity of traits identified between wild and cultivated *Cicer* species.

While the hydroponics system described in this study has proven to be reliable for the purpose of studying *P. medicaginis*-chickpea interactions, specific requirements in terms of greenhouse facilities, materials for hydroponics aeration systems for proper oxygenation and nutrient circulation can be modified while maintaining the basic principles conferring its efficiency. The disease pressure to induce the required level of PRR infection can be varied by altering the concentration of compatible *P. medicaginis* zoospores applied as the inoculum. Furthermore, consideration can be given to the use of zoospores of more than one *P. medicaginis* isolate, which could prove to be beneficial in a breeding program when screening large number of diverse genotypes for partial resistance to PRR. The use of zoospore inoculum to cause PRR disease enabled the generation of a uniform disease across the large number of plants grown in hydroponics system. In field disease conditions of PRR, the lesions formed at the base of the chickpea stem may themselves liberate zoospores, forming a secondary source of zoospore inoculum able to reinfect neighbouring chickpeas [24]. Additionally, the use of hydroponics as a phenotyping system enabled the phytophthora zoospores to access both the roots and hypocotyl region of the cotyledon for pathogen invasion. Thus, we report that adopting the right choice of inoculum in suitable plant growth system will facilitate the appropriate expression of virulence and avirulence factors in the pathogen and resistance genes in the host plant under controlled environments. Given that the zoospore is the infecting stage of the phytophthora life cycle, using it as the inoculum of choice can promptly and evenly cause PRR infection in the host plant. In contrast to applying oospores or mycelium slurry, the use of zoospores allows specific control of infection timing which will be beneficial for research aimed at the identification of specific genes or biological processes involved in the temporal plant response to PRR infection. Furthermore, this system proves advantageous for easy sampling of plant tissues like roots free from soil for molecular studies. The similarity in the underlying genetic components of the phenotype traits KME-survival, canker length and survival index using a model-based correlation analysis, support the application of this hydroponic phenotyping method as a viable alternative in breeding to laborious and relatively expensive field-based protocols that are impacted by environmental variation.

Conclusion

The present study describes a hydroponics screening system to study *P. medicaginis*–chickpea interactions using a zoospore inoculation technique. This system has been validated both qualitatively, based on observation of characteristic PRR symptom development, and quantitatively based on the pathogen DNA quantification in roots, thereby making it suitable to conduct both small- and large-scale experiments for PRR resistance. Two phenotyping traits, plant KME-survival and canker length, used to select for PRR resistance showed a high genetic correlation. QTL analysis and model-based correlation analysis has shown this phenotyping method enables the expression of the same PRR resistance in both the field and under controlled environment. Thus, the application of this method will facilitate current and future efforts in breeding for PRR resistance in chickpea, as well as genetics studies aimed at identifying both PRR resistance genes in chickpea and virulence factors in *P. medicaginis*.

Methods

Aim and design of the study

The main objective of this study was to develop a screening system as an efficient phenotyping method under controlled environment to study PRR resistance in chickpea and potentially be applied in breeding. The specific objective included the analysis of PRR resistance related

traits using linear mixed modelling approach to quantify the genetic potential underlying each chickpea genotype and use it to identify QTL associated with PRR resistance in chickpea. Further, a multi-trait multi-environment analysis was used to assess the genetic connection between PRR traits derived from the hydroponics system and previously published plant survival traits obtained from field experiments.

Plant and fungal material

One each of an intraspecific and interspecific F_6 derived RIL mapping population was used in this study. The intraspecific F_6 derived RIL population, herein referred to as YG, consisted of 192 RIL individuals derived from a cross between the moderately PRR resistant chickpea variety Yorker (pedigree: 8507-28H/946-31) and the moderately PRR susceptible variety Genesis 114 (pedigree: FLIP91-150C/FLIP90-124C//S9231). The interspecific F_6 derived population, herein referred to as RB, consisted of 212 RIL individuals derived from a cross between a highly PRR resistant breeding line 04067-81-2-1-1 (a backcross derivative from *C. echinospermum* pedigree: Howzat/ILWC 245//99039-1013) and a PRR susceptible chickpea variety Rupali (pedigree: FLIP84-15C/ICCV88516//Amethyst). The *P. medicaginis* isolate 1129-1, which was recovered from the field in Yetman, New South Wales was used to infect chickpea.

Hydroponics based *in planta* infection

An *in-planta* infection method to screen chickpea for PRR resistance was developed using hydroponically-grown seedlings inoculated with *P. medicaginis* zoospore suspension culture. Three chickpea genotypes were utilised in the initial pilot scale study: PRR susceptible Rupali, moderately susceptible Genesis 114 and the highly PRR resistant breeding line 04067-81-2-1-1 (a backcross derivative from *C. echinospermum*). The experiment was conducted in a temperature-controlled growth room at the University of Adelaide, Waite campus, South Australia, Australia at 20/14 ± 2 °C day/night temperatures with a 16 h photoperiod. Covered plastic pots (4.5 L) were used to grow plants in continuously aerated nutrient solution. The composition of the full-strength nutrient solution, in deionized water, was (mM): 5.0 Ca^{2+}, 5.0 K^{+}, 0.625 NH^{4+}, 0.4 Mg^{2+}, 0.2 Na^{+}, 5.4 SO_4^{2-}, 4.4 NO_3^{-}, 0.2 $H_2PO_4^{-}$, 0.1 SiO_3^{2-}, 0.1 Fe-sequestrene, 0.05 Cl^{-}, 0.025 BO_3^{3-}, 0.002 Mn^{2+}, 0.002 Zn^{2+}, 0.0005 Cu^{2+}, 0.0005 MoO_4^{2-} and 0.001 Ni^{2+} [25]. The solution was buffered with 1.0 mM MES (2-[N-morpholino] ethane sulfonic acid) and adjusted to pH 6.5 using KOH. Seeds were washed with commercial bleach (0.042% (w/v) sodium hypochlorite) added to deionized water for 5 min, rinsed twice in tap water and imbibed at 4 °C for 48 h. Imbibed seeds were then germinated on mesh in 10% aerated nutrient solution in the dark for 3 d and seedlings were then transferred to continuously aerated 25% nutrient solution and exposed to light. Each pot had one healthy individual from each genotype and the pots and position of each genotype was set up in a completely randomised block design with six replicates in control (no inoculation) and in treatment (with inoculation). *P. medicaginis* zoospore suspension culture was added to the treatment pots at a concentration of 1.5×10^5 spores mL^{-1}. Plants were examined daily after inoculation for PRR symptoms including canker development, chlorosis and wilting/death. The experiment was terminated at 16 days after inoculation and repeated three times.

Zoospore production

P. medicaginis zoospore production was based on a protocol developed for zoospores of *P. sojae* and *P. cajani* [26, 27]. One piece of mycelial mat (5 mm) from a pure culture of *P. medicaginis* isolate 1129-1 was used to inoculate 100 mL of sterile 20% (v/v) V8 broth containing 0.2% (w/v) calcium carbonate in a 250 mL conical flask and incubated in the dark at 25 °C for 72 h. The V8 broth was then decanted and replaced with sterile deionized water, which was immediately decanted and replaced with salt solution (per litre: 0.294 g $CaC1_2.2H_20$, 0.247 g $MgSO_4.7H_20$, and 0.075 g KC1). The mycelial culture was washed five times with the salt solution at 30-minute intervals with incubation at 20 °C, and finally incubated in 25% nutrient solution for about 20 h in the dark. The development of zoospores was confirmed by visualisation using an optical microscope. Mycelial growth was removed by centrifugation at 100 x g for 5 minutes and the zoospores were harvested in the nutrient solution. The concentration of the zoospores was determined using a haemocytometer. An average concentration of 8×10^5 zoospores per mL was obtained for the *P. medicaginis* isolate.

Molecular quantification of *P. medicaginis* in chickpea roots grown in in planta infection system

The roots of control and treated chickpea varieties Rupali, Genesis114 and breeding line 04067-81-2-1-1 were harvested 16 h after inoculation, rinsed thoroughly with tap water, patted dry on clean paper towel, weighed and snap-frozen in liquid nitrogen. Frozen roots were freeze-dried and the amount of *P. medicaginis* DNA in chickpea roots quantified using a TaqMan MGB assay developed for *P. medicaginis* at the South Australian Research and Development Institute (SARDI) [20, 28, 29].

Phenotyping two RIL mapping populations (YG and RB) for PRR resistance

Phenotyping experiments to screen two RIL mapping populations were conducted consecutively in the same controlled-environment growth room that was used for the pilot experiment. Seeds from each RIL population, parental genotypes and three check varieties (PBA Slasher, PBA HatTrick and PBA Boundary) were used. Surface-sterilised and imbibed seeds were germinated in plastic pots containing equal volumes of perlite: vermiculite mix covered with aluminium foil. After 7 days the germinated seedlings were transplanted into a scaled-up hydroponics system. Plastic tanks (12.5 L) were used to grow plants in continuously aerated nutrient solution, with each tank holding up to 24 seedlings. The experiment included four replicates of each of the RILs, parental genotypes and check varieties in a completely randomised block design. *P. medicaginis* zoospore suspension culture was added at a final concentration in the nutrient solution of 1.5×10^5 spores mL^{-1} for PRR disease development. The plants were assessed daily for wilting or plant death. The phenotyping experiment was terminated at 20 and 24 days for the RB and YG populations, respectively, based on the time of death of the PRR-susceptible RIL population parent. Stem canker length beginning from the hypocotyl region and proceeding upwards on the stem was measured for each plant using electronic digital 0–150 mm Vernier callipers.

Genotyping data

Genotyping of all RIL progenies including the parental genotypes of YG and RB was performed by Diversity Arrays Technology Pty. Ltd. (Canberra, Australia) using chickpea DArT Seq version 1.0. Further details on the development of the linkage maps for both YG and RB RIL mapping populations and the molecular marker data are provided in Amalraj et al. [8].

Statistical methods

Survival probability calculation

To ensure an effective quantitative measure was used for analyses of plant survival, Kaplan–Meier (KM) estimates of survival probability (KME-survival) [30] were calculated using the examined survival time of each of the plants. Let $t_1, \ldots, t_n$ be the time periods the experiment was examined over. The KM estimate of a plant surviving at time t_i is then

$$S(t_i) = \prod_{i=1}^{n} \left(1 - \frac{d_i}{n_i}\right)$$

where d_i are the number of plants that die during the t_i th time period and n_i are the number of plants at risk at the beginning of time period t_i. The ordered set of KM estimates $S(t_1), \ldots, S(t_n)$ represent an estimate of the true survival function of the population when plants are infected with PRR. KM estimates approaching one signify early time of death and increased disease susceptibility, whereas estimates approaching zero suggest a prolonged survival time and resistance to PRR. This KM estimator also naturally allows censoring of individuals that did not germinate in the initial stages of the experiment through the appropriate reduction of the numbers of individuals at risk in the first time period. No additional transformation was required for this trait in the analysis models that follow.

Hydroponics univariate trait model

For each of the RIL populations, the KME-survival and canker length phenotypic traits were analysed using a linear mixed model (LMM) that partitioned and accounted for genetic and non-genetic sources of variation. Let $\boldsymbol{y} = (y_1, \ldots, y_n)$ be the phenotypic response, then the linear mixed model was defined as

$$\boldsymbol{y} = \boldsymbol{X\tau} + \boldsymbol{Zu} + \boldsymbol{Z}_g\boldsymbol{g} + \boldsymbol{e} \quad (1)$$

where $\boldsymbol{X\tau}$ was the fixed component of the model and contained a population type factor to estimate the overall mean of the progeny population as well as means of the parental and control lines. The term $\boldsymbol{Zu}$ was the random component containing factors to model sources of non-genetic variation including differences between the two sides of the controlled environment as well as differences between tanks containing the isolates used for inoculation. Additional extraneous variation was captured with the residual model error term, $\boldsymbol{e}$, and was assumed to be distributed $\boldsymbol{e} \sim N(\boldsymbol{0}, \sigma^2\boldsymbol{I}_n)$. Underlying genetic variation of the RIL population was modelled using the random component term $\boldsymbol{Z}_g\boldsymbol{g}$ where the genetic random effects, $\boldsymbol{g}$, are an r length vector and assumed to be distributed $\boldsymbol{g} \sim N(\boldsymbol{0}, \sigma_g^2\boldsymbol{I}_r)$. The fixing of the parental and check varieties in the fixed component of the LMM ensured σ_g^2 reflects only the genetic diversity of the progeny population. Under this LMM structure, the effects, $(\boldsymbol{u}, \boldsymbol{g}, \boldsymbol{e})$, were considered to be mutually independent. For each population, best linear unbiased predictions (BLUPs) of the RIL progeny as well as their prediction error variances, were extracted from each of the fitted trait models and used to calculate broad sense generalized heritabilities with the formula derived in [10], namely

$$H_g^2 = 1 - \frac{PEV_a}{2\sigma_g^2}$$

where PEV_a is the average of the prediction error variances of all elementary contrasts between the progeny lines of the RIL population.

Hydroponics bivariate trait model

To understand the underlying genetic and phenotypic inter-relatedness between the KME-survival and canker length in each population, a bivariate LMM (BLMM) was fitted using an extension of (1). In this extension, the fixed component of the model consisted of an interaction of a two-level trait factor with the population type factor to ensure the means of the progeny, parental and check varieties for each of the traits were estimated separately for each trait. Extraneous sources of environmental variation were modelled for each trait using separate random effect terms. An important feature of the BLMM was the incorporation of terms that appropriately model the relatedness of the traits at the phenotypic and genetic level. Consequently, a multiplicative structure was assumed for the model error with a distribution $\boldsymbol{e} \sim N(\mathbf{0}, \boldsymbol{R}_b \otimes \boldsymbol{I}_n)$, where $\boldsymbol{R}_b$ is a 2 by 2 correlation matrix that reflects the residual variation within each trait as well as the residual phenotypic relationship between traits. Similarly, the genetic effects of the BLMM were assumed to have a multiplicative structure with distribution $\boldsymbol{g} \sim N(\mathbf{0}, \boldsymbol{G}_b \otimes \boldsymbol{I}_r)$, where $\boldsymbol{G}_b$ is a 2 by 2 correlation matrix with diagonal elements reflecting the underlying genetic variation of each of the traits for the RIL population and an off-diagonal element capturing the true genetic correlation between the traits.

Quantitative trait loci analysis

For the phenotypic traits, KME-survival and canker length, a QTL analysis was conducted using the whole genome average interval mapping (WGAIM) approach of Verbyla et al. [31] and Verbyla et al. [32]. The WGAIM approach initially considers an extension of the LMM defined in (1) through a partitioning of the genetic effects, $\boldsymbol{g}$, namely

$$\boldsymbol{g} = \boldsymbol{a} + \boldsymbol{p} \tag{2}$$

where $\boldsymbol{a}$ is a set of additive genetic effects with assumed distribution $\boldsymbol{a} \sim N(\mathbf{0}, \sigma_a^2 \boldsymbol{M}\boldsymbol{M}^T)$ and $\boldsymbol{M}$ is a complete $(r \times q)$ matrix of interval markers (typically $q > r$) calculated using the rules defined in Verbyla et al. [31]. Here, $\boldsymbol{M}\boldsymbol{M}^T$ is an $(r \times r)$ additive relationship matrix used widely in the genetic association analysis literature [30, 31] to explore the underpinning genetic relationships between the lines and to provide computational efficiency to complex analyses. The remaining effects, $\boldsymbol{p}$, on the right-hand side of (2) are polygenic or residual genetic effects and are assumed to be distributed $\boldsymbol{p} \sim N(\mathbf{0}, \sigma_p^2 \boldsymbol{I}_r)$. To determine whether interval markers were significantly linked to putative QTL, the additive variance parameter σ_a^2 was tested for significance by comparing the extended LMM with the baseline LMM defined in (1) through a simple likelihood ratio test. If significant, predicted interval marker effects are calculated through the back transformation $\tilde{\boldsymbol{q}} = \boldsymbol{M}^T \left(\boldsymbol{M}\boldsymbol{M}^T\right)^{-1} \tilde{\boldsymbol{a}}$ [32–34], along with the predicted error variances, and outlier statistics are calculated for each interval marker using the methods derived in Verbyla et al. [31]. The interval marker with the largest outlier statistic is then removed from $\boldsymbol{M}$ and placed as a separate random covariate in the extended LMM. This selection procedure was repeated until σ_a^2 was found to be non-significant. Selected interval markers are then independently tested using the techniques of Verbyla et al. [32] and summarized with their effect size, approximate contribution to the genetic variance and their LOD score.

Combined hydroponics and field trait model

An important component of this research is understanding the underlying genetic connection between the hydroponics phenotypic traits with the plant survival traits collected from multiple field environments and analyzed in Amalraj et al. [8]. Similar to the BLMM discussed earlier, the KME-survival and canker length can be combined with the plant survival field traits and analyzed using a multivariate multi-environment LMM (MVE-LMM). In this extension of (1) the fixed component of the MVE-LMM consisted of an interaction of a five-level trait factor with a population factor ensuring parental, control and progeny line means were estimated separately for each trait. The fixed component also contained terms to model extraneous environmental trends relevant for each of the traits. Other extraneous sources of variation associated with the field or glasshouse design as well as potential non-linear trends across row or columns of the layouts was modelled using separate random effects for each trait. Similar to the BLMM, terms were required for the MVE-LMM to ensure the genetic and phenotypic relatedness between traits was appropriately modelled. Specifically, if the phenotypic traits are ordered by field then glasshouse then the MVE-LMM residual error was assumed to be distributed

$$\boldsymbol{e} \sim N\left(\begin{bmatrix}\mathbf{0}\\ \mathbf{0}\end{bmatrix}, \begin{bmatrix}\oplus_{i=1}^{3}\boldsymbol{R}_{fi} & \mathbf{0}\\ \mathbf{0} & \boldsymbol{R}_b \otimes \boldsymbol{I}_n\end{bmatrix}\right)$$

where $\oplus_{i=1}^{3}\boldsymbol{R}_{fi} = \text{diag}\left(\boldsymbol{R}_{fi}\right)$ and $\oplus$ is the so-called direct sum operator and used contextually in Butler et al. [27]. Here, $\boldsymbol{R}_{fi}$ is a residual correlation matrix containing for the ith field site containing a parameterization for an AR1 × AR1 (AR1 = autoregressive structure of order 1) to appropriately capture the correlation of the neighboring

observations in the row and column directions of the field layout. The inclusion of the residual correlation structure $\boldsymbol{R}_b \otimes \boldsymbol{I}_n$ ensures the phenotypic relatedness of hydroponics traits are captured. The genetic effects of the MVE-LMM were assumed to have a multiplicative structure with distribution $\boldsymbol{g} \sim N(\boldsymbol{0}, \boldsymbol{G}_m \otimes \boldsymbol{I}_r)$ where $\boldsymbol{G}_m$ is a 5 × 5 correlation matrix with diagonal elements consisting of genetic variances for each of the traits and off diagonal elements capturing the genetic correlation between traits. From the fitted MVE-LMM, the estimated genetic correlation matrix was extracted and summarized.

Computations

All univariate, bivariate and multivariate multi-environment linear mixed modelling was conducted using the ASReml-R package [35] available in the R Statistical Computing Environment (R Core Team 2018) [36]. ASReml-R uses a Residual Maximum Likelihood (REML) approach to estimation of model parameters [37] and is commercially available through VSN International (VSNi) at https://www.vsni.co.uk/software/asreml-r/. Univariate QTL analysis was conducted using the WGAIM R package [38] freely available from Comprehensive R Archive Network (CRAN) repository https://cran.r-project.org/web/packages/wgaim/index.html.

Abbreviations

PRR: Phytophthora root rot; DNA: deoxyribonucleic acid; KME-survival: Kaplan–Meier estimates of plant survival; QTL: quantitative trait loci; WGAIM: whole genome average interval mapping; KM: Kaplan–Meier; RIL: recombinant inbred line; MGB: minor groove binder; BLUPs: best linear unbiased predictions; BLMM: bivariate linear mixed model; LMM: linear mixed model; MVE-LMM: multi-environment linear mixed model; SCAR: Sequence Characterised Amplified Region; QDR: quantitative disease resistance; F_6: Filial generation; PBA: Pulse Breeding Australia; DArT: Diversity Arrays Technology; LOD: Logarithm of the odds; REML: Residual Maximum Likelihood.

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Authors' contributions

AA and TS were involved in the conceptualization and design of the zoospore inoculation and hydroponics screening system. AA conducted all experiments described in this study. JT performed statistical analysis. AA and JT drafted the manuscript. All authors reviewed and revised the manuscript. TS supervised the project. All authors read and approved the final manuscript.

Availability of data and materials

The materials and datasets used and/or analyzed in this current study are available from the corresponding author on reasonable request.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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Publisher's Note

Link to Chapter 5

The development of an *in planta* infection system to study PRR disease in chickpea facilitated the undertaking of molecular studies to identify changes in gene expression linked with PRR resistance and susceptibility following PRR infection. Three chickpea genotypes with contrasting levels of PRR resistance were used in an RNA-seq experiment: A PRR resistant chickpea breeding line with a resistance source derived from the wild *Cicer* species *C. echinospermum*, a moderately PRR resistant chickpea variety Yorker with resistance derived from *C. arietinum*, and a PRR susceptible chickpea variety Rupali. This study describes differentially expressed genes (DEG) linked with PRR resistance and susceptibility following PRR infection. The study reports candidate resistance genes and identifies similarities and differences in signalling events associated with PRR resistance derived from *C. arietinum* and *C. echinospermum*. This work was performed during my PhD candidature and is written in manuscript format which will shortly be submitted for publication. Supplementary material included within this chapter is provided in the appendix section of the thesis.

Statement of Authorship

Title of Paper	Using RNA-sequencing to unravel the early defence response in chickpea (*Cicer arietinum* L.) induced by *Phytophthora medicaginis* (E. M Hansen and D. P. Maxwell)
Publication Status	☐ Published ☐ Accepted for Publication ☐ Submitted for Publication ☑ Unpublished and Unsubmitted w ork w ritten in manuscript style
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Principal Author

Name of Principal Author (Candidate)	Amritha Amalraj
Contribution to the Paper	Contributed to the design and conduct of all experiments, computational analysis, result interpretation and drafting of the manuscript.
Overall percentage (%)	80%
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.
Signature	Date 5/11/2019

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

Name of Co-Author	Ute Baumann
Contribution to the Paper	Involved in the design of the sequencing experiment, computational analysis and revision of the manuscript.
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Name of Co-Author	Tim Sutton
Contribution to the Paper	Involved in the design of the experiments, manuscript revision and overall supervision of the project.
Signature	Date 5/11/2019

Please cut and paste additional co-author panels here as required.

Using RNA-sequencing to unravel the molecular changes underlying the defence response in chickpea (*Cicer arietinum L.*) induced by *Phytophthora medicaginis* (E. M Hansen and D. P. Maxwell)

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Abstract:

Phytophthora root rot (PRR) caused by *P. medicaginis* is a major soil borne disease in chickpea growing regions of Australia. Breeding for PRR resistance is considered to be an effective approach to avoid significant yield loss in chickpea. Sources of PRR resistance have been identified in cultivated chickpea *C. arietinum*, and in the wild relative, *C. echinospermum*. Recent genetic studies based on plant survival traits from both field-based and glasshouse phenotyping experiments identified specific genomic regions associated with PRR resistance and suggested that these two sources of resistance are independent. However, the molecular mechanisms associated with PRR resistance are not yet known. In this study, RNA-sequencing was used to identify changes in plant gene expression in roots of three chickpea genotypes following PRR infection caused by *P. medicaginis* zoospores. An initial experiment based on the molecular quantification of pathogen DNA in chickpea roots at different time points after inoculation showed no significant change in the amount of *P. medicaginis* DNA in chickpea roots at 8 hours after inoculation in both the PRR-resistant and PRR-susceptible genotypes. Hence, this time point was chosen to capture the transcriptomic changes associated with defence response in the three chickpea genotypes against *P. medicaginis*. The analysis of differential expression of genes obtained from RNA-sequencing data followed by gene ontology analysis identified several key categories such as plasma membrane bound cell wall enzymes including protein kinases/phosphatases, ion channels, transcription factors and proteolytic machinery. Redox processes, an important element of early defence responses, were found to be modulated in all three PRR-resistant chickpea genotypes signifying successful pathogen recognition by host plant. A difference in the signalling events was observed between the two sources of resistance, wherein brassinosteroid and jasmonic acid hormone signalling processes were activated in the cultivated chickpea variety, while mitogen-activated protein kinase (MAPK) cascades were upregulated leading to the expression of defence-related

transcription factors in a PRR- resistant chickpea genotype derived from *C. echinospermum*. These contrasting molecular changes in the defence responses of the two PRR-resistant chickpea genotypes could potentially lead to a difference in the genetic factors that take part in minimizing the long-term effects of infection and in conferring resistance against *P. medicaginis* in chickpea. Furthermore, several differentially expressed genes were observed from QTL regions associated with PRR resistance from the two different sources that were identified in genetic studies. The gene Ca_24447 coding for aquaporin SIP1-2 located on chromosome 6 and within the interval *QRBprrsi04* was identified as a DEG for both PRR-resistant chickpea genotypes in response to infection in comparison to PRR-susceptible Rupali. Thus, this RNA-sequencing study provided evidence for a difference in the molecular response of two PRR-resistant chickpea genotypes (one with a resistance source derived from *C. echinospermum*, the other from *C. arietinum*), following PRR infection. Knowledge of these genes will be useful in understanding the molecular genetic control of PRR resistance in chickpea, and will ultimately support the development of resistant elite varieties through molecular breeding and/or transgenic approaches in crop resistance breeding.

Introduction:

Chickpea (*Cicer arietinum* L.) is a self-pollinating diploid with eight chromosomes and a genome size of ~ 740 Mb (Varshney et al, 2013). It is a nutritious, protein-rich pulse crop grown in more than 50 countries around the world. India is the largest producer of chickpea, accounting for 61.4% of global production, followed by Australia with 13.6% (FAOSTAT 2017). In Australia, chickpea is grown as a commercial crop in all mainland states with major areas under cultivation in northern New South Wales and southern Queensland (Knights, 2007). In Australia, 10% of total chickpea production is retained for domestic consumption, whilst the majority is exported to developing countries like India and its subcontinent where demand often exceeds the local supply (Knights, 2007). Besides its nutritional benefits, chickpea is grown in rotation with cereals for its ability to support biological nitrogen fixation through symbiosis with *Rhizobium* bacteria, thus improving soil fertility (Saraf et al, 1998).

Phytophthora root rot (PRR) caused by *Phytophthora medicaginis* is a major soil-borne disease affecting chickpea production in northern New South Wales and southern Queensland (Knights et al, 2008). The pathogen usually survives as oospores and when there is prolonged soil saturation following a rainfall event and/or when water stagnates, oospores mature into sporangia which then develop into motile zoospores that can invade a susceptible host plant root, causing disease. Thus, yield losses are greater during wet seasons than in normal seasons (Irwin et al, 1995). Symptoms of PRR include decaying of lateral and tap roots, defoliation from the ground up, chlorosis and wilting, leading to the eventual death of the plant. Dark brown to black lesions on the roots extending upwards to the stem can be observed in PRR-infected plants. This leads to loss of lateral roots and plants being dislodged from the soil (Schwinghamer, 2011). There is no effective treatment for a crop infected with PRR. Yield losses attributable to PRR in chickpea are estimated to cost growers up to $8.2 million per year

in Australia (Murray. GM 2012). Breeding for PRR resistance is the only practical solution to prevent yield loss and protect the crop from this significant disease.

Field PRR resistance was identified in a cultivated *C. arietinum* accession (CPI 56564 = ICC11870) and this source was incorporated into some early Australian chickpea varieties such as Barwon, Moti, Jimbour and Yorker (Dale & Irwin, 1991b). However, under high disease pressure conditions such as an increased inoculum load and heavy rainfall, these moderately resistant varieties become susceptible. Failure to identify an improved source of PRR resistance in *C. arietinum* was attributed to a narrowing of the genetic diversity within the species, through prolonged domestication and breeding (Abbo et al, 2003). An alternative source with improved PRR resistance was identified in *C. echinospermum*, a wild relative of chickpea (Knights et al, 2008). This resistance source has recently been incorporated into adapted backgrounds to generate interspecific hybrids which were subsequently used to develop bi-parental recombinant-inbred line (RIL) mapping populations. A recent genetic study based on field resistance identified independent loci associated with PRR resistance in cultivated chickpea and its wild relative (Amalraj et al, 2018). However, the major genes, metabolic pathways and molecular mechanisms underlying PRR resistance in chickpea are not clearly understood.

Plants possess complex defence mechanisms to protect themselves from a wide range of microbes, insects and soil borne pathogens in their natural environment. Plants have a capacity to detect pathogens/microbes and respond through complex, orchestrated networks of molecular, cellular and tissue-based defence events to prevent pathogen spread and limit the infection. Plant-pathogen interactions include host-specific recognition wherein a plant resistance (R) gene interacts directly or indirectly with its corresponding virulence factor in the pathogen. The non-host specific interaction includes a series of signal transduction cellular events leading to the expression of defence related genes in plants. This type of defence

response in plants is activated through the recognition of pathogen-associated molecular patterns (PAMP) by receptor proteins called pattern recognition receptors (PRRs), and the immune response expressed in the host is termed as PAMP-triggered immunity (PTI) (Boller & Felix, 2009). Another pathway for perception involves the recognition by intracellular receptors of pathogen virulence molecules called effectors, which leads to effector-triggered immunity (ETI). The PTI- and ETI-related gene expressions are similar but vary in magnitude (Dodds & Rathjen, 2010). The genes involved in pathogen recognition and in the following signalling transduction cellular events are believed to play a major role in defence response in plants to prevent pathogen spread and limit the infection. Therefore, it is essential to identify these key genes and their function associated with a resistance response in breeding for crop resistance. Research conducted on the plant-pathogen interaction in other phytophthora pathosystems, such as *P. sojae* that causes root rot and phytophthora blight in leguminous plants such as soybean (Sugimoto et al, 2011), has revealed the existence of a R-gene mediated resistance mechanism (Dorrance, 2013). However, in the case of *P. capsici* that causes foliar blight in pepper (Barchenger et al, 2018), there is a lack of evidence for R genes and/or presence of an inhibitor gene (*Ipcr*) (Reeves et al, 2013). As a foliar based pathogen, the underlying genetics of the resistance mechanism in *P. capsici* may be less relevant to that of *P. medicaginis* resistance in chickpea (Chuberre et al, 2018). Phytophthora species have specific host ranges (Erwin & Ribeiro, 1996) and it is not known if the same or different genes are associated with PRR resistance in chickpea to *P. medicaginis*. The work presented here can provide a basis for the analysis of the molecular mechanisms underlying the defence response in chickpea against *P. medicaginis*, to improve our understanding of resistance to this disease.

In recent years, advancements in next generation sequencing (NGS) technologies have made the application of genomics to crop improvement possible. It is applied in RNA-sequencing (RNA-seq) to determine the expression of RNA in a given sample at a given time

(Van Dijk et al, 2014), and to compare control and treatment conditions to study abiotic and biotic stress responses in different genotypes or tissue types. In the case of disease resistance, comparisons can be made between resistant and susceptible genotypes, with and without pathogen inoculation. Computational approaches can reveal gene expression changes, identify novel genes and isoforms, and detect variants such as expressed SNPs and InDels to ultimately answer biological questions associated with the trait (Wang et al, 2009). In several crop improvement studies including chickpea, RNA-sequencing has been applied to identify molecular changes underlying tolerance and resistance responses (Choudhary et al, 2012; Fracasso et al, 2016; Kim et al, 2011). A recent study enabled the identification of differentially expressed genes and physiological responses under drought in root and shoot tissues in a kabuli chickpea type (Mashaki et al, 2018).

In this study, RNA-seq was used to identify changes in plant gene expression associated with the defence response to PRR in chickpea roots. Three chickpea genotypes with contrasting levels of PRR resistance were selected, to complement recent genetic studies in this area (Amalraj et al, 2018). An initial experiment was performed to determine an appropriate time point for capturing transcriptomic changes occurring during defence response in chickpea roots to PRR infection. RNA-seq data obtained from the Illumina platform provided a molecular profile of the expression changes occurring in two PRR-resistant chickpea genotypes, 04067-81-2-1-1 and Yorker, with resistance sources derived from *C. echinospermum* and *C. arietinum*, respectively, in response to *P. medicaginis* inoculation. This enabled the identification of several categories of key genes and molecular pathways associated with the defence response to PRR.

Materials and Methods:

Plant and fungal material:

Three chickpea genotypes were selected with different levels of PRR resistance that had been used as parental genotypes to develop bi-parental RIL mapping populations for PRR genetic studies. These include a breeding line 04067-81-2-1-1 (a backcross derivative from *C. echinospermum* with pedigree: Howzat/ ILWC 245//99039-1013) with high PRR resistance, an Australian chickpea variety Yorker (pedigree: 8507-28H/946-31) of moderate PRR resistance, and a chickpea variety Rupali (pedigree: FLIP84-15C/ ICCV88516// Amethyst) that is susceptible to PRR. The chickpea breeding line and chickpea varieties used in this study were developed and maintained by the National Chickpea breeding program based at the Department of Primary Industries, Tamworth, New South Wales. The *P. medicaginis* isolate 1129-1, which was recovered from the field in Yetman, New South Wales (Southwell & Crocker, 2005), was used to inoculate chickpea. Zoospores from isolate 1129-1 were produced following the conditions described in Amalraj et al. (2019).

Plant growth conditions and PRR infection system:

The experiment was conducted in a temperature-controlled growth room at the University of Adelaide, Waite Campus, South Australia, Australia; 20/14 ± 2°C day/night with a 16 h photoperiod (250 – 300 microeinstein, metal-halide). Plastic pots (4.5 L) covered with aluminium foil were used to grow plants in continuously aerated nutrient solution. The composition of the full-strength nutrient solution prepared in deionized water was (mM): 5.0 Ca^{2+}, 5.0 K^{+}, 0.625 NH^{4+}, 0.4 Mg^{2+}, 0.2 Na^{+}, 5.4 SO_4^{2-}, 4.4 NO_3^{-},0.2 $H_2PO_4^{-}$, 0.1 SiO_3^{2-}, 0.1 Fe-sequestrene, 0.05 Cl^{-}, 0.025 BO_3^{3-},0.002 Mn^{2+}, 0.002 Zn^{2+}, 0.0005 Cu^{2+}, 0.0005 MoO_4^{2-} and 0.001 Ni^{2+}. The solution was buffered with 1.0 mM MES (2-[N-morpholino] ethane sulfonic acid) and adjusted to pH 6.5 using KOH (Samineni et al, 2011). Seeds were washed with commercial bleach (0.042% (w/v) sodium hypochlorite) in deionized water for 5 minutes,

rinsed twice in tap water, and imbibed at 4°C for 48 h. Imbibed seeds were then germinated on mesh in 10% aerated nutrient solution in the dark for 3 days. Seedlings were transferred to 25% aerated nutrient solution and exposed to light. Each pot contained a healthy individual from each of the three selected chickpea genotypes and the pots and positions of each genotype were set up in a completely randomised block design with three replicates in control (no inoculation) and in treatment (with inoculation). *P. medicaginis* zoospore suspension culture was added to the treatment pots containing 7 days old seedlings at a concentration of 1.5×10^5 spores/ mL for PRR disease infection.

Molecular quantification of P. medicaginis penetration in chickpea roots at different time points:

To identify an appropriate time point to study the molecular defence response in chickpea to PRR, an experiment was set up to quantify pathogen DNA in root tissue at different times after inoculation. For this, root tissues from the PRR-susceptible chickpea variety Rupali and PRR-resistant breeding line 04067-81-2-1-1 were harvested at 0, 1, 2, 4, 8, 16 and 32 hours after inoculation, rinsed thoroughly with tap water, patted dry on clean paper towel, weighed and snap-frozen in liquid nitrogen. Frozen roots were freeze-dried, and their dry weight was determined using a weighing balance. The amount of *P. medicaginis* DNA per mg of dry root weight in each sample was quantified using a TaqMan MGB assay developed for *P. medicaginis* at the South Australian Research and Development Institute (SARDI) (Alan McKay, 2018; Sean Bithell, 2015). Six biological replicates for each chickpea genotype and at each time point were included in this experiment.

RNA extraction and RNA-sequence data generation:

At 8 h after inoculation, root tissue from three replicates from each of the control and inoculated treatments of three chickpea genotypes were harvested for RNA extraction. Total RNA was extracted using Spectrum™ Plant Total RNA Kit (Sigma Aldrich) according to the

manufacturer's instructions. The concentration of RNA was determined using a spectrophotometer (NanoDrop Technologies, Wilmington, USA) and the quality of RNA was determined based on the RNA integrity value calculated from the ratio of 28S to 18S rRNA (RIN) value using an Agilent BioAnalyzer (Agilent Technologies Inc., Santa Clara, CA, USA). Stranded Illumina TruSeq libraries were prepared using high-quality RNA (RIN ≥ 8) and the sequence data were generated using a HiSeq 2500 (Australian Genome Research Facility Limited, Melbourne, Victoria, Australia). The 18 libraries from three chickpea genotypes, two treatment conditions and three biological replicates were spread across four sequencing lanes.

RNA sequence data analysis:

The RNA-sequence raw data were subjected to quality control using FastQC version 0.11.4 (Andrews, 2016) (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and the adapter sequences were removed using Trimmomatic version 0.36 (Bolger et al, 2014). Adapter trimming was performed in paired-end mode with min_len=50, palindromeClipthreshold=30, simpleClipThreshold=10 and –phred 33. The trimmed reads were then aligned to the chickpea reference genome, CDC Frontier v1.0, kabuli type chickpea *C. arietinum* (Varshney et al, 2013) using HISAT2 version 2.1.0 (Kim et al, 2015). A chickpea reference Genome Index was generated using hisat2-build which is based on Karkkainen's blockwise algorithm. The Genome Index enables the aligner to trade-off between running time and memory usage in determining the potential start of the query sequence. SAMtools was used for post processing the alignments in SAM format for indexing and alignment (Li et al, 2009). The read alignments from each sample were then used to perform reference annotation-based transcript assembly together with the chickpea genome v1.0 GFF using Stringtie version 1.3.5 (Pertea et al, 2015). The stringtie-merge option was used to generate a non-redundant set of transcripts observed in all samples for downstream analysis. The read counts mapped to a particular genomic feature

such as a gene were quantified, and a count matrix for each sample was generated for downstream analysis.

Differential expression analyses:

Differentially expressed genes (DEG) between the chickpea genotypes and PRR treatments were determined using the R package edgeR (Nikolayeva & Robinson, 2014) and linear models included in Limma (Smyth, 2005). The generated count matrix along with the experimental group information was used to create the DGEList object built within the edgeR package. Six experimental groups were created according to genotype and treatment conditions: 04067-81-2-1-1-control (Bc-C), 04067-81-2-1-1-inoculated (Bc-I), Yorker-control (Yor-C), Yorker-inoculated (Yor-I), Rupali-control (Rup-C) and Rupali-inoculated (Rup-I). Normalisation factors calculated using a trimmed mean M-values (TMM) method were used as a scaling factor for the library sizes (Robinson & Oshlack, 2010). For subsequent analysis, genes that were expressed in at least one group were retained by gene expression level filtering based on CPM (counts per million reads). Contrast matrices were designed to identify differentially expressed genes under different conditions to identify potential candidate genes associated with PRR resistance in the wild chickpea relative 04067-81-2-1-1 and in the cultivated species Yorker as described in Table 1. Linear modelling was carried out using precision weights calculated by the voom function to remove fluctuations caused by genes of very low expression level on the mean-variance relationship. Linear modelling in Limma was carried out using the lmfit and contrast.fit functions to identify genes that respond to the comparisons of interests as described in the contrast matrix. Empirical Bayes moderation was carried out to obtain precise estimates of gene-wise variability. False discovery rate correction was carried out using the Benjamini and Hochberg method (Benjamini & Hochberg, 1995) with statistical significance defined using an adjusted p-value cut off of $p<0.05$. The genes exhibiting significant differences of at least two-fold change with the corrected p-value< 0.01 in each of the

conditions analysed were regarded as differentially expressed genes. In order to understand the functional classification of DEG, the DEG were subjected to BLASTX similarity searches against the NCBI non-redundant protein database with an e-value threshold of $\leq 10^{-5}$ followed by their annotation using Blast2go (Conesa et al, 2005). Subsequently, the DEG were subjected to GO enrichment analysis using agriGO v2.0 (Tian et al, 2017).

Table 1. Description of the contrast matrices design used in RNA-seq data analysis to identify differential expression of genes in different treatments and genotypes.

Serial number	Contrast condition	Effect analysed	Observation
1	Bc-I vs Bc-C	Treatment within the genotype	DEGs in PRR resistant breeding line 04067-81-2-1-1following PRR infection (Bc-I)
2	Yor-I vs Yor-C	Treatment within the genotype	DEGs in moderately PRR resistant genotype, Yorker following PRR infection (Yor-I)
3	Rup-I vs Rup-C	Treatment within the genotype	DEGs in PRR susceptible genotype, Rupali following PRR infection (Rup-I)
4	(Bc-I vs Bc-C) vs (Rup-I vs Rup-C)	Interaction 1	DEGs in PRR resistant breeding line 04067-81-2-1-1 compared to PRR susceptible genotype, Rupali following PRR infection
5	(Bc-I vs Bc-C) vs (Yor-I vs Yor-C)	Interaction 2	DEGs in PRR resistant breeding line 04067-81-2-1-1 compared to moderately PRR resistant genotype, Yorker following PRR infection
6	(Yor-I vs Yor-C) vs (Rup-I vs Rup-C)	Interaction 3	DEGs in moderately PRR resistant genotype, Yorker compared to PRR susceptible genotype, Rupali following PRR infection
7	Bc-C vs Rup-C	Genotype (control)	DEGs in PRR resistant breeding line 04067-81-2-1-1 compared to PRR susceptible genotype, Rupali in the absence of PRR infection
8	Bc-C vs Yor-C	Genotype (control)	DEGs in PRR resistant breeding line 04067-81-2-1-1 compared to moderately PRR resistant genotype, Yorker in the absence of PRR infection
9	Yor-C vs Rup-C	Genotype (control)	DEGs in moderately PRR resistant genotype, Yorker compared to PRR susceptible genotype, Rupali in the absence of PRR infection

MapMan Pathway analysis:

Identification of the molecular pathways involved during chickpea defence response in PRR infection was performed using MapMan software tool, Mercator4 v2.0 (Schwacke et al, 2019). MapMan software relies on its own ontology to generate a redundancy–reduced mapping file consisting of hierarchical categories referred to as 'BIN' and 'subBIN', using the user-provided assembled transcript/gene dataset. It provides a modular system to visualize results on a gene-by-gene basis in the context of schematic diagrams of pathways and biological processes (Lohse et al, 2014; Thimm et al, 2004). A chickpea mapping file was generated using the assembled transcript data generated from this experiment. This chickpea mapping file and the experimental files containing the log2 ratios of fold change values calculated from the treatment effect for each of the three-chickpea genotypes (Bc-I, Yor-I and Rup-I), as described above, were supplied to MapMan software and the DEG were assigned to corresponding functional groups defined as BINs. BINs were imported by an ImageAnnotator module to organise and display the results as schematic diagrams of pathways and/or biological processes.

Quantitative real-time PCR (qRT-PCR) analysis:

To validate the results from the *in-silico* analysis of RNA-sequencing data, six DEG from the different conditions analysed were selected (Table S1) for quantitative real-time PCR (qRT-PCR) experiment. Elongation factor 1-alpha (EF1-α) was used as a reference gene because it showed stable expression among the three chickpea genotypes in both control and inoculated conditions. Gene-specific primer pairs were designed using Primer 3 (version 0.4.0) software. The RNA samples from three chickpea genotypes including three biological replicates used for sequencing (described above) were used for validation. Total RNA was reverse-transcribed using a SuperScript™ IV First-Strand Synthesis System (Thermo Fischer Scientific, USA) following the manufacturer's instructions. The concentration of cDNA was determined using a spectrophotometer (Nanodrop® ND-100- BIOLAB) and quality was verified from PCR

amplification of the reference gene EF1-α. qRT-PCR was performed with Precision Fast 2x qPCR Master Mix premixed with SYBR green (Primerdesign Ltd., UK). The amplification run was real-time monitored on a QuantStudio™ 6 Flex Real-Time PCR system (Applied Biosystems, USA). Each qPCR reaction included three technical replicates. The amplification data obtained from each qPCR run was processed with LinRegPCR software (Ruijter et al, 2009). PCR efficiencies and Ct values (fractional number of cycles needed to reach the fluorescence threshold) obtained were used for further calculations. Data for each gene of interest was then normalised using the mean Ct values of the reference gene EF1-α. Normalised relative quantities (NRQ) defined by the gene expression level for a given target gene were calculated using the following formula (Pfaffl, 2001):

$$NRQ = \frac{E_{goi}^{\Delta Ct,goi}}{E_{ref}^{\Delta Ct,ref}}$$

Where, goi refers to the gene of interest and ref refers to the reference gene. A geometric mean of the NRQ values from the three biological replicates was calculated for each target gene. Log2 ratios of fold changes between each of the desired conditions as described in the contrast matrices of RNA-sequencing data analysis were then determined and presented graphically.

Results:

The penetration of P. medicaginis pathogen in chickpea roots at different time points:

The pathogen penetration in chickpea roots following PRR infection at 0, 1, 2, 4, 8, 16 and 32 hours after inoculation was determined from the amount of *P. medicaginis* DNA in root tissues of PRR-resistant breeding line 04067-81-2-1-1 and PRR-susceptible variety Rupali, quantified using a TaqMan PCR assay. An increase in pathogen content with time was observed in both genotypes. However, in both genotypes, the levels of pathogen DNA appeared to plateau from eight hours after inoculation (Fig. 1). Therefore, eight hours after inoculation was selected as an appropriate time point to study the molecular defence response in chickpea to PRR infection. There were increased levels of pathogen DNA in the PRR-susceptible chickpea variety Rupali compared to the PRR-resistant breeding line 04067-81-2-1-1 at most time points (Fig. 1). This observation is broadly in accordance with field-based resistance rankings of the two genotypes, however the direct relationship between root pathogen content and field resistance rating needs to be examined experimentally.

RNA sequencing and data assembly:

A total of 521.93 million paired-end reads were generated from transcriptome sequencing of six RNA sample types (three chickpea genotypes with control and inoculated treatments), with about 75.6 to 91.4 million reads per sample. Reads with adapter contamination and low base quality were removed using Trimmomatic. Consequently, a total of 496.34 million (95.09%) high quality reads were obtained. A total of 430.34 million reads (86.7%) were mapped to the chickpea reference genome v1.0 (Varshney et al., 2013) using HISAT2 software. An average of 71.7 million reads (98.27%) were mapped to the reference genome for each sample (Table 2).

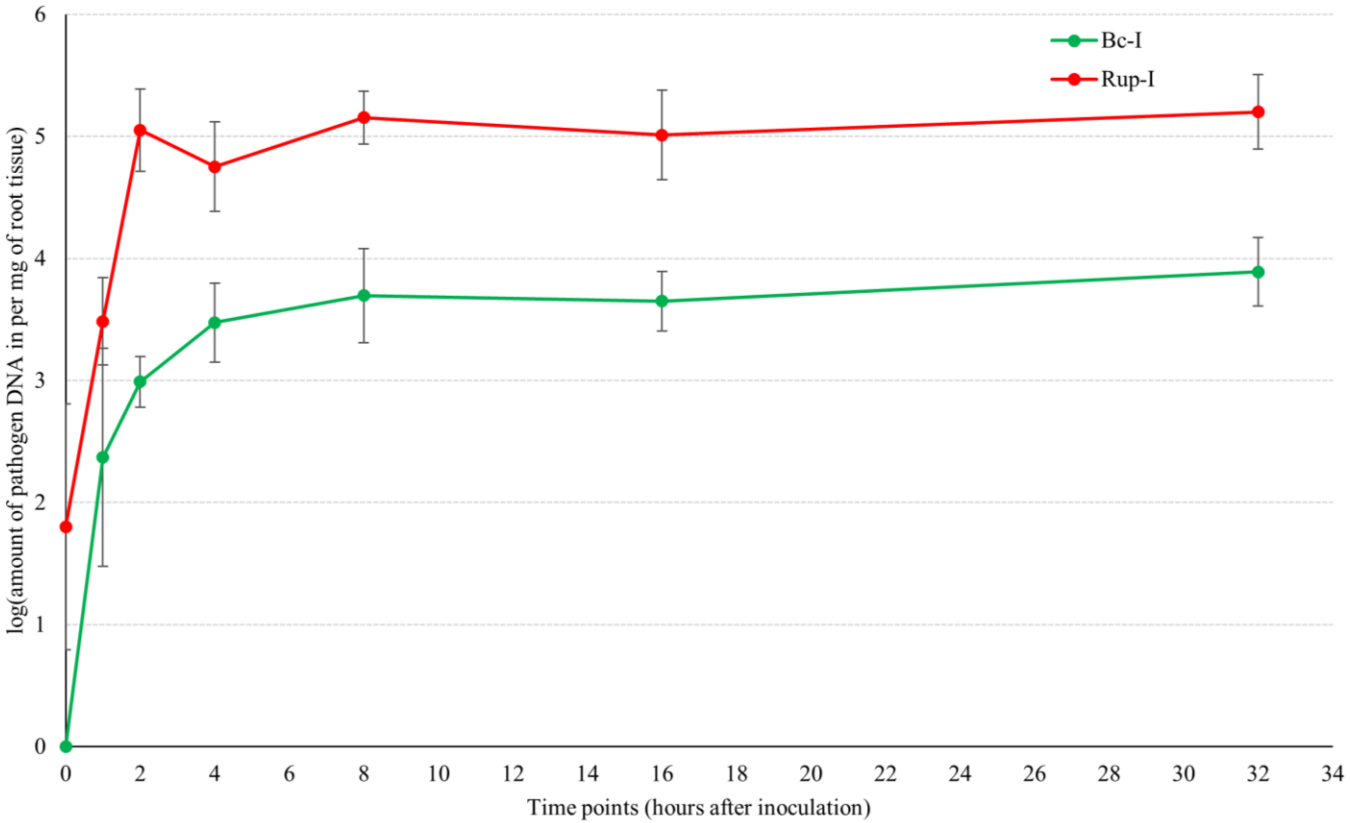


Fig. 1. Molecular quantification of *P. medicaginis* DNA in roots of PRR resistant breeding line 04067-81-2-1-1 (Bc-I) and PRR susceptible chickpea variety Rupali (Rup-I). The log-transformed values of the amounts of *P. medicaginis* DNA determined by a TaqMan PCR assay is presented. Error bars represent the standard error of the mean of six biological replicates.

Table 2. Summary of Illumina sequencing data and mapped reads for the samples.

Genotype	Described PRR resistance level	Treatment	Sample ID	Total reads (bp)	Mapped reads (bp)	Mapping rate (%)	Unique match (bp)	Multi-position match (bp)
04067-81-2-1-1	Resistant	Control	Bc-C	91,443,176	76,412,453	98.92	70,257,728	6,154,725
		Inoculated	Bc-I	75,658,674	62,283,177	98.80	56,881,693	5,401,484
Yorker	Moderately resistant	Control	Yor-C	88,459,749	72,699,344	98.03	66,105,966	6,593,378
		Inoculated	Yor-I	87,090,381	71,968,298	98.68	64,395,589	7,572,709
Rupali	Susceptible	Control	Rup-C	88,884,902	71,918,841	97.09	63,682,750	8,236,091
		Inoculated	Rup-I	90,399,787	75,065,712	98.12	67,147,765	7,917,947
Total				521,936,669	430,347,825			
Average				86,989,444.83	71,724,637.5	98.27		

Overall gene expression analysis:

A gene was considered expressed if its CPM ≥ 1. In total, 21,380 genes were expressed in at least one of the six samples analysed. The distribution of gene expression in each sample was visualized using density plots of raw and filtered data (Fig. 2). The density plot produced using filtered data (Fig. 2B) showed that the distribution of expression values was similar across all samples within the dataset. The unsupervised clustering of samples for gene expression analyses grouped the three chickpea genotypes separately in accordance to their described levels of PRR resistance as shown in a multi-dimensional scaling (MDS) plot (Fig. 3). This clustering showed that samples grouped well within the genotypes, a primary condition of interest to this study.

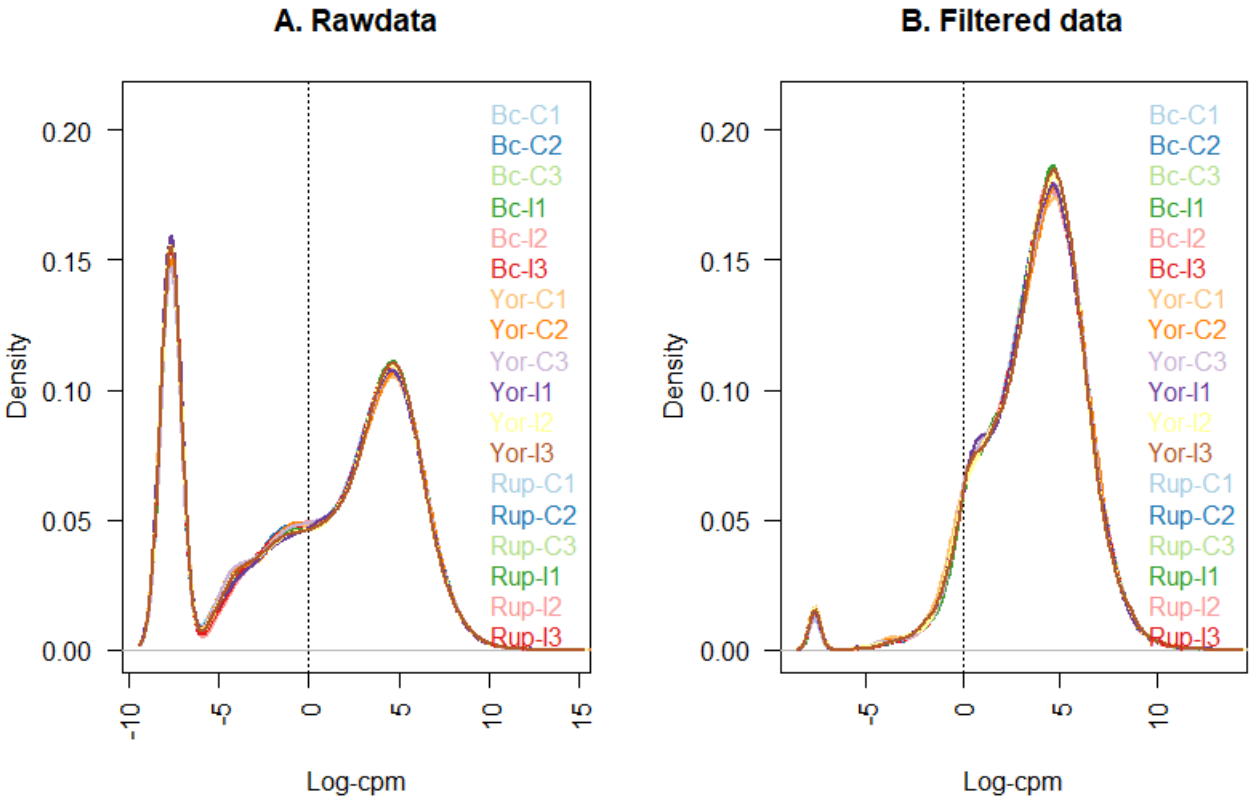


Fig. 2. Density plots of log-CPM expression values for raw (pre-filtered data) (A) and post-filtered data (B) are shown for each sample. Dotted vertical lines mark the log-CPM expression values of zero threshold (equivalent to 1 CPM) used in the filtering process.

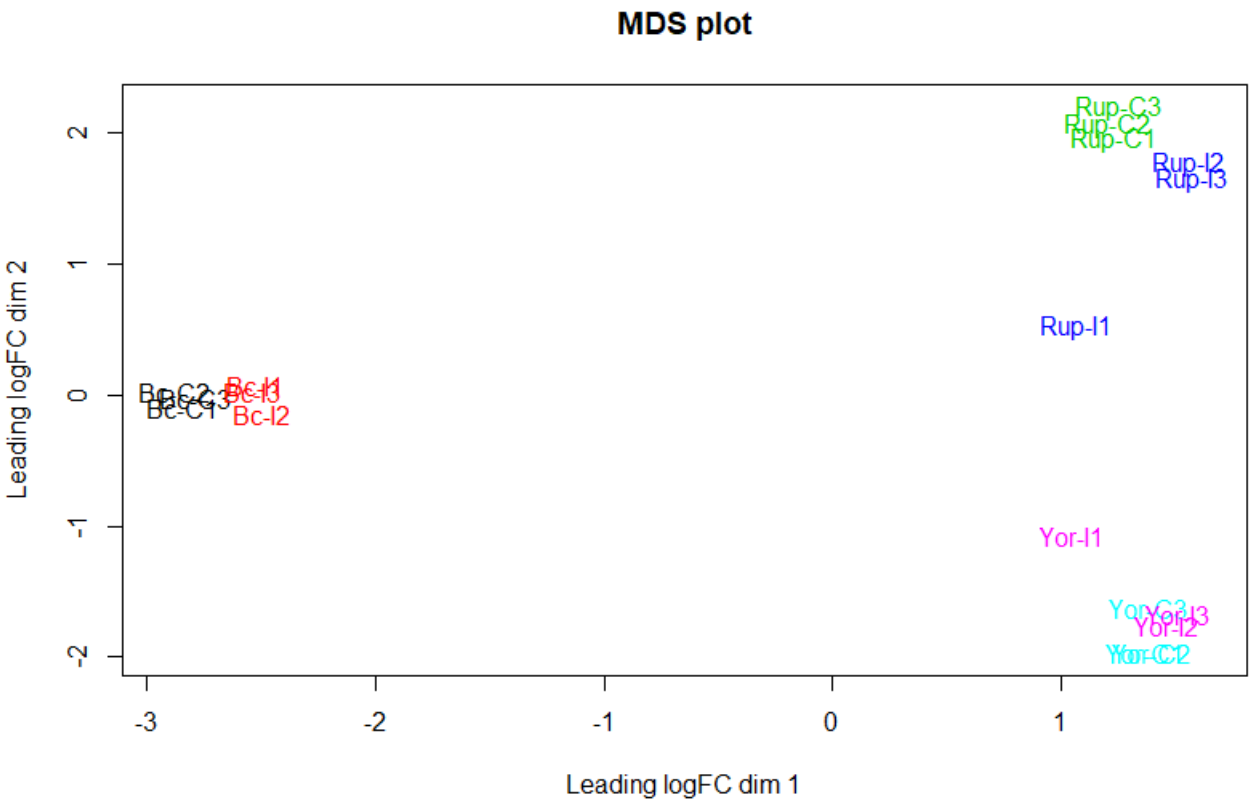


Fig. 3. Multidimensional scaling (MDS) plots of log-CPM values over dimensions 1 and 2 with samples coloured and labelled. Distances on the plot correspond to the leading fold-change between each pair of samples.

Differentially expressed genes (DEG):

A total of 4,005 DEG were identified by comparing the six samples in nine different genotype/treatment comparisons, as described in Table 1. Lists of the DEG for each comparison are provided in Supplementary Tables 2 – 10. Comparisons between genotypes under control conditions identified the highest number of DEG. There were 1,779 DEG between 04067-81-2-1-1 and Yorker (Bc-C vs Yor-C), followed by 1,690 DEG between 04067-81-2-1-1 and Rupali (Bc-C vs Rup-C) and 1,364 DEG between Yorker and Rupali (Yor-C vs Rup-C) (Table 3). The analysis of treatment effects within each of the three chickpea genotypes identified the highest number of DEG (1,054) in the PRR- susceptible variety Rupali (Rup-I vs Rup-C), followed by 532 DEG in the moderately PRR-resistant Yorker (Yor-I vs

Yor-C) and the lowest number of DEG (412) in the PRR-resistant line 04067-81-2-1-1 (Bc-I vs Bc-C) (Table 3). These groups represent genes that are differently expressed in each chickpea genotype specifically following PRR infection and could potentially be used to determine the molecular mechanism underlying the defence response each genotype based on their described levels of resistance. Analysis of the interaction terms in each of the three intended contrast conditions analysed in this study identified 152 DEG in Interaction 1 (Bc-I vs Bc-C) vs (Rup-I vs Rup-C). This group represents genes that are differently expressed in the PRR-resistant breeding line 04067-81-2-1-1 compared to the PRR-susceptible chickpea variety Rupali following PRR infection. There were 13 DEG identified following PRR infection in Interaction 2 (Bc-I vs Bc-C) vs (Yor-I vs Yor-C), which represents genes differently expressed in the breeding line 04067-81-2-1-1 with PRR resistance derived from *C. echinospermum* compared to the moderately PRR-resistant chickpea variety Yorker with resistance derived from the cultivated variety, *C. arietinum.*. This group of DEG could potentially be further used to understand the similarities and/or differences existing between the two different sources of PRR resistance. In Interaction 3 (Yor-I vs Yor-C) vs (Rup-I vs Rup-C), representing genes differently expressed in the moderately PRR- resistant chickpea variety Yorker compared to the PRR- susceptible variety Rupali during infection 564 DEG were identified. Following PRR infection in the three chickpea genotypes of contrasting PRR resistance levels, the number of down- regulated genes were observed to be higher than the number of up-regulated genes (Table 3). However, the number of up- regulated genes were observed to be high in the interaction analyses (Interaction 1 and Interaction 3) of the PRR- resistant and PRR- susceptible genotypes following PRR infection. The overlapping DEG amongst the three chickpea genotypes following PRR infection (Bc-I, Yor-I and Rup-I) was analysed and is presented in Fig. 4A. In a comparison between PRR- resistant breeding line 04067-81-2-1-1 (Bc-I) and moderately PRR- resistant Yorker (Yor-I), 197 DEG associated with PRR resistance were

Table 3. Summary of observed differentially expressed genes in each of the different effect analysed.

Contrasts of interest	**Effect analysed**	**Up regulation**	**Down regulation**	**Total number of DEGs**
Bc-I vs Bc-C	Treatment (within each genotype)	146	266	412
Yor-I vs Yor-C	Treatment (within each genotype)	240	292	532
Rup-I vs Rup-C	Treatment (within each genotype)	437	611	1048
(Bc-I vs Bc-C) vs (Rup-I vs Rup-C)	Interaction 1	91	61	152
(Bc-I vs Bc-C) vs (Yor-I vs Yor-C)	Interaction 2	3	10	13
(Yor-I vs Yor-C) vs (Rup-I vs Rup-C)	Interaction 3	354	210	564
Bc-C vs Rup-C	Genotype (control)	921	769	1690
Bc-C vs Yor-C	Genotype (control)	1139	640	1779
Yor-C vs Rup-C	Genotype (control)	447	917	1364

observed to overlap, comprising 66 up-regulated genes and 131 down- regulated genes. In another comparison between Yorker (Yor-I) and Rupali (Rup-I), 181 DEG were found to overlap, of which 54 and 49 genes were up-regulated in Yorker and Rupali, respectively. In a comparison between 04067-81-2-1-1 (Bc-I) and Rupali (Rup-I) about 200 DEG including 55 up-regulated and 145 down-regulated genes were found to overlap following PRR infection. There were 119 DEG common to all three chickpea genotypes following PRR infection. Similarly, the overlapping DEG among the three interaction terms used to analyse the effects of both the treatment and genotype are shown in Fig. 4B. Similarly, 97 DEG were observed to overlap between Interaction 1 and Interaction 3, indicating common genes associated with PRR resistance derived from *C. echinospermum* and *C. arietinum* compared to the PRR-susceptible variety Rupali. Two DEG were observed to overlap between Interaction 1 and Interaction 2 which indicates the common genes expressed in *C. echinospermum* source of PRR resistance compared to the PRR-susceptible Rupali and moderately PRR-resistant Yorker. Nine DEG were observed to overlap between Interaction 2 and 3. One gene (Ca_24447, coding for aquaporin SIP1-2 belonging to the major intrinsic protein superfamily), was found to overlap in all three comparisons, suggesting an association of this gene with PRR resistance in chickpea.

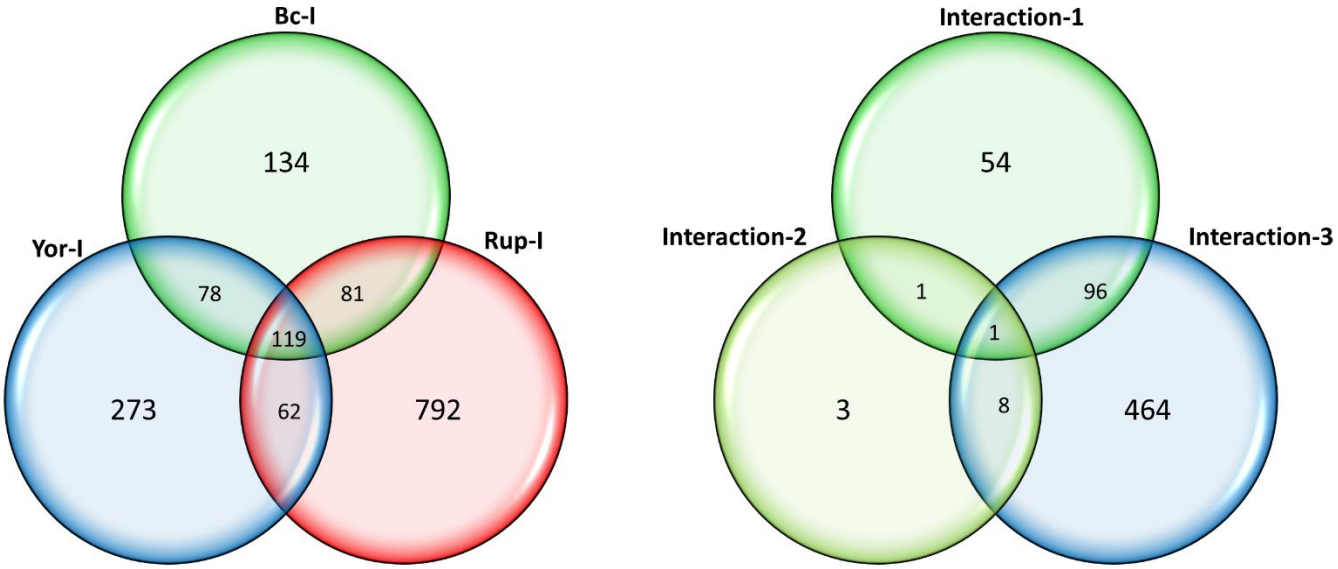


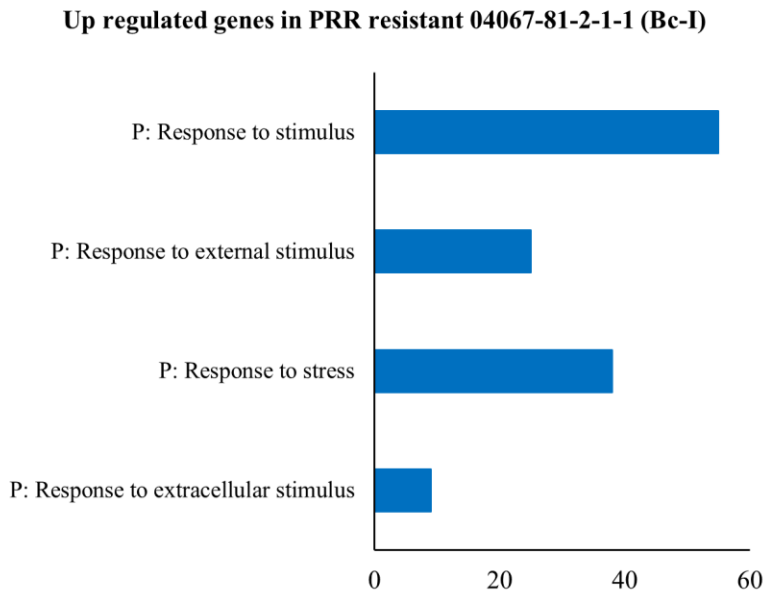
Fig. 4. Venn diagrams showing (A) the overlapping DEG between chickpea genotypes following PRR infection; (B) the overlapping DEGs when comparing the different interaction terms to identify genes that respond differently to PRR infection compared to their contrast of interest i.e., Interaction 1: (Bc-I vs Bc-C) vs (Rup-I vs Rup-C), Interaction 2: (Bc-I vs Bc-C) vs (Yor-I vs Yor-C) and Interaction 3 (Yor-I vs Yor-C) vs (Rup-I vs Rup-C).

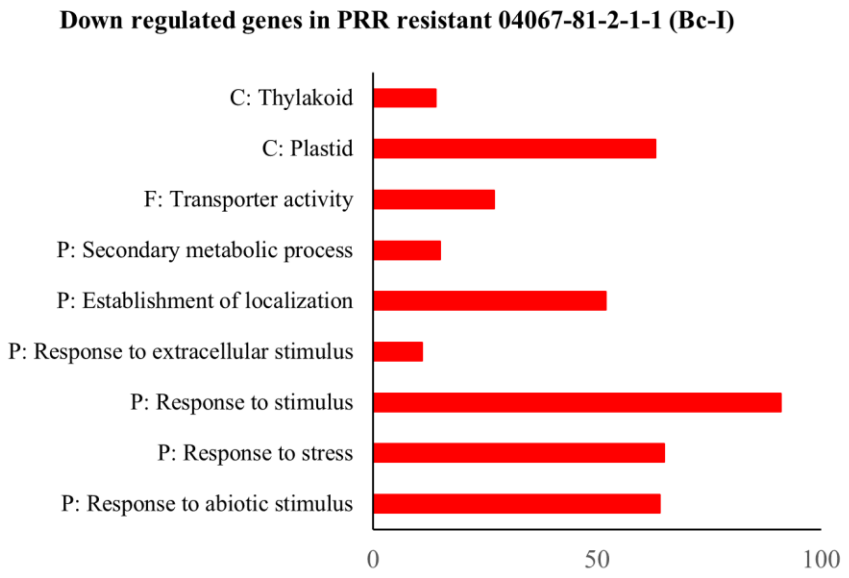
Functional classification of DEG:

Gene ontology (GO) analysis classified the identified DEG into three principal categories: molecular function, biological process and cellular component. Further analysis grouped DEG into several sub-categories of molecular function, biological process and cellular component, as shown in Fig.5. Following PRR infection in the PRR- resistant chickpea breeding line 04067-81-2-1-1 (Bc-I), a large number of up-regulated genes were observed to be enriched in the major sub-categories of biological process that included response to stimulus, response to external stimulus, response to stress and response to extracellular stimulus, while genes categorised under cellular component such as thylakoid and plastid and under molecular function such as transporter activity and localization, were found to be down-regulated (Fig. 5A). However, in the moderately PRR-resistant variety Yorker, the major subcategories of biological process that included lipid metabolic process and photosynthesis were found to be

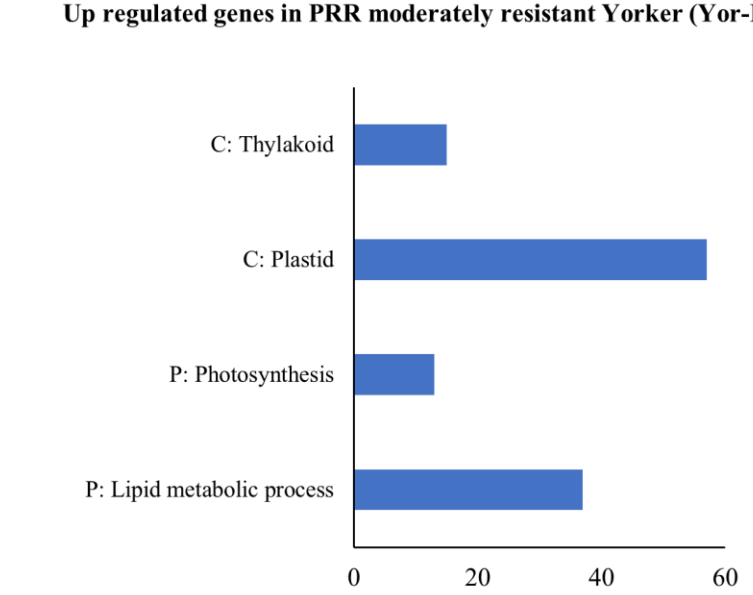
enriched along with the cellular component sub-categories thylakoid and plastid (Fig. 5B). In the PRR-susceptible variety Rupali following PRR infection (Rup-I), a high number of major sub-categories in biological process, molecular function and cellular component were observed to be enriched (Fig. 5C). The molecular function category which includes catalytic activity, receptor activity, cell death and cell communication was observed to be markedly enriched in the PRR-susceptible genotype but not in PRR-resistant genotypes during infection. These differences in the DEG groupings based on functional classification between PRR-resistant and PRR-susceptible genotypes imply a difference in the defence response to *P. medicaginis* following PRR infection. Also, the observed differences in the sets of genes enriched in roots of Yor-I and Bc-I suggest a difference associated with PRR resistance derived from *C. arietinum* and *C. echinospermum*, respectively.

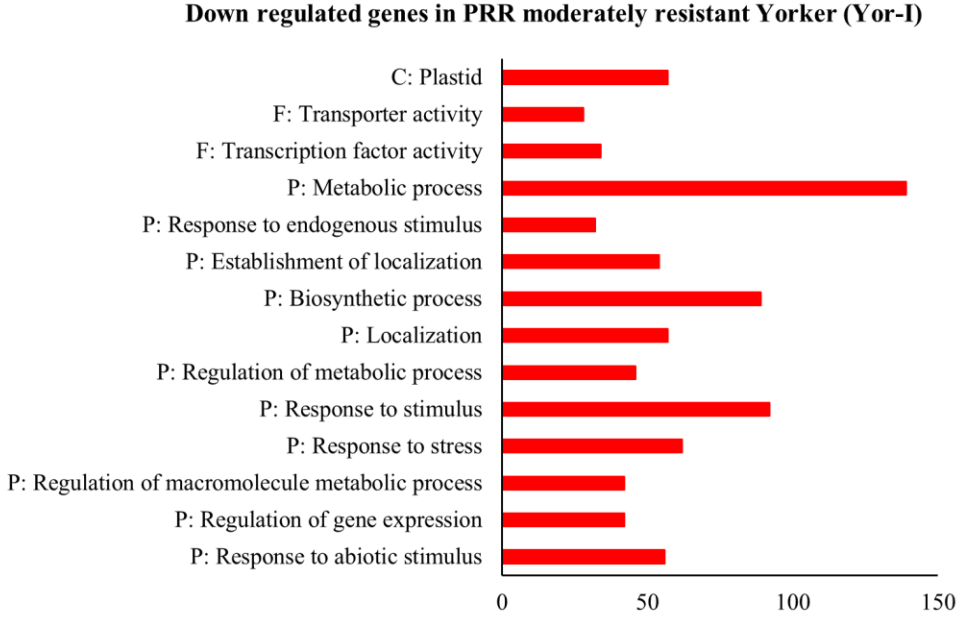
A


Up regulated genes in PRR resistant 04067-81-2-1-1 (Bc-I)
P: Response to stimulus
P: Response to external stimulus
P: Response to stress
P: Response to extracellular stimulus
0
20
40
60


Down regulated genes in PRR resistant 04067-81-2-1-1 (Bc-I)
C: Thylakoid
C: Plastid
F: Transporter activity
P: Secondary metabolic process
P: Establishment of localization
P: Response to extracellular stimulus
P: Response to stimulus
P: Response to stress
P: Response to abiotic stimulus
0
50
100

B


Up regulated genes in PRR moderately resistant Yorker (Yor-I)
C: Thylakoid
C: Plastid
P: Photosynthesis
P: Lipid metabolic process
0
20
40
60


Down regulated genes in PRR moderately resistant Yorker (Yor-I)
C: Plastid
F: Transporter activity
F: Transcription factor activity
P: Metabolic process
P: Response to endogenous stimulus
P: Establishment of localization
P: Biosynthetic process
P: Localization
P: Regulation of metabolic process
P: Response to stimulus
P: Response to stress
P: Regulation of macromolecule metabolic process
P: Regulation of gene expression
P: Response to abiotic stimulus
0
50
100
150

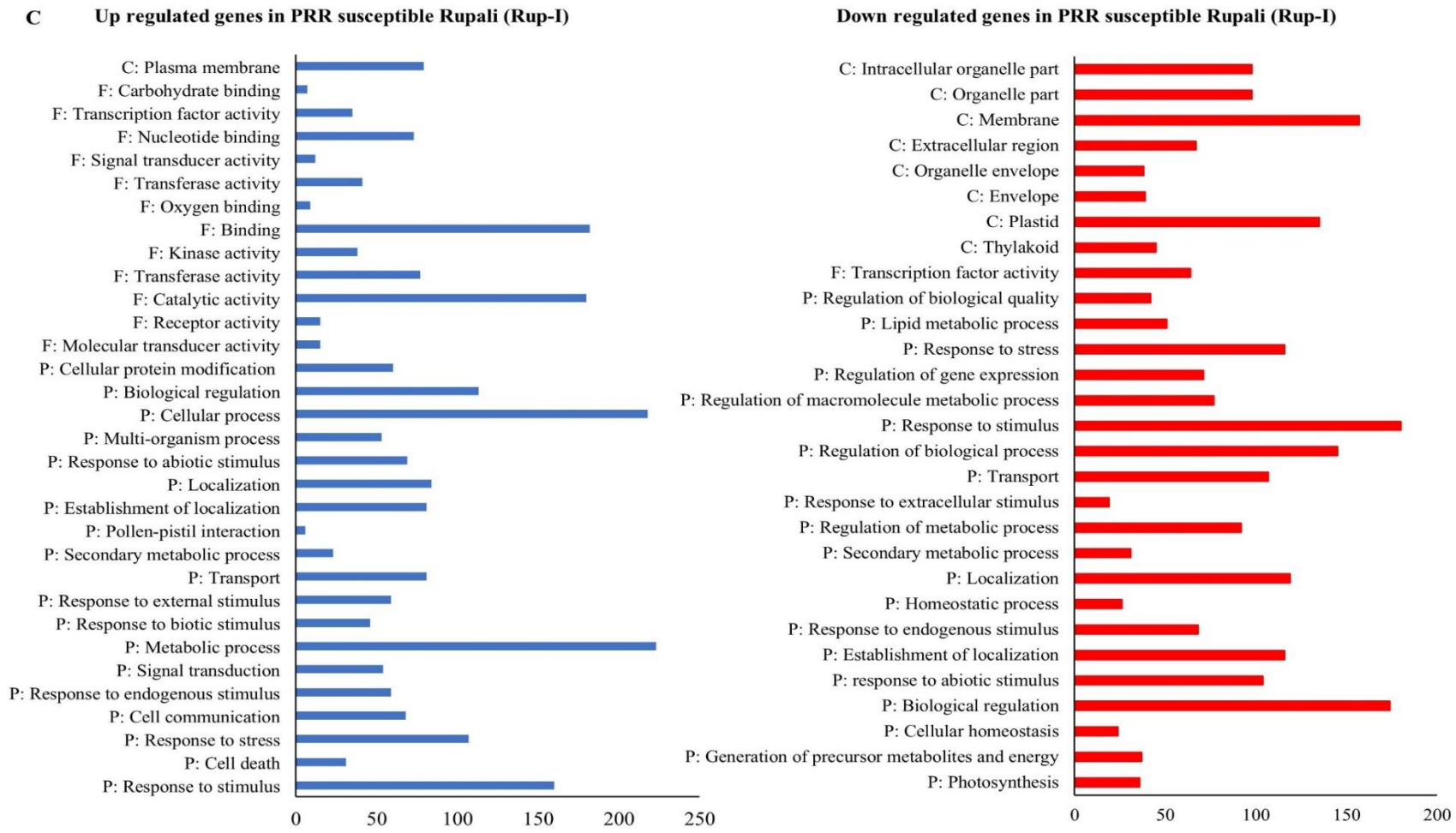


Fig. 5. GO enrichment analysis of DEGs identified in each of the three chickpea genotypes (A) PRR resistant 04067-81-2-1-1 (B) PRR moderately resistant Yorker (C) PRR susceptible Rupali following PRR infection. The abbreviations P, F and C refer to the biological process, molecular function and cellular component.

Differential expression of genes associated with MapMan pathway analysis:

MapMan analysis initially grouped all assembled transcripts into functional groups defined as 'BINs'. Based on the assignment to different BINs, an attempt was made to understand the roles of identified DEG for each genotype in response to PRR infection. This was performed by classification into primary metabolic reactions that commonly modulate various cellular functioning during biotic stress caused by pathogen attack as built into the MapMan software tool. The pathways of energy metabolism, signalling, transcription factors, cell wall modification, proteolysis and biosynthesis of secondary metabolites were observed to be enriched in the roots of genotypes 04067-81-2-1-1 (Bc-I), Yorker (Yor-I) and Rupali (Rup-I) following PRR infection. However, there were differences in the number and in the direction of gene regulation associated with energy metabolism involving redox state, peroxidases and glutathione-S-transferases, signalling, WRKY and MYB transcription factors, cell wall modification, proteolysis, heat shock proteins and biosynthesis of secondary metabolites, in the roots of the PRR-resistant 04067-81-2-1-1, the PRR moderately resistant variety Yorker and PRR-susceptible Rupali (Fig. 6A, B and C). Genes involved in redox state signalling and hormone signalling such as auxins, abscisic acid (ABA) and ethylene (ET) were observed to be specifically down-regulated in PRR-resistant 04067-81-2-1-1. It is also notable that Mitogen-activated protein kinase (MAPK) cascades were activated only in 04067-81-2-1-1 following PRR infection. Similarly, jasmonate (JA) hormone signalling and brassinosteroid signalling pathways were observed to be oppositely regulated in PRR-moderately resistant Yorker and PRR-susceptible Rupali. However, a high number of genes associated with oxidative burst and R-gene signalling during pathogen recognition and pathogenesis-related (PR) proteins in response to pathogen attack were activated in Rupali. This could be attributed to the susceptible response observed in Rupali wherein the R-gene and PR proteins activated following PRR infection in this genotype (Rupali) are not appropriate to counteract the effector

molecules from *P. medicaginis*. The distinct differences observed in the molecular pathways modulated during plant defence response to pathogen attack between the two PRR-resistant chickpea genotypes could be attributed to the different sources of PRR resistance derived from *C. echinospermum* and *C. arietinum* involved in the response to infection.

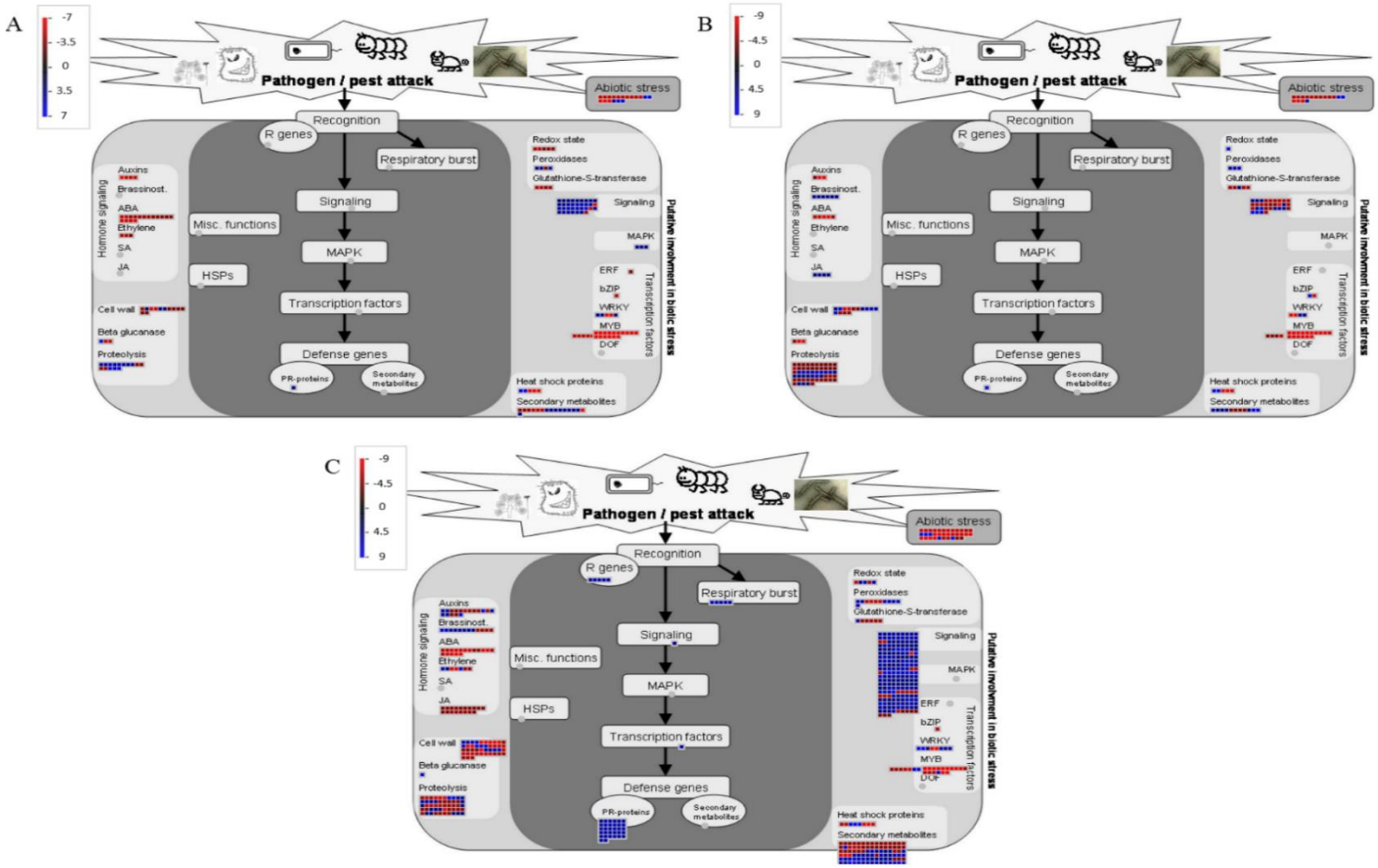


Fig. 6. Distribution of differentially expressed genes in different metabolic pathways in the root tissues of (A) PRR resistant breeding line 04067-81-2-1-1 (Bc-I), (B) PRR moderately resistant Yorker (Yor-I), (C) PRR susceptible Rupali (Rup-I) at eight hours after PRR infection. DEG from each genotype were subjected to MapMan Pathway analysis (Lohse et al., 2014), with up regulation and down regulation genes shown in blue and red colours, respectively. Each square represents a single DEG.

DEG coincidental with PRR resistance-related QTL regions:

The genomic locations of DEG identified following PRR infection in the two PRR-resistant genotypes, 04067-81-2-1-1 (Bc-I) and Yorker (Yor-I), were compared to previously identified regions associated with PRR resistance in bi-parental mapping populations derived from crosses of these parental genotypes (Amalraj et al., 2018). A total of 39 DEG were located within the QTL *QYGprrsi02* on chromosome 5 found in a Yorker x Genesis114 population (Table 4). Of these, four DEG (Ca_11390, Ca_07421, Ca_04067 and unannotated transcript which could potentially code for sucrose-like protein) were found to be differently expressed both in response to treatment and in comparison, with the susceptible genotype following PRR infection. In addition, 20 genes were differently expressed in Yorker compared to Rupali following PRR infection. A total of ten DEG were localised to the interval *QYGprrsi03* on chromosome 6 (Table 4). Of these, six genes (Ca_06379, Ca_06474, Ca_06356, Ca_06384, Ca_06380 and Ca_06488) showed differences in expression patterns in Yorker compared to Rupali under treatment. The gene Ca_06369 located in the interval *QYGprrsi03*, coding for GDSL lipase associated with lipid metabolism, was observed to be differently expressed in Yorker variety both in response to treatment and in comparison, with the susceptible genotype. Likewise, for the genomic regions associated with PRR resistance from the chickpea breeding line 04067-81-2-1-1, three DEG were localised to *QYBprrsi02* on chromosome 6 identified for PRR resistance in a Yorker x 04067-81-2-1-1 mapping population (Amalraj et al., 2018), and two of these genes (Ca_16452 and Ca_16443) were observed to be differently expressed in PRR-resistant 04067-81-2-1-1 during infection compared to Rupali (Table 5). Two DEG identified from the treatment effect in PRR- resistant 04067-81-2-1-1 (Bc-I) were found to be in the interval *QRBprrsi01* on chromosome 3 identified for PRR resistance in the Rupali x 04067-81-2-1-1 population. The gene Ca_24447 coding for aquaporin SIP1-2 found to be differently expressed in wild *Cicer* source of PRR resistance (Bc-I) in comparison to both

Yorker and Rupali was located in the major PRR resistance QTL interval *QRBprrsi04* on chromosome 6 (Table 5). Furthermore, the genes Ca_21371 and an unannotated transcript which is predicted to encode for cytochrome P450 were differently expressed in 04067-81-2-1-1 compared to Rupali were found to be in the interval *QRBprrkms05* and *QRBprrck05* on chromosome 7. This locus was found to co-locate for both plant survival and canker length traits linked to PRR resistance in chickpea. Additionally, five DEG expressed in 04067-81-2-1-1 (Bc-I) following PRR infection were also mapped to the same QTL. Also, two DEG identified in PRR- resistant 04067-81-2-1-1 during infection were found to be located within *QRBprrkms03* and *QRBprrck03* QTL on chromosome 4. Similarly, nine DEG were found to be localised in the interval *QRBprrck04* on chromosome 6 and of these six genes (Ca_13864, Ca_15792, Ca_23154, Ca_24868, Ca_23252 and an unannotated transcript potentially coding for ABC transporter like protein) were differently expressed in the roots of PRR- resistant 04067-81-2-1-1 compared to Rupali following PRR infection.

Table 4. Summary of the differentially expressed genes in the PRR moderately resistant chickpea variety Yorker (Yor-I) under inoculation co-locating previously reported QTL regions associated with PRR resistance in a Yorker x Genesis114 RIL population (Amalraj et al., 2018).

QTL name	Gene-working id	Chickpea reference gene id	Chromosome	Direction of regulation	Functional annotation of the gene
QYGprrsi02	MSTRG.13274	Ca_07641	Ca5	Up regulation	zinc finger protein constans-like 9
QYGprrsi02	MSTRG.13182	Ca_07542	Ca5	Up regulation	alcohol dehydrogenase-like 7
QYGprrsi02	MSTRG.13310	Ca_19234	Ca5	Up regulation	nudix hydrolase 2
QYGprrsi02	MSTRG.13266	Ca_07635	Ca5	Up regulation	subtilisin-like protease SBT5.3
QYGprrsi02	MSTRG.13344	Ca_11406	Ca5	Up regulation	cysteine desulfurase 1
QYGprrsi02	MSTRG.13683	Ca_03988	Ca5	Down regulation	RING-H2 finger protein ATL65
QYGprrsi02	MSTRG.13524	Ca_12665	Ca5	Down regulation	uncharacterized protein At4g08330
QYGprrsi02	MSTRG.13614	Ca_03916	Ca5	Down regulation	F-box protein SKP2A-like
QYGprrsi02	MSTRG.13647	Ca_03953	Ca5	Down regulation	RNA polymerase sigma factor sigE
QYGprrsi02	MSTRG.13155	Ca_07516	Ca5	Down regulation	thiol-disulfide oxidoreductase DCC
QYGprrsi02	MSTRG.13773	Ca_04080	Ca5	Down regulation	protein response to low sulfur 2-like
QYGprrsi02	MSTRG.13060	Ca_07420	Ca5	Down regulation	BTB/POZ and TAZ domain-containing protein 1-like
QYGprrsi02	MSTRG.13518	-	Ca5	Down regulation	hypothetical protein MTR_3g087890
QYGprrsi02	MSTRG.13381	-	Ca5	Down regulation	transmembrane protein, putative
QYGprrsi02	MSTRG.13809	Ca_04111	Ca5	Down regulation	putative GATA-type transcription activator
QYGprrsi02	**MSTRG.13357**	**Ca_11390**	Ca5	Up regulation	probable xyloglucan galactosyltransferase GT14
QYGprrsi02	**MSTRG.13377**	**Ca_11365**	Ca5	Up regulation	15-cis-zeta-carotene isomerase
QYGprrsi02	**MSTRG.13239**	**Ca_07604**	Ca5	Up regulation	oligopeptide transporter 7-like
QYGprrsi02	**MSTRG.13061**	**Ca_07421**	Ca5	Up regulation	probable pectate lyase 5
QYGprrsi02	**MSTRG.13220**	**Ca_07584**	Ca5	Up regulation	endoglucanase 11
QYGprrsi02	**MSTRG.13162**	**Ca_07522**	Ca5	Up regulation	betaine aldehyde dehydrogenase 1
QYGprrsi02	**MSTRG.13284**	**Ca_11424**	Ca5	Up regulation	glucan endo-1,3-beta-glucosidase 4
QYGprrsi02	**MSTRG.13125**	**Ca_07483**	Ca5	Up regulation	probable boron transporter 2 isoform X1
QYGprrsi02	**MSTRG.13735**	**Ca_04041**	Ca5	Up regulation	RNA-binding protein 38-like
QYGprrsi02	**MSTRG.13365**	**Ca_11381**	Ca5	Up regulation	xyloglucan endotransglucosylase/hydrolase 2

QYGprrsi02	**MSTRG.13750**	**Ca_04055**	Ca5	Up regulation	ribosome-binding factor PSRP1
QYGprrsi02	**MSTRG.13278**	**Ca_07645**	Ca5	Up regulation	transmembrane protein, putative
QYGprrsi02	**MSTRG.13782**	**Ca_04085**	Ca5	Up regulation	cytochrome P450 714A1-like
QYGprrsi02	**MSTRG.13634**	**Ca_03943**	Ca5	Down regulation	protein MKS1
QYGprrsi02	**MSTRG.13497**	**Ca_12695**	Ca5	Down regulation	putative C2 domain-containing protein
QYGprrsi02	**MSTRG.13495**	**Ca_12697**	Ca5	Down regulation	putative C2 domain-containing protein
QYGprrsi02	**MSTRG.13751**	**Ca_04056**	Ca5	Down regulation	two-component response regulator-like APRR5 isoform X1
QYGprrsi02	**MSTRG.13302**	**Ca_11408**	Ca5	Down regulation	chalcone synthase 4-like
QYGprrsi02	**MSTRG.13145**	**Ca_07508**	Ca5	Down regulation	probable alpha-trehalose-phosphate synthase [UDP-forming] 9
QYGprrsi02	**MSTRG.13196**	**Ca_07559**	Ca5	Down regulation	NADH--cytochrome b5 reductase 1-like
QYGprrsi02	**MSTRG.13189**	**Ca_07550**	Ca5	Down regulation	UPF0481 protein At3g47200-like
QYGprrsi02	**MSTRG.13507**	**Ca_12684**	Ca5	Down regulation	protein downstream of flc
QYGprrsi02	**MSTRG.13764**	**Ca_04067**	Ca5	Down regulation	heavy metal-associated isoprenylated plant protein 9
QYGprrsi02	**MSTRG.13059**	**-**	Ca5	Down regulation	sucrase-like protein
QYGprrsi03	MSTRG.15565	Ca_06354	Ca6	Up regulation	putative methyltransferase
QYGprrsi03	MSTRG.15698	Ca_06485	Ca6	Up regulation	Serine/Threonine kinase, plant-type protein, putative
QYGprrsi03	MSTRG.15573	Ca_06357	Ca6	Up regulation	isoflavone synthase
QYGprrsi03	MSTRG.15589	Ca_06379	Ca6	Down regulation	flagellar basal body L-ring protein
QYGprrsi03	**MSTRG.15580**	**Ca_06369**	Ca6	Up regulation	GDSL esterase/lipase At5g45960
QYGprrsi03	**MSTRG.15689**	**Ca_06474**	Ca6	Up regulation	filament-like plant protein 7
QYGprrsi03	**MSTRG.15568**	**Ca_06356**	Ca6	Down regulation	isoflavone 4'-O-methyltransferase
QYGprrsi03	**MSTRG.15593**	**Ca_06384**	Ca6	Down regulation	protein trichome birefringence-like 38
QYGprrsi03	**MSTRG.15590**	**Ca_06380**	Ca6	Down regulation	phospholipase A1-IIgamma
QYGprrsi03	**MSTRG.15704**	**Ca_06488**	Ca6	Down regulation	plastid movement impaired protein

The gene working id and the corresponding available chickpea reference id highlighted in bold represent the DEG expressed in PRR moderately resistant Yorker in comparison to the PRR susceptible Rupali.

Table 5. Summary of the differentially expressed genes in PRR resistant chickpea breeding line 04067-81-2-1-1 (Bc-I) under inoculation co-locating with previously reported QTL regions associated with PRR resistance in a 04067-81-2-1-1 x Rupali RIL population (Amalraj et al., 2018, Amalraj et al., 2019).

QTL name	Gene-working id	Chickpea reference gene id	Chromosome	Direction of regulation	Functional annotation of the gene
QYBprrsi02	MSTRG.16434	-	Ca6	Down regulation	glucan endo-1,3-beta-glucosidase 14
QYBprrsi02	**MSTRG.16400**	**Ca_16452**	Ca6	Up regulation	probable 2-carboxy-D-arabinitol-1-phosphatase
QYBprrsi02	**MSTRG.16389**	**Ca_16443**	Ca6	Up regulation	glucomannan 4-beta-mannosyltransferase 2
QRBprrsi04	**MSTRG.16533**	**Ca_24447**	Ca6	Up regulation	aquaporin SIP1-2
QRBprrsi01	MSTRG.6977	Ca_00734	Ca3	Up regulation	purine-uracil permease NCS1
QRBprrsi01	MSTRG.6967	Ca_00727	Ca3	Down regulation	UDP-glycosyltransferase 73C2
QRBprrkms05	MSTRG.20169	Ca_13791	Ca7	Up regulation	K(+) efflux antiporter 2
QRBprrkms05	MSTRG.20246	Ca_16441	Ca7	Up regulation	BON1-associated-like protein
QRBprrkms05	MSTRG.20369	-	Ca7	Down regulation	uncharacterized protein LOC101511185
QRBprrkms05	MSTRG.20049	Ca_17633	Ca7	Down regulation	transmembrane protein, putative
QRBprrkms05	MSTRG.20363	Ca_20210	Ca7	Down regulation	protein LNK3
QRBprrkms05	**MSTRG.20407**	**Ca_21371**	Ca7	Up regulation	protein YLS3-like
QRBprrkms05	**MSTRG.20252**	**-**	Ca7	Down regulation	cytochrome P450 704C1-like
QRBprrkms03	MSTRG.9119	Ca_05658	Ca4	Down regulation	phytosulfokines 3
QRBprrkms03	MSTRG.9128	Ca_05651	Ca4	Down regulation	LIM domain-containing protein WLIM1-like
QRBprrkms02	MSTRG.6569	Ca_07308	Ca3	Down regulation	lactosylceramide 4-alpha-glycosyltransferase
QRBprrkms02	**MSTRG.6570**	**Ca_07309**	Ca3	Up regulation	seed maturation protein LEA 4
QRBprrck04	MSTRG.16606	Ca_15777	Ca6	Up regulation	serine/threonine-protein kinase-like protein CCR4
QRBprrck04	MSTRG.16847	Ca_13814	Ca6	Down regulation	heme-binding-like protein At3g10130
QRBprrck04	MSTRG.16621	Ca_26435	Ca6	Down regulation	NAD(P)H-quinone oxidoreductase subunit T
QRBprrck04	**MSTRG.16749**	**-**	Ca6	Up regulation	ABC transporter A family member 7-like protein
QRBprrck04	**MSTRG.16803**	**Ca_23252**	Ca6	Up regulation	BTB/POZ domain-containing protein At5g48800
QRBprrck04	**MSTRG.16817**	**Ca_24868**	Ca6	Up regulation	protein exordium-like 3
QRBprrck04	**MSTRG.16773**	**Ca_23154**	Ca6	Up regulation	ELMO domain-containing protein A isoform X3
QRBprrck04	**MSTRG.16596**	**Ca_15792**	Ca6	Down regulation	protein BEARSKIN2-like
QRBprrck04	**MSTRG.16893**	**Ca_13864**	Ca6	Down regulation	cytochrome P450 71D9-like

The gene working id and the corresponding available chickpea reference id highlighted in bold represent the DEG expressed in PRR resistant chickpea breeding line 04067-81-2-1-1 in comparison to the PRR susceptible Rupali.

Validation of differentially expressed genes:

In order to validate the results of DEG obtained from the *in-silico* analysis of RNA-sequencing data, qRT-PCR was performed using six DEG associated with the PRR response. qRT-PCR validation revealed similar expression patterns for all selected genes, supporting the *in-silico* analysis of RNA-sequencing data (Fig. 7). The gene Ca_15276 was up-regulated in both Yorker (Yor-I) and 04067-81-2-1-1 (Bc-I) during infection while the gene Ca_01365 was down-regulated in both genotypes. Similarly, in the PRR-susceptible genotype Rupali (Rup-I) following PRR infection, the genes Ca_01309 and Ca_15106 showed up and down-regulation patterns respectively, in accordance with DEG analysis of the RNA-sequencing data. Importantly, the DEG Ca_24447 that was observed in each of the three genotype/treatment interactions studied, showed similar patterns of expression in both *in-silico* and qRT-PCR analyses. Comparisons of the expression values of RNA-sequencing data and qRT-PCR across genotypes and treatments showed a strong correlation ($r^2 = 0.9007$) between the two data sets.

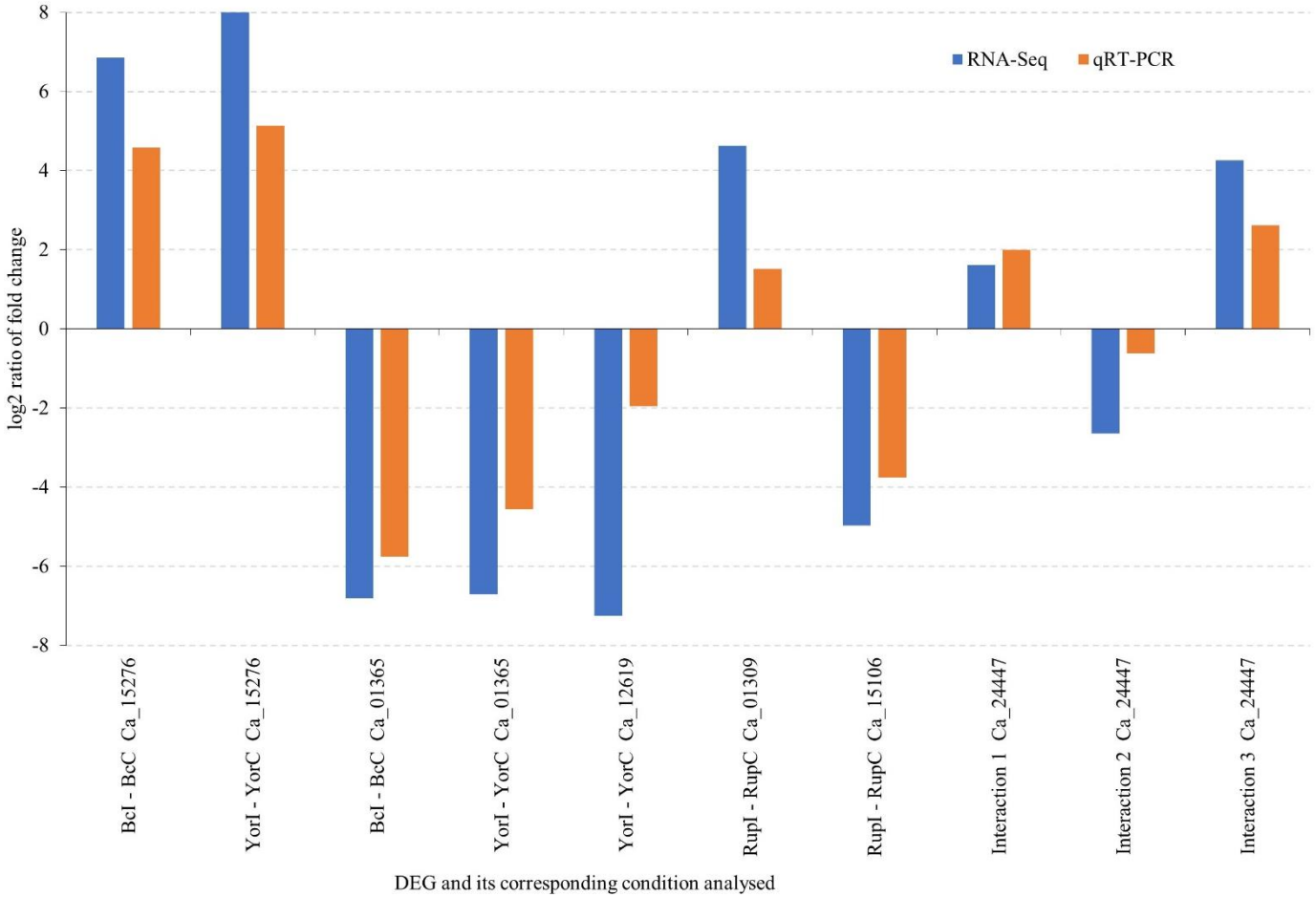


Fig. 7. Comparison of *in-silico* analysis of RNA-sequencing data and qRT-PCR validation experiment using six selected DEG analysed in ten conditions.

Discussion:

This study aimed to identify genes that are differentially expressed in the roots of three chickpea genotypes contrasting in their level of PRR resistance during infection by the *P. medicaginis* isolate 1129-1, and therefore to contribute to the knowledge of resistance to PRR in chickpea. For this, PRR-resistant 04067-81-2-1-1 (with PRR resistance derived from *C. echinospermum*) and moderately PRR-resistant variety Yorker (with PRR resistance source derived from *C. arietinum*) and the PRR-susceptible variety Rupali were selected. Studies from other plant pathogen systems suggested that plants can detect infection almost immediately and that first-line defensive reactions can occur rapidly after pathogen attack (Staskawicz et al, 1995). Therefore, it is important to study the key genes associated with defence response in plants to the pathogen. Knowledge of these genes will be useful in understanding the molecular genetic control of PRR resistance in chickpea which will ultimately support the development of resistant elite varieties through molecular breeding and/or transgenic approaches in crop resistance breeding. The defence response in plants is time-based, involving several signal transduction events at both the molecular and cellular levels, and therefore it is necessary to choose an appropriate time point(s) of infection to study the plant defence response. To define this, an experiment to determine pathogen levels in chickpea roots of PRR-resistant and PRR-susceptible genotypes at different times following inoculation with *P. medicaginis* zoospores was performed. The results clearly demonstrated that the amount of pathogen DNA in chickpea roots of both genotypes reached a plateau at 8 hours after inoculation with zoospore culture. Reaching a plateau at this time point implied that further pathogen invasion and development may have ceased in both genotypes, although it was observed there was a high amount of pathogen DNA accumulated in the roots of Rupali compared to that of 04067-81-2-1-1. For practical reasons such as the time involved and the cost of sequencing, it was determined that

8 hours after inoculation is an appropriate starting point to study the molecular defence response in chickpea against *P. medicaginis* in our system.

The differential expression of genes was analysed between control and infected roots at 8 hours after inoculation in each of three chickpea genotypes, to identify specific changes in expression of genes in each genotype following PRR infection. Additionally, DEG analysis was examined in two PRR-resistant genotypes in comparison with PRR-susceptible Rupali (described as Interactions 1 and 3). This was followed by GO enrichment analysis that functionally classified the DEG identified. The analysis suggested that up-regulated genes belonging to biological processes such as response to stimulus, response to external stimulus, response to extracellular stimulus and response to stress were clearly associated with PRR resistance in the roots of 04067-81-2-1-1. By contrast, the up-regulation of genes associated with lipid metabolic process and photosynthesis were actively involved in the defence signalling process in the roots of Yorker. A relatively higher number of DEG and consequently more GO terms were identified in PRR-susceptible Rupali (Rup-I) compared to the two PRR-resistant genotypes (Yor-I and Bc-I). This implied that intense transcriptional re-programming occurred during the susceptible/compatible interaction compared to the resistant/incompatible interaction of chickpea with *P. medicaginis* at 8 hours after inoculation. Given that this RNA-sequencing study is based on a single time point (8 hours after inoculation), it is possible that the major transcriptional changes occurring in the PRR-resistant genotypes might have taken place earlier to the chosen time point. Therefore, it is proposed that in future, conducting histopathological studies to track the time point at which *P. medicaginis* zoospores come in contact and move into chickpea roots will provide biological information to better understand the host-pathogen interaction. This will also compliment the observed profile of accumulation of pathogen DNA in different chickpea genotypes observed in this study. During the defence response of the plant to pathogen attack, the activation of signalling pathways may either lead

to cell death or activate resistance mechanisms at the site of infection and subsequently in other parts of the plant (Talarczyk et al, 2001). Interestingly, some processes such as response to stress and response to stimulus identified in the PRR-resistant genotypes, were also enriched in roots of PRR-susceptible Rupali along with processes of cell death. A possible explanation could be that a weak, or delayed strength of signalling occurred in roots of Rupali, resulting from the absence of allelic variation or the gene associated with a resistance/ incompatible response has led to its failure to limit pathogen spread or further development of PRR disease symptoms. This also correlated with a higher amount of pathogen DNA in Rupali compared to that of the 04067-81-2-1-1, observed in the TaqMan PCR experiment.

The pathogens belonging to the genera Phytophthora are known to propagate as zoospores through the extracellular spaces of plant tissue, in this case roots, spreading hyphae. Hyphae form feeding structures called haustoria to penetrate the host cell wall (Davison, 1998). Molecules released from the pathogen such as lipopolysaccharides, flagellin, chitin and other pathogen-associated molecular patterns (PAMP) are recognised by cell surface receptors and activate the PAMP-triggered immune response (PTI) in the host plant. Following is a discussion of cellular events associated with the PTI response in plants in the context of patterns of DEG observed in this study.

Plant cell membranes are actively involved in pathogen recognition and signal transduction processes during the early defence response to a pathogen. Following pathogen contact, there is a rapid change in plant cell membrane permeability, resulting in the activation of ion fluxes and oxidative bursts. These events are believed to be mediated through the regulation of plasma membrane-bound enzymes such as Ca^{2+}-ATPase and H^{+}-ATPase, the activation of ion channels and the induction of membrane-bound NADPH oxidase (Gelli et al, 1997; Lam et al, 1998; Neill et al, 2002; Vera-Estrella et al, 1994). Changes in the electrical potential across the plasma membrane can affect the NADPH oxidase energy metabolism,

causing oxidative burst of reactive oxygen species (ROS) such as H_2O_2 and O_2^-. It is currently understood that these pathways mediate changes involving the membrane-bound enzyme NADPH oxidoreductase, G proteins and changes in cytosolic Ca^{2+} concentration, which is known as an important signal associated with the activation of enzymes such as protein kinases, DNA-phosphorylation and gene expression (Aharon et al, 1998; Xing et al, 1997). Plant cells are normally protected from the damaging effects of ROS by various peroxidases and carotenes. We observed up-regulation of peroxidases in roots of PRR-resistant genotypes 04067-81-2-1-1 and Yorker following PRR infection, suggesting a protective role following damage caused in chickpea roots during *P. medicaginis* invasion. Additionally, the up-regulation of DEG coding for receptor kinases, glycoproteins, G-proteins, phosphinositides and leucine-rich repeat (LRR) proteins observed in the roots of 04067-81-2-1-1 likely play an important role in the signalling events associated with PRR resistance in chickpea. We observed similar genes also enriched in the roots of PRR moderately-resistant Yorker, although a variation in the number and direction of regulation of some of these DEG was observed. Furthermore, the gene Ca_24447 located on chromosome 6 and within the interval *QRBprrsi04* associated with PRR resistance in chickpea (Amalraj et al, 2018), was identified as a DEG for both PRR- resistant chickpea genotypes in response to infection (Bc-I and Yor-I) in comparison to Rupali. This gene encodes an aquaporin, SIP1-2. Aquaporins belonging to the major intrinsic protein (MIP) family in plants play an important role in the transport of water, glycerol, H_2O_2 and carbon dioxide (Baiges et al, 2002). It has been reported that in *Arabidopsis thaliana*, AtPIP1;4 is present at the stomatal opening and is involved in H_2O_2 translocation, influencing defence signalling pathways associated with resistance response to *Pseudomonas syringae* (Tian et al, 2016). Similarly, a study in *Capsicum annum* L. has reported that the expression of *CaPIP1-1* encoding for aquaporin is infection stage-specific during phytophthora foliar blight infection caused by *P. capsici* (Yin et al, 2015). This PIP aquaporin was observed to be up-

regulated during spore germination bringing about changes in the plant metabolic pathways associated with resistance response to *P. capsici*. Based on an earlier finding of Dale & Irwin (1991a) that stomata present in chickpea roots act as in entry point for *P. medicaginis* zoospores in surface water, it is possible that Ca_24447 could be involved in the defence response in chickpea, with a role limiting pathogen growth and also activating downstream signalling molecules that participate in the resistance response. Future research should focus on understanding the complete functional role of Ca_24447 in the chickpea-phytophthora interaction regulating the resistance response.

Another important cellular event associated with the PTI response in resistant plants is the activation of mitogen-activated protein kinase (MAPK) cascades. These are ubiquitous signal transduction components involved in the transfer of signals from extracellular receptors to cellular responses in plants (Pitzschke et al, 2009). They function through several phosphorylation-dependent mechanisms regulating the activity of different substrates such as transcription factors and other protein kinases (Gómez-Gómez et al, 2001). It has been reported in *A. thaliana* that MAPK cascades are associated with the resistance response to flagellin peptide flg22 from *P. syringae*, by modulating the expression of WRKY transcription factors (Suarez-Rodriguez et al, 2007). Congruently, in this study three DEG coding for MAPK were observed to be up-regulated specifically in the roots of PRR-resistant 04067-81-2-1-1 following PRR infection (Bc-I). Also, the expression of various transcription factors such as ERF (ethylene responsive factor), bZIP (basic leucine zipper domain) and MYB were down-regulated while three WRKY genes were up-regulated and one showed down regulation. We propose that the activation of MAPK cascades brings about the observed changes in the expression of resistance-related transcription factors in 04067-81-2-1-1.

The hormone signalling pathways for compounds such as salicylic acid (SA), jasmonic acid (JA), ethylene (ET), brassinosteroid, auxin and ABA are key regulators for the expression

of defence-related genes including various transcription factors in plants during pathogen attack. Cross- talk between JA-ET pathways and the exact pattern of response are not clearly understood but are believed to be dependent on pathogen type and the physiological state of the plant. Transcriptomic analysis in avocado (*Persea americana* Mill.) has shown that activation of JA signalling pathways contributes to the resistance response against *P. cinnamomi* during early stages of infection (van den Berg et al, 2018). The association of brassinosteroid hormone signalling with plant immune responses has been demonstrated in *A. thaliana* in response to the perception of bacterial-derived flagellin FLS2, in which BRI1-associated receptor kinase 1 (BAK1) binds to brassinosteroid insensitive 1 (BRI1) receptor, triggering downstream phosphorylation events for the expression of defence-related genes (Li et al, 2002). In chickpea, the activation of JA and brassinosteroid pathways was observed specifically in the roots of moderately PRR-resistant Yorker following PRR infection. The activation of JA and brassinosteroid hormone signalling pathways may have led to the expression of defence-related WRKY and MYB transcription factors following PRR infection in Yorker.

Proteolytic enzymes such as proteases are involved in plant growth and development and in regulatory functions in cells of intact or pathogen-infected plant tissues. During pathogen attack, pathogen-derived proteases are secreted into plant cells to modify plant proteins. The activation of different signalling pathways leads to post-translational modification of plant proteases through proteolytic processing, thereby regulating plant defence response to the pathogen (Xia, 2004). DEG associated with post-translational modification of proteolytic machinery such as proteases, subtilases and cysteine proteases, were observed to be enriched in the roots of 04067-81-2-1-1 and Yorker and could potentially contribute to PRR resistance in chickpea during infection. These could counteract the *P. medicaginis*-derived virulence molecules, limiting the spread of pathogen in infected chickpea

roots. Furthermore, genes associated with secondary metabolite pathways such as flavonoids, isoprenoids and chalcones were observed to be differently expressed in the roots of PRR-resistant 04067-81-2-1-1 during infection. In PRR moderately-resistant Yorker, genes associated with the biosynthesis of secondary metabolites such as phenylpropanoids, flavonoids and glucosinolates, were found to be differently expressed following PRR infection. These plant secondary metabolites may directly exhibit antimicrobial effects on the pathogen or be involved in establishing a physical barrier (eg. lignin biosynthesis), reducing the penetration efficiency of the pathogen into the host (Talarczyk & Hennig, 2001).

RNA-sequencing analysis identified genes associated with PRR resistance in different categories such as plasma membrane bound cell wall enzymes including protein kinases/phosphatases, ion channels, transcription factors and defence-related genes like pathogenesis-related proteins. The molecular pathways of redox processes, signalling, proteolysis and biosynthesis of secondary metabolites were observed to be enriched in the roots of both PRR-resistant chickpea genotypes during infection. The contrast in signalling events observed between Yorker and 04067-81-2-1-1 (brassinosteroid and JA hormone signalling processes activated in the cultivated chickpea variety, Yorker and the activation of MAPK cascades activated in the genotype 04067-81-2-1-1) may relate to a difference in the defence responses involving the expression of genes responsible for reducing undesirable effects of the infection (plant survival) and in conferring resistance against *P. medicaginis* in these two resistance sources. However, further detailed molecular, biochemical and cell biological studies are warranted to determine the key differences underlying the two sources of PRR resistance. Several DEG were mapped to QTL regions associated with PRR resistance in Yorker and 04067-81-2-1-1 (Amalraj et al, 2018; Amalraj et al, 2019) using the chickpea reference genome v1.0 (Varshney et al., 2013) for the variety CDC Frontier which is different from the genotypes used in this study. One limitation of this study is that causal genes

associated with PRR resistance from *C. echinospermum* could be either absent or significantly different in sequence compared to the reference genome. In order to address this, the utilisation of a chickpea reference genome derived from *Cicer* echinospermum (when available) could be used to identify DEG and alternative alleles underlying the PRR resistance QTL regions. These genes/ novel alleles could be important targets when developing molecular markers or fine mapping resistance loci and in developing improved chickpea varieties facilitated by molecular breeding and/or transgenic approaches. Thus, this RNA-sequencing study has provided evidence supporting differences in the molecular changes occurring in two PRR-resistant chickpea genotypes, 04067-81-2-1-1 and Yorker, with resistance sources derived from *C. echinospermum* and *C. arietinum* respectively. The outcomes from this study establish a sound foundation for future research aimed at improving the genetic resistance of chickpea to the *P. medicaginis* pathogen.

Authors' contribution:

AA, UB and TS were involved in design of the experiment. AA conducted all experiments described in this study. AA performed computational analysis with assistance from UB. AA drafted the manuscript. All authors reviewed and revised the manuscript. TS supervised the project.

Competing interests:

The authors declare that they have no competing interests.

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Chapter 6

General discussion and future directions:

Genetic diversity existing within landraces and crop wild relatives can provide variation necessary for improvement of agronomical traits, stress tolerance and disease resistance. In modern plant breeding, marker-assisted selection (MAS) is utilised as a primary tool to introgress diversity into breeding programs whilst minimising associated genetic drag from donor genotypes in the secondary and tertiary genetic pools. Prior to this research, there was very little known about the genetic basis of PRR resistance in chickpea against *P. medicaginis*. The knowledge developed in this research will support progress in molecular genetics aspects of a multidisciplinary breeding strategy towards the improvement of PRR resistance in developing future chickpea varieties for the Northern pulse growing region of Australia, where the disease is most prevalent.

Early research on PRR identified two sources of field-based resistance in chickpea. The first was derived from the cultivated *C. arietinum* accession CPI 56564 (ICC11870) (Dale & Irwin, 1991b) and the other, stronger source from a number of accessions of the wild chickpea species *C. echinospermum* (Knights et al, 2008). Subsequently, the *C. arietinum* source of resistance was incorporated into selected Australian chickpea varieties, such as Yorker. However, even under heavy rainfall and high inoculum load, moderately PRR-resistant chickpea varieties such as Yorker can become highly susceptible to the disease, resulting in significant yield loss. A higher level of PRR resistance, identified in the secondary gene pool of the wild chickpea species *C. echinospermum*, was also incorporated into a cultivated chickpea background to form interspecific hybrids (Knights et al, 2008) as the basis for breeding improved resistance. To facilitate genetic studies, crosses from both sources of resistance were used

to develop one intra-specific and two interspecific bi-parental RIL mapping populations referred as YG, RB and YB, respectively, as described in Chapter 3 (Amalraj et al, 2018).

As a first step to understand the genetic basis for PRR resistance in chickpea, this research aimed to identify genomic regions (QTL) associated with resistance, derived from the wild and the cultivated donors. GBS-based DArT-sequencing was used to generate polymorphic markers for linkage map construction. GBS is a sequencing-based genotyping method that has been extensively used in crop species, including legumes, to identify genome-wide SNPs applicable for the development of high-density genetic maps and subsequent QTL analysis, GWAS and genomic selection (GS) applications in breeding (Elshire et al, 2011). Comparison of linkage maps from three RIL mapping populations revealed a low level of polymorphism in the intra-specific population YG compared to the two interspecific populations, RB and YB. The relatively reduced level of polymorphism observed in the progeny of intra-specific crosses of cultivated chickpea species can be attributed to the reduced genetic diversity existing in the parental genotypes, compared to that derived from a cross involving a wild species. Also, this observation substantiates the utilization of a crop's wild relatives from the secondary genetic pool as a source of novel alleles and potentially new genes for improving disease resistance traits (in this case PRR) in chickpea breeding.

The three RIL mapping populations were field-phenotyped for PRR resistance (plant survival trait SI-t3) across three target environments including 2014 rainfed, 2015 rainfed and 2015 irrigated using a mixture of ten *P. medicaginis* isolates. Very little is known about the relative dominance (based on virulence) of *P. medicaginis* isolates collected from field soil samples in the Northern growing regions. There is also no genetic information to support the existence of specific avirulence genes matched to plant resistance genes, and no clear evidence for the existence of race-specific resistance in the chickpea-phytophthora pathosystem. As this research represents the first field-based

genetic study focussed on the chickpea/Phytophthora pathosystem, it was considered appropriate to use a mixture of *P. medicaginis* isolates for inoculation as opposed to using a single isolate.

Based on the relative incidence of PRR disease, the three environments were described as having low (2014 rainfed), moderate (2015 rainfed) and high (2015 irrigated) disease pressure; classifications that were reflected in heritability values calculated for populations across each of the three environments. Heritability for the SI-t3 trait was high from interspecific populations RB and YB in the 2015 rainfed (moderate disease) and 2015 irrigated (high disease) environments, indicating that phenotyping for the plant survival trait SI-t3 in field-based environments with sufficient disease pressure is an effective approach for the selection of PRR resistance in the chickpea breeding program. Subsequently, QTL analyses were performed for each of the populations and in each of the environments. The single environment analyses revealed a significant influence of the environment component in the expression of PRR resistance and to address this, multiple environment QTL analysis was undertaken. This approach enabled the identification of markers linked to PRR resistance QTL across multiple target environments. In the RB population, three major effect QTL (*QRBprrsi01* on chromosome 3, *QRBprrsi02* on chromosome 4 and *QRBprrsi04* on chromosome 6) and one minor effect QTL (*QRBprrsi03* on chromosome 8) were identified with the resistance source derived from *C. echinospermum*. Similarly, in the YB population, two major effect QTL (*QYBprrsi01* on chromosome 3 and *QYBprrsi02* on chromosome 6) were identified with the resistance source derived from *C. echinospermum*. The loci on chromosomes 3 and 6 co-locate in two mapping populations (YB and RB) and across three environments. This result implies that loci derived from the wild relative of chickpea are strongly linked to PRR resistance in chickpea and offer good potential for varietal improvement. In the case of the intra-specific population YG, two major effect

QTL (*QYGprrsi02* on chromosome 5 and *QYGprrsi03* on chromosome 6) were identified across the target environments. The observation that the locations of major QTL for PRR resistance in interspecific and intra-specific populations are physically distinct, provides evidence for independent sources of PRR resistance derived from *C. arietinum* and *C. echinospermum* and informs the way forward for breeding improved PRR resistance. Now that linked markers have been identified and KASP assays are available, future research should encompass validation experiments, examining the association of linked molecular markers with PRR resistance in a large collection of Australian chickpea breeding germplasm. This work will deliver important information to the breeding program to potentially implement routine MAS and pyramid PRR resistance genes in chickpea.

With major QTL for PRR resistance identified, future opportunities are now evident to advance research towards the fine mapping of loci and identification of causal PRR resistance genes. Progress in fine mapping of loci will enable identification of molecular markers closely linked to the resistance gene, minimising the incidence of marker/trait dis-association through recombination in breeding germplasm. A high marker-trait association will be beneficial in a breeding strategy for PRR resistance involving QTL deployment and MAS. Future fine mapping research could involve the development of genetic resources such as near isogenic lines (NILs) or segregating populations derived from RIL inter-crosses. The NIL populations for each locus could be developed rapidly from the selfing of F_6 RILs identified as having residual heterozygosity across PRR resistance QTL. Targeted sequence capture methods could also provide accurate sequence data from a collection of chickpea breeding lines or genetic stocks differing in their response to Phytophthora, providing an opportunity to associate haplotype variation with resistance and susceptibility. This approach would enable the generation of additional markers to support fine mapping of QTL. Additional

markers from QTL regions could also be obtained from publically available re-sequencing data resources for chickpea. New genome level information combined with reliable PRR resistance phenotypic data from key recombinants in regions of interest could be used to delimit resistance QTL and identify the resistance genes.

For plant breeding programs, one of the long term challenges has been the ability to gather informative, cost effective and reproducible phenotypic data relating to essential breeding traits. This is often difficult to achieve, either because the methods are not available, they are not able to be scaled up sufficiently, or they involve field-based trials that are subject to significant environmental variation and cost. When this research began, the only methods available for assessing breeding germplasm or new potential sources of variation to PRR were field-based nurseries. No methods were available for phenotypic assessment of PRR under controlled conditions that were applicable at a scale essential for a large and complex plant breeding program.

To address this need, the second objective of this research was to develop a scalable, hydroponics based phenotyping method for PRR disease screening using zoospore inoculation, as described in Chapter 4 (Amalraj et al, 2019). Initially, pilot-scale experiments were performed to test the efficiency of the system to cause PRR infection by *P. medicaginis* isolate 1129-1. This specific isolate was chosen based on unpublished inoculated glasshouse experiments testing phytophthora isolates, where 1129-1 showed a similar pattern of pathogen-host interaction profile (based on plant mortality) to the mixture of 10 *P. medicaginis* isolates used in field experiments and in breeding trials (Sean Bithell, personal communication). Three chickpea genotypes with known levels of PRR resistance were used in the pilot study. The hydroponics system was validated qualitatively based on observations of PRR symptom development including measurements of plant wilting and canker development on roots and at the base of the stem. For all of these phenotypic measurements a good discrimination between

genotypes was observed. Infection assessment was also made by molecular quantification of amounts of *P. medicaginis* DNA in chickpea roots using a TaqMan MGB assay for *P. medicaginis* (Alan McKay, 2018). This approach resulted in the ranking of disease severity in genotypes similar to visual assessments of plant survival and stem canker length.

The subsequent scaling up of the pilot hydroponics system allowed for high-throughput screening of a larger number of genotypes, to measure and validate quantitative traits linked to PRR resistance, and support method implementation as a future selection tool for resistance in chickpea breeding. Using the scaled-up system, one intra-specific (YG) and one interspecific (RB) RIL mapping populations were screened in consecutive experiments. PRR disease assessments were made during the early stages of disease progression to avoid the complication that older chickpea plants are able to survive by generating new roots from the upper main tap root. In each of the screenings, plant survival time after inoculation was measured and used to derive Kaplan-Meier estimates of plant survival (KME-survival). This provided a basis to objectively measure specific traits linked to PRR resistance in chickpea and undertake genetic analysis.

Genetic analyses of PRR-linked traits demonstrated strong positive correlation between KME-survival and canker length in both the intra-specific (YG, $r^2 = 0.642$) and interspecific (RB, $r^2 = 0.917$) RIL mapping populations. This was also evident from the co-location of KME-survival and canker length QTL on chromosome 4 (*QRBprrkms03* and *QRBprrck03*) and on chromosome 7 (*QRBprrkms05* and *QRBprrck05*) in the RB population with the resistance source derived from the wild species *C. echinospermum*. Additionally, a model-based correlation analysis demonstrated strong negative correlations between KME-survival and canker length from hydroponics and the plant survival trait (SI-t3) from the field (described in Chapter 3). This observation was also supported by the co-location of the major chromosome 4 QTL (*QRBprrkms03* and

QRBprrck03, RB-SNP-79(C): RB-SNP-72(C), respectively) in the RB population under both rainfed field conditions and in hydroponics. Additionally, the major QTL *QRBprrck04* on chromosome 6 identified in hydroponics is directly adjacent to a genetic interval *QRBprrsi04* reported across multiple field experiments from the field-based genetic study (Chapter 3). This result implies that the expression of genetic factors related to PRR resistance under both field and controlled environments are similar. The similarity of PRR QTL for the traits phenotyped in hydroponics and in the field not only provide evidence for genetic similarity in the plant response to this disease across different environments, but also supports the selection of isolate 1129-1 as a single inoculum source for the hydroponics method. The comparable host-pathogen interaction for a range of chickpea genotypes inoculated with *P. medicaginis* isolate 1129-1 and with a more complex mixture of *P. medicaginis* isolates suggests that 1129-1 could initially be used in a relevant breeding selection strategy. Future research could utilise the high-throughput method developed here to screen additional *P. medicaginis* isolates, such as those combined in the cocktail inoculum applied in field nurseries to establish virulence and the interaction with plant genotype.

In the intra-specific population (YG) under hydroponics, genetic correlation and the heritability values were weak. An explanation for this observation could be that PRR disease pressure in hydroponics was relatively high for the intraspecific population, preventing adequate differential expression of resistant and susceptible phenotypes. This observation is in agreement with the field-based PRR resistance study, which also showed low to moderate heritability values from traits measured in the YG population across three environments. Moreover, in the field-based study it was shown that Yorker, the resistant parent in the YG population was classified to be moderately resistant to PRR and known to become susceptible under high inoculum loads when disease pressure was high. These observations suggest that breeding for PRR resistance in chickpea should

primarily focus on the utilisation of resistance genes/alleles from wild crop relatives, to provide enhanced adaptation under severe disease conditions compared to the available genetic variants in the *C. arietinum* gene pool. It is recommended that in future, when screening for YG population in hydroponics, reducing the disease pressure will achieve better discrimination between the moderately PRR resistant Yorker and the susceptible Genesis114. The disease pressure required to cause PRR infection can be varied by altering the concentration of zoospores applied as the inoculum. Consideration can also easily be given to the use of zoospores of more than one *P. medicaginis* isolate, which could prove to be beneficial in a breeding program when screening for partial resistance to PRR or if there is knowledge that certain isolates are prevalent in specific environments.

The hydroponics phenotyping method developed in this research provides an opportunity to overcome some of the major limitations presented by current PRR field-based screening systems, while still allowing for a natural course of PRR infection and appropriate expression of resistance in host chickpea plants. The use of *P. medicaginis* zoospores as the inoculum is considered to be key for achieving uniform disease pressure both in small and large scale screening of PRR, thereby eliminating environmental sources of variation caused by flooding and draining regimes that are needed for the development of phytophthora infection when using *P. medicaginis* oospores as the inoculum. Another advantage of the use of zoospores as opposed to applying oospores or a mycelium slurry is the ability to promptly cause PRR infection and initiate a resistance/susceptibility response in the host plant. This control of infection timing is important as it also facilitates temporal control of the plant response to pathogen infection. This detailed level of control is particularly relevant for molecular studies aimed at identification of specific genes or biological processes involved in the temporal plant response to PRR infection. Additionally, molecular studies with hydroponically

grown plants permit the relatively simple and efficient harvest of clean root and shoot tissue samples that are free from soil and other pathogen contaminants associated with field-grown plant samples.

Following the development of an *in planta* infection system to phenotype PRR resistance, a complementary genomics approach based on RNA-sequencing was undertaken to identify genes differentially expressed in roots of chickpea genotypes differing in their levels of PRR resistance (Chapter 5). In this approach, the PRR-resistant line 04067-81-2-1-1 (with the *C. echinospermum* source of PRR resistance), the moderately PRR-resistant variety Yorker (with the *C. arietinum* source of PRR resistance) and the PRR-susceptible variety Rupali were selected. From other pathosystems, it has been well documented that the plant response to pathogen attack is time-based involving a complex network of signalling events that leads to expression of defence-related genes (Talarczyk & Hennig, 2001). It was therefore desirable to determine a suitable time point of PRR infection that would enable the study of plant defence response gene expression changes to *P. medicaginis* in chickpea. To achieve this, an experiment to quantify the amount of phytophthora DNA in chickpea roots of PRR resistant and susceptible genotypes at different time points after inoculation was performed using the TaqMan MGB assay (Alan McKay, 2018). The results showed that the amount of pathogen DNA accumulated in roots of both chickpea genotypes reached a plateau at 8 hours after inoculation indicating the cessation of further pathogen invasion or multiplication in chickpea roots after this time. Therefore, 8 hours after inoculation was chosen as an appropriate time point to study gene expression aspects of the early plant defence response in chickpea against *P. medicaginis*.

The differential expression of gene analysis was conducted from the expression data obtained from control and treated root tissues at 8 hours after inoculation in each of the three chickpea genotypes. Additionally, DEG analysis was performed in the two PRR

resistant genotypes, in comparison with PRR-susceptible Rupali following PRR infection. DEG analysis was followed by GO analysis that functionally classified the DEG identified. Overall, this research demonstrated that genes belonging to biological processes such as response to stimulus, response to external stimulus, response to extracellular stimulus and response to stress were up-regulated in the roots of 04067-81-2-1-1 following infection. In the moderately PRR resistant variety Yorker, genes associated with lipid metabolic process and photosynthesis were up-regulated, contributing to early defence signalling processes. A relatively higher number of DEG were identified in PRR-susceptible Rupali compared 04067-81-2-1-1 and Yorker at 8 hours after inoculation, indicating that a more intense transcriptional re-programming occurred during the susceptible/compatible interaction compared to the resistant/incompatible interaction of chickpea with *P. medicaginis*. An explanation for this observation is that a weak or delayed signalling response post-infection in Rupali was ineffective at limiting pathogen growth and preventing further infection. This interpretation could also be attributed to the use of a single time point (8 hours after inoculation) selected for RNA-sequencing. It is possible that major transcriptional changes occurring in PRR-resistant genotypes might have taken place earlier than the point 8 hours after inoculation. Future experimental examination should involve histopathological studies to determine the specific timing of *P. medicaginis* zoospore contact with chickpea roots, and the rate of zoospore movement inside the roots should be investigated This information will assist in the understanding and interpretation of biologically relevant timepoints associated with the Phytophthora-Chickpea interaction.

The differentially expressed genes identified in PRR-resistant and susceptible chickpea genotypes following infection were used to categorise pathways associated with signalling processes during pathogen attack using MapMan software tools (Lohse et al, 2014; Thimm et al, 2004). In general terms, when a pathogen comes in contact with a

host plant, events such as the synthesis of reactive oxygen species (H_2O_2 and O_2^-), altered ion fluxes, cytoskeletal rearrangements, protein phosphorylation/dephosphorylation, transcriptional and post-translational modification of transcription factors are all associated with the first line of plant defence, limiting the spread of the pathogen and the incidence of disease. Among these, specific changes in ion fluxes and protein phosphorylation are known to serve as signals initiating transcription-dependent aspects of the defence response at the infection site, as well as the starting point for systemic signal transduction to other parts of the plant (Talarczyk & Hennig, 2001). In this study, the up-regulation of genes encoding peroxidases in the roots of the two PRR-resistant genotypes was observed following infection, implying a protective role following root damage caused during *P. medicaginis* infection. In addition to these changes, the up-regulation of DEG coding for receptor kinases, glycoproteins, G-proteins, phosphinositides and leucine rich repeat (LRR) genes observed in roots of the two PRR-resistant chickpea genotypes are hypothesised to play an important role in signalling events associated with the PRR resistance mechanism in chickpea.

One identified DEG, Ca_24447 was shown to be expressed in both 04067-81-2-1-1 and Yorker during infection, in comparison to Rupali. BLAST analysis of the chickpea genome revealed that it is located on chromosome 6 with the interval *QRBprrsi04*. Ca_24447 encodes for the aquaporin protein SIP1-2. Aquaporins belong to the major intrinsic protein (MIP) family of transmembrane channels in plants and are involved in regulating the flux of water and other small solutes such as glycerol, H_2O_2 and carbon dioxide (Baiges et al, 2002). Besides their role in plant physiological process, recent studies have associated the expression of aquaporins with biological process related to plant-pathogen interactions. In Arabidopsis, it has been reported that during inoculation with *Pseudomonas syringae*, the aquaporin AtPIP1;4 is involved in apoplastic translocation of H_2O_2 to the cytoplasm which activates PAMP-triggered

immunity (PTI) pathways influencing resistance-related response against pathogens (Tian et al, 2016). Similarly, analysis in *Capsicum annuum* L. has shown that during phytophthora foliar blight infection the expression of aquaporin *CaPIP1-1* is infection stage-specific (Yin et al, 2015). *CaPIP1-1* is up-regulated during the spore germination process, bringing about changes in plant secondary metabolite pathways as a part of the defence response to *P. capsici*. Rodrigues et al, (2017) proposed a model in which the activation of aquaporin P1P2;1 by flg22 (eubacterial flagellin-derived protein, a PAMP) and ABA enabled the translocation of water and H_2O_2 produced during pathogen recognition, leading to stomatal closure and activation of downstream signalling pathways and prevention of further pathogen invasion. Based on the observed differential gene expression of Ca_24447 (SIP1-2) between PRR-resistant and susceptible genotypes, and in combination with earlier findings of Dale & Irwin, (1991a) that stomata present in chickpea roots act as an infection site for *P. medicaginis* zoospores present in surface water, it is proposed that SIP1-2 could have a similar role in PRR resistance in chickpea.

From this discovery, a number of future research opportunities across different disciplines can be considered. Initial research questions should focus on identifying potential non-synonymous sequence variation in the *SIP1-2* gene between PRR-resistant and susceptible genotypes that could affect protein function. Identification of the SIP1-2 gene promoter sequence would also enable investigation into polymorphism related to the observed expression difference of the SIP1-2 mRNA, and characterisation of putative regulatory elements with a role associated with disease resistance. Microscopy methods such as *in situ* hybridisation could provide insight into the role of SIP1-2 in PRR resistance, by localising expression to specific root tissues. Furthermore, to determine specific transport properties of SIP1-2, protein analysis techniques involving the recombinant expression of membrane proteins in heterologous systems such as *Xenopus*

laevis oocytes could be considered. Recently, significant advancements in nanotechnology tools has also enabled the development of methods for the *in vitro* synthesis of plant membrane proteins under "native" conditions using tethered bilayer lipid membranes comprising proteo-liposomes, detergents, ampiphols, and surfactant peptides to ensure proteins are in properly folded and functional forms with appropriate yield suitable for structural and functional studies (Periasamy et al, 2013). The synthesised proteins can subsequently be used in transport assays based on impedance spectroscopy (Terrettaz & Vogel, 2005) and stopped-flow measurements (Tyerman et al, 1999), to determine specific transport characteristics that can be related to PRR resistance in chickpea.

Differences in DEG and response pathways were evident between the two sources of resistance to PRR; Yorker (*C. arietinum*) and 04067-81-2-1-1 (*C. echinospermum* derivative). Following infection, genes encoding MAPK were up-regulated specifically in the roots of the PRR-resistant genotype 04067-81-2-1-1. Based on analogies with disease resistance literature (Pitzschke et al, 2009; Suarez-Rodriguez et al, 2007), we propose that the activation of MAPK is responsible for changes also observed in the expression of defence-related transcription factors such as ERF (ethylene responsive factor), bZIP (basic leucine zipper domain), MYB and WRKY in 04067-81-2-1-1. In the moderately PRR-resistant variety Yorker, the activation of JA and brassinosteroid hormone signalling pathways was observed to be specific to this genotype following infection. We propose that this can lead to the observed changes in the expression of defence-related WRKY and MYB transcription factors following infection in Yorker. This observed difference in signalling events between cultivated and *C. echinospermum* sources of resistance can lead to differences in their respective late defence responses conferring resistance against *P. medicaginis*.

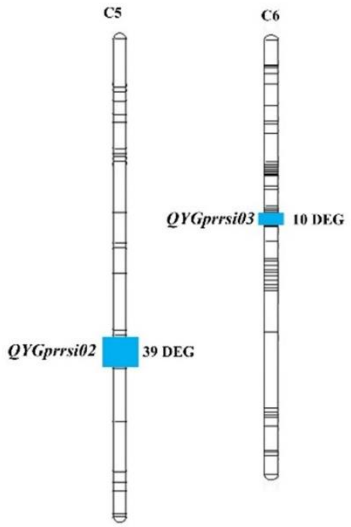
The differentially expressed genes encoding proteins associated with post translational modification of proteolytic machinery such as proteases, subtilases and cysteine proteases were observed to be regulated in the roots of 04067-81-2-1-1 and Yorker following infection, potentially contributing to a component of PRR resistance in chickpea. One role that these molecules could have in contributing to resistance may be involved in interaction with *P. medicaginis* derived effector molecules to limit pathogen spread in infected roots. Moreover, DEG predicted to encode secondary metabolite pathways such as flavonoids, isoprenoids and chalcones were observed to be expressed specifically in the roots of PRR resistant 04067-81-2-1-1, while in moderately PRR resistant Yorker, phenylpropanoid and glucosinolates were found to be expressed following infection. Plant secondary metabolites may either directly exhibit antimicrobial effect on the pathogen or may be involved in establishing a physical barrier (e.g. lignin biosynthesis) thereby retarding the penetration efficiency of the pathogen into the host. These observations provide an opportunity for future research opportunities to clarify the role of these processes in the resistance mechanism, and to elucidate differences between the two sources of resistance. As a first step, a detailed temporal analysis of the expression responses to PRR infection of these secondary metabolite pathway genes could be undertaken. Associated metabolomics experiments could reveal more clearly the roles of specific metabolites in resistance responses.

In summary, the approaches adopted in this research have revealed substantiated differences in PRR resistance derived from cultivated and wild *Cicer* sources. Determining the physical locations of DEG in the chickpea reference genome enabled the prioritisation of candidates that physically mapped to QTL regions associated with PRR resistance identified in genetic studies (Amalraj, Taylor et al. 2018; Chapter 3, Amalraj, Taylor et al. 2019; Chapter 4). A limitation of this RNA-sequencing study, however, relates to the use of the chickpea reference genome v1.0 (Varshney et al., 2013)

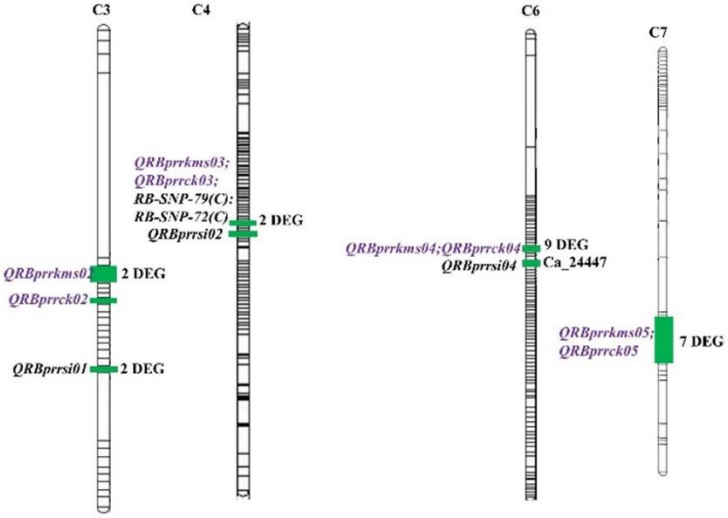
derived from the *Cicer arietinum* variety CDC Frontier. It is possible that causal genes associated with PRR resistance derived from *C. echinospermum* could be either absent in CDC Frontier or be significantly different in sequence compared to the reference genome that they were not identified as QTL-candidates in this approach. This can be addressed in future studies by using a chickpea reference genome derived from *C. echinospermum* (when available) for identifying DEG and/or alternative alleles underlying the PRR resistance QTL regions. These novel genes/ alleles should be considered important targets for future research aimed at identifying the underlying causal genetic factors regulating PRR resistance in chickpea. Transcript sequences of specific genes from resistant and susceptible genotypes could be aligned and examined for polymorphism to correlate non-synonymous variation with phenotypic variation. Additional sequence variation could be determined with targeted re-sequencing using sequence capture across the major PRR resistance loci from a number of resistant and susceptible chickpea genotypes. The resistant loci of major interest are the QTL *QRBprrsi04* and *QYBprrsi02* on chromosome 6 and, *QRBprrsi01* and *QYBprrsi01* co-locating on chromosome 3 with resistance source derived from *C. echinospermum* (Fig. 6.1). This will enable the construction of comprehensive haplotypes for the PRR resistance QTL regions to potentially identify candidate genes associated with PRR resistance in chickpea. An alternative approach would be to employ sequence-based trait mapping, by sequencing the pooled samples of extreme phenotypes selected from the RIL populations. Bulked segregant RNA-seq (BSR-seq) is based on expression as opposed to bulk segregant analysis using DNA (Michelmore et al, 1991). A recent application of this technique was described by Liu et al, (2012), who demonstrated the use of BSR-seq to identify the gene *GPC-B1* for grain protein content in wheat. To date, there is no study that has been reported to use this approach for trait mapping in legumes,

and it would be interesting to explore the outcomes of such an approach in chickpea to determine the genetic basis of PRR resistance.

YG


C5
C6
QYGprrsi03
10 DEG
QYGprrsi02
39 DEG

RB


C3
C4
C6
C7
QRBprrkms03;
QRBprrck03;
RB-SNP-79(C);
RB-SNP-72(C)
QRBprrsi02
2 DEG
QRBprrkms01
2 DEG
QRBprrck02
QRBprrsi01
2 DEG
QRBprrkms04;QRBprrck04
9 DEG
QRBprrsi04
Ca_24447
QRBprrkms05;
QRBprrck05
7 DEG

YB

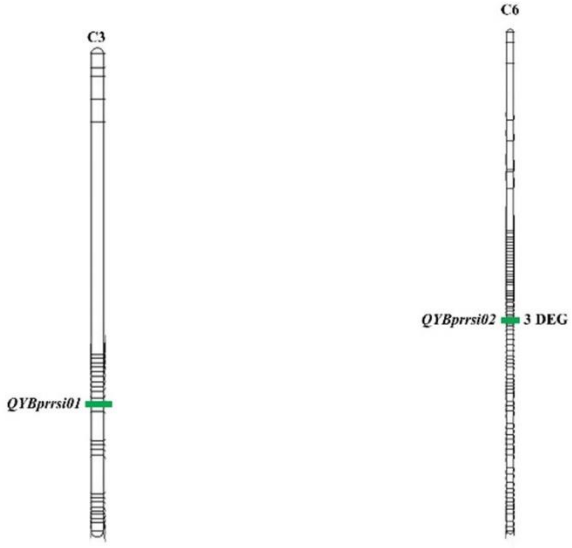

C3
C6
QYBprrsi01
QYBprrsi02
3 DEG

Fig. 6.1 Schematic representation of PRR resistance QTL regions on genetic map identified in this research. Shown are QTL from the intra-specific population YG (at top), RB, (Centre) and YB (bottom). Resistance sources derived from *C. arietinum* are shown as blue shading, those derived from *C. echinospermum* as green shading. In each population, QTL identified from field experiments are written in black and from hydroponics in purple. The number of DEG identified as physically mapping to the corresponding QTL interval are shown.

An additional area of knowledge that will support ongoing research of the chickpea/ PRR interaction relates to the *P. medicaginis* pathosystem. This could be addressed by exploring the field pathogenomics of *P. medicaginis*, by collecting genomic and transcriptomic data from field samples of the pathogen, and determining the population structure and genetic diversity in pathogen populations (Möller & Stukenbrock, 2017). Such data, when monitored both temporally and spatially will prove to be beneficial in predicting an emerging outbreak based on changes in the genetic diversity and population structure shifts of the pathogen (Hubbard et al, 2015). This type of research effort at the genomic-level of the pathogen will not only provide information regarding the pathogen effector molecules but also on the evolutionary process of the pathogen. This combination of knowledge from both the host plant and pathogen will open avenues for new approaches in resistance breeding.

As a result of pre-breeding and breeding research for improved PRR resistance, it is now evident that resistance sources from wild *Cicer* relatives are more effective and provide more agronomically relevant adaptation to PRR under severe disease pressure than those offered by cultivated varieties. This research has highlighted specific differences in the genetic factors underlying PRR resistance from wild *Cicer* and cultivated sources. A decision to focus efforts on wild *Cicer* resistance characterisation and introgression would be well-informed by the research presented in this thesis, and

aligns with a current broader investment strategy for pulses related to the development of genetic and genomic resources for wild relatives of *Cicer* for use in chickpea breeding. Developments in NGS-based genotyping platforms along with complex computational pipelines for improved sequence assembly has made it possible to generate reference genomes for multiple cultivated chickpea varieties, in addition to more recent progress on the reference genomes for wild *Cicer* species (von Wettberg et al, 2018). It is anticipated that these new genomic resources will accelerate the rate of discovery of key chickpea resistance genes such as for PRR, and the development of knowledge of allelic variation across diverse germplasm collections, providing breeders with a toolkit for application in selection programs. In future, the application of relatively new molecular genetic techniques such as CRISPR/Cas9 in crop breeding will be instrumental in developing crop varieties with a tailored trait combination that will provide improved adaptation and increased yield potential under challenging environmental conditions.

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Appendix 1

Online resource 1:
Documented PRR disease ratings for the three varieties (GRDC 2013) and breeding line 04067-81-2-1-1 used as parents for RIL population development.

Chickpea variety/ breeding line	Resistance to PRR
Rupali	Susceptible
Genesis114	Susceptible
Yorker	Moderately resistant
04067-81-2-1-1	Resistant

Conditions for three field experiments. Irrigation was applied on two separate dates, mm water applied in each application cited.

Experiment	Amount of in-crop rainfall/ irrigation	*P. medicaginis* oospores per m of row
2014 Rainfed	67 mm	17420
2015 Rainfed	78 mm	15931
2015 Irrigated	73 mm + irrigation 66/105 mm	15053

Online resource 2:
Linkage map details for the RIL mapping population YG (Yorker x Genesis114)

Linkage groups	Chromosome	Number of markers	Linkage group length	Average spacing of markers	Maximum spacing of markers
L.1	C1	106	168	1.6	23.6
L.2	C3	27	98.3	3.8	22.5
L.3	C2	86	97.6	1.1	12.4
L.4	C6	94	173.3	1.9	23.3
L.5	C4	113	140.3	1.3	18.1
L.6	C5	42	120.2	2.9	14.7
L.7	C7	88	122.9	1.4	12
L.8	C8	17	73.3	4.6	30.7
Overall		573	993.8	1.8	30.7

Linkage map details for the RIL mapping population RB (Rupali x 04067-81-2-1-1)

Linkage groups	Chromosome	Number of markers	Linkage group length	Average spacing of markers	Maximum spacing of markers
L.1	C1	275	77.8	0.3	10.6
L.2	C2	33	85.2	2.7	27.4
L.3	C3	194	111	0.6	42.9
L.4	C4	535	177.2	0.3	10.8
L.5	C5	107	118.2	1.1	20.3
L.6	C7	153	151.7	1	19.9
L.7	C8	168	76.3	0.5	14.3
L.8	C6	475	159.5	0.3	31.8
Overall		1940	956.9	0.5	42.9

Linkage map details for the RIL mapping population YB (Yorker x 04067-81-2-1-1)

Linkage groups	Chromosome	Number of markers	Linkage group length	Average spacing of markers	Maximum spacing of markers
L.1	C1	271	207.1	0.8	43.6
L.2	C2	33	106.4	3.3	26
L.3	C3	221	133.7	0.6	65.2
L.4	C4	467	151.6	0.3	22.5
L.5	C5	116	165.8	1.4	32
L.6	C6	507	220.2	0.4	25
L.7	C7	282	208.5	0.7	54
L.8	C8	164	141.4	0.9	17.4
Overall		2061	1334.7	0.7	65.2

Online resource 3:

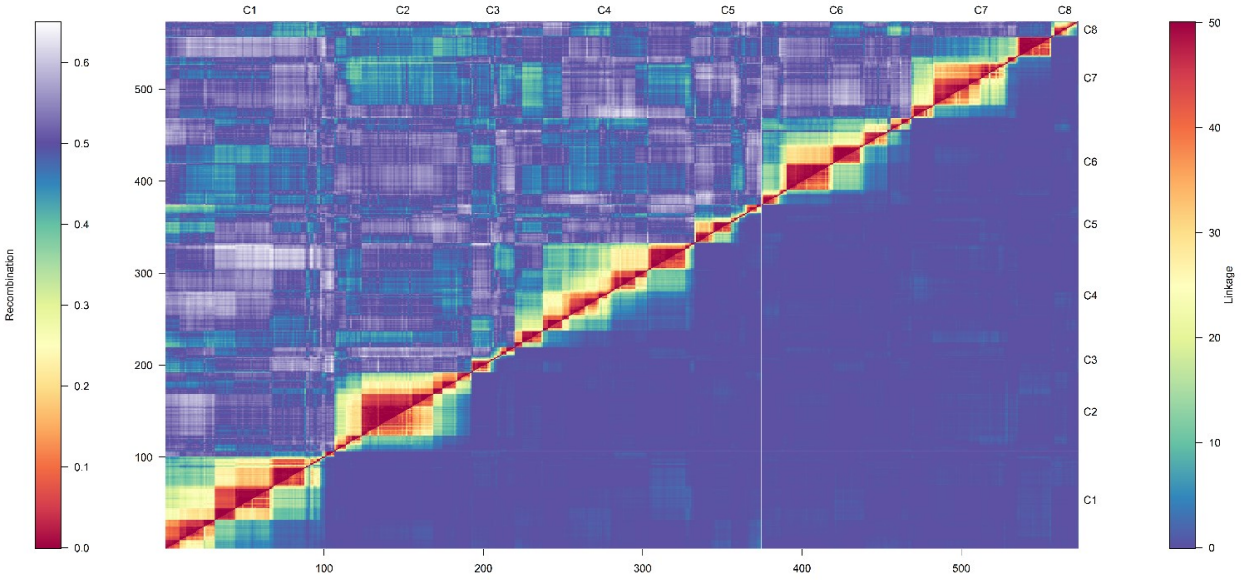

Fig. S1
Heat map showing the tight linkage of markers within the linkage groups for the RIL mapping population YG. The red areas on the heat map indicate strong linkage between the markers and blue areas indicate weak or no linkage between the markers.

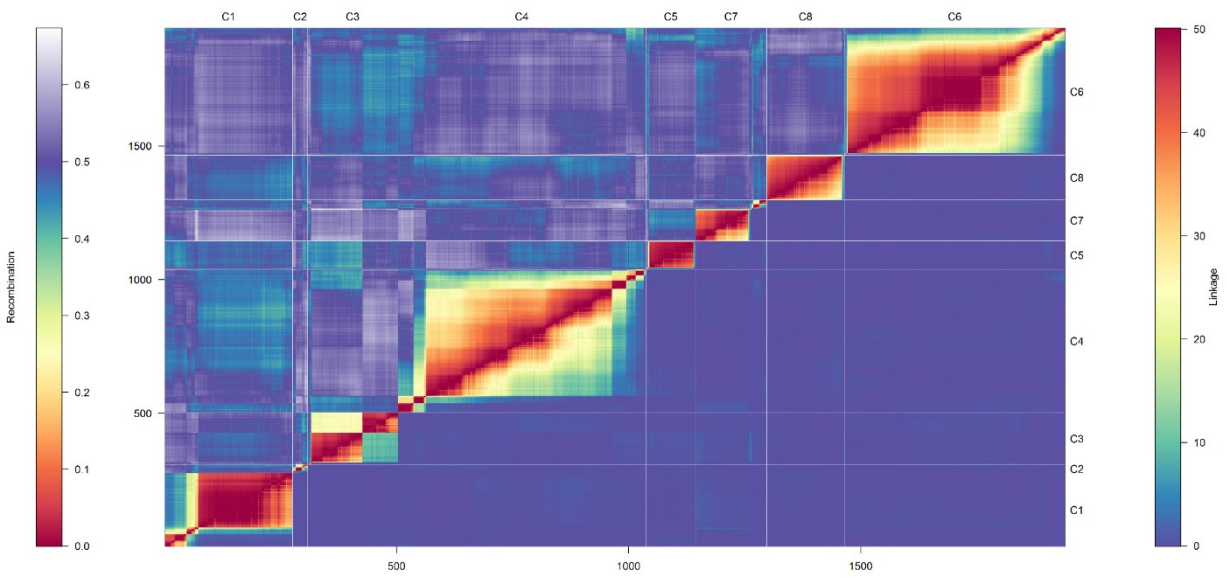

Fig. S2

Heat map showing the tight linkage of markers within the linkage groups for the RIL mapping population RB. The red areas on the heat map indicate strong linkage between the markers and blue areas indicate weak or no linkage between the markers.

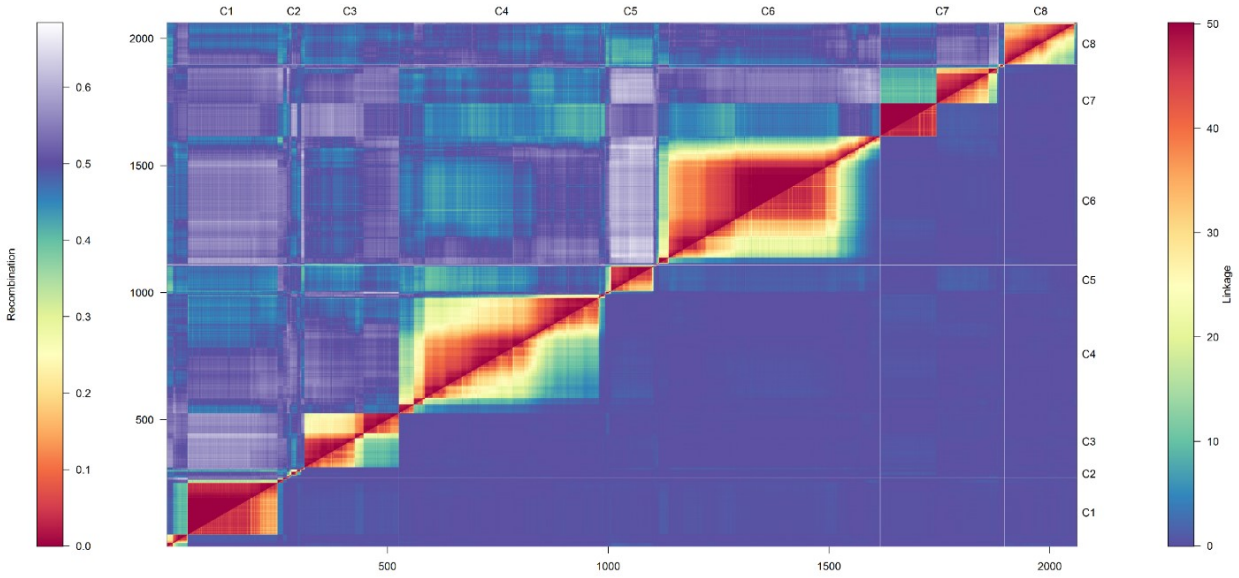

Fig. S3
Heat map showing the tight linkage of markers within the linkage groups for the RIL mapping population YB. The red areas on the heat map indicate strong linkage between the markers and blue areas indicate weak or no linkage between the markers.

Online resource 4, 5 and 6:

It includes the genetic maps for the YG, RB and YB mapping populations. Please follow the link below to access the supplementary files online.

https://link.springer.com/article/10.1007%2Fs00122-018-3256-6

Appendix 2

S1. List of primer sequences used in the qRT-PCR experiment

Gene ID	**Forward primer sequence**	**Reverse primer sequence**
AJ004960 (EF1-α)	GCCTGGTGTGATCGTTACCT	AGTTGGCAGCTTCCTTAGCA
Ca_15276	TTGGTGAAACGCAGAATTGA	CCGAAGGAAGAAGTTGCTTG
Ca_01365	AGGATCATCAGATGGGCAAC	TTAGCAGTCCCTCCTCCTCA
Ca_12619	CGTTTTGTTCCAATGGCTTT	GCAATCACTGCCTTCACAAA
Ca_01309	ATTCACCCCAATGGAAGACA	AGTCTCTGCGGCATTCTGTT
Ca_15106	ACTGCAACCCTGAGTGGAAT	CCATTTGGGAGAGAGGACAA
Ca_24447	CTGTGGTGACTTTGGTTTTGG	CCAAAGCAGCAAAAGTAGCC

Supplementary Table 2: PRR resistance genes in PRR resistant breeding line 04067-81-2-1-1 differently expressed under inoculation (Bc-I)

Serial number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)	Description of the gene
1	MSTRG.147	Ca_27893	C11165044	3.413	-2.704	zinc finger protein CONSTANS-LIKE 2-like
2	MSTRG.165	Ca_27557	C11172910	4.534	-2.269	tonoplast dicarboxylate transporter
3	MSTRG.842	Ca_00665	Ca1	-1.244	6.889	chaperonin-like RBCX protein 1, chloroplastic
4	MSTRG.1888	Ca_06938	Ca1	-1.487	2.561	organic cation/carnitine transporter 4
5	MSTRG.2961	Ca_12939	Ca1	3.652	2.095	B-box zinc finger protein 22
6	MSTRG.1981	Ca_22779	Ca1	7.814	1.901	glucan endo-1,3-beta-glucosidase, basic isoform
7	MSTRG.958	-	Ca1	-0.889	1.828	PKS-NRPS hybrid synthetase CHGG_01239-like
8	MSTRG.1438	Ca_02609	Ca1	4.840	1.775	putative E3 ubiquitin-protein ligase XBAT31
9	MSTRG.881	Ca_00698	Ca1	4.722	1.633	cysteine proteinase inhibitor 1
10	MSTRG.367	Ca_00160	Ca1	2.525	1.589	costars family protein
11	MSTRG.2339	Ca_20295	Ca1	1.993	1.575	protein SRG1
12	MSTRG.2966	Ca_12936	Ca1	4.006	1.545	protein trichome birefringence-like 41
13	MSTRG.858	Ca_00679	Ca1	4.002	1.427	ubiquinol oxidase 4, chloroplastic/chromoplastic
14	MSTRG.997	Ca_07988	Ca1	5.582	1.384	peroxidase 15
15	MSTRG.2753	Ca_22519	Ca1	7.432	1.300	proline-rich extensin-like protein EPR1
16	MSTRG.1231	Ca_02818	Ca1	3.436	1.252	dynein light chain 1, cytoplasmic-like
17	MSTRG.2122	Ca_08869	Ca1	1.001	1.223	Peroxidase 16
18	MSTRG.2286	Ca_25078	Ca1	4.267	1.212	probable WRKY transcription factor 47
19	MSTRG.525	Ca_00322	Ca1	8.481	1.155	dormancy-associated protein 1
20	MSTRG.623	Ca_00419	Ca1	4.030	1.136	DUF1685 family protein
21	MSTRG.999	Ca_07981	Ca1	10.701	1.129	peroxidase family protein
22	MSTRG.1230	Ca_02819	Ca1	6.338	1.096	late embryogenesis abundant protein
23	MSTRG.615	Ca_00410	Ca1	2.502	1.074	probable LRR receptor-like serine/threonine-protein kinase At3g47570 isoform X1
24	MSTRG.2009	Ca_14776	Ca1	9.755	1.054	class-10 pathogenesis-related protein 1
25	MSTRG.1919	Ca_06909	Ca1	7.262	1.047	root cap/late embryogenesis-like protein
26	MSTRG.2784	Ca_22663	Ca1	0.728	1.047	SKP1-like protein 14
27	MSTRG.1724	Ca_07110	Ca1	5.671	1.044	cellulose synthase-like protein H1
28	MSTRG.605	Ca_00398	Ca1	2.402	1.021	plant cysteine oxidase 4-like
29	MSTRG.1332	Ca_02707	Ca1	3.072	1.018	transmembrane protein, putative
30	MSTRG.1237	Ca_02810	Ca1	6.446	1.015	protein PLANT CADMIUM RESISTANCE 8
31	MSTRG.1029	Ca_08020	Ca1	2.785	1.008	transmembrane protein, putative

32	MSTRG.2974	Ca_12925	Ca1	2.806	1.000	BES1/BZR1 homolog protein 4
33	MSTRG.324	Ca_00127	Ca1	6.008	-1.063	protein LNK1-like isoform X4
34	MSTRG.497	Ca_00295	Ca1	1.689	-1.112	dof zinc finger protein DOF1.4
35	MSTRG.2321	Ca_18618	Ca1	0.714	-1.127	chloroplast envelope quinone oxidoreductase homolog
36	MSTRG.1910	Ca_06916	Ca1	4.356	-1.168	myosin-2 isoform X2
37	MSTRG.1107	Ca_02938	Ca1	1.115	-1.169	fasciclin-like arabinogalactan protein 14
38	MSTRG.410	Ca_00205	Ca1	1.282	-1.183	putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 3
39	MSTRG.2120	Ca_17338	Ca1	2.798	-1.217	nifU-like protein 3, chloroplastic
40	MSTRG.1651	Ca_14118	Ca1	3.913	-1.230	coumaroyl-CoA:anthocyanidin 3-O-glucoside-6"-O-coumaroyltransferase 1-like
41	MSTRG.1914	Ca_06912	Ca1	5.539	-1.239	cotton fiber
42	MSTRG.746	Ca_00559	Ca1	4.591	-1.346	plant/F10N7-170 protein, putative
43	MSTRG.2246	Ca_19281	Ca1	3.007	-1.350	transmembrane protein, putative
44	MSTRG.1678	Ca_14141	Ca1	2.066	-1.359	formin-like protein 3
45	MSTRG.774	Ca_00589	Ca1	3.343	-1.446	transmembrane protein 45A-like
46	MSTRG.1679	-	Ca1	3.368	-1.503	cysteine-rich repeat secretory protein 38-like
47	MSTRG.2825	Ca_13567	Ca1	3.102	-1.523	1-aminocyclopropane-1-carboxylate oxidase homolog 1-like
48	MSTRG.2726	Ca_23112	Ca1	8.159	-1.530	probable glutathione S-transferase
49	MSTRG.1451	Ca_02593	Ca1	6.218	-1.565	myb transcription factor
50	MSTRG.1395	Ca_02643	Ca1	3.683	-1.747	aluminum-activated citrate transporter
51	MSTRG.2626	Ca_13966	Ca1	3.484	-1.789	oxidoreductase/transition metal ion-binding protein
52	MSTRG.3010	Ca_12885	Ca1	0.397	-1.811	AAA-ATPase At3g50940
53	MSTRG.481	Ca_00278	Ca1	3.878	-1.953	polyphenol oxidase A1, chloroplastic
54	MSTRG.1665	Ca_14127	Ca1	3.465	-2.081	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130
55	MSTRG.1741	-	Ca1	3.161	-2.130	protein FAF-like, chloroplastic
56	MSTRG.1904	Ca_06917	Ca1	6.451	-2.375	chlorophyll a-b binding protein 13, chloroplastic
57	MSTRG.1548	Ca_02491	Ca1	3.682	-2.451	phosphoenolpyruvate carboxylase 2
58	MSTRG.1830	Ca_07000	Ca1	1.361	-2.472	protein SENSITIVE TO PROTON RHIZOTOXICITY 2
59	MSTRG.1442	Ca_02605	Ca1	2.416	-2.848	fusaric acid resistance-like protein
60	MSTRG.1345	Ca_02689	Ca1	6.327	-3.366	salt tolerance protein
61	MSTRG.2429	-	Ca1	-2.402	-4.115	---NA---
62	MSTRG.1684	-	Ca1	-0.180	-4.240	B-box domain protein 30
63	MSTRG.4808	Ca_15276	Ca2	-1.149	6.853	Small heat shock protein C2
64	MSTRG.4231	Ca_17243	Ca2	-0.954	4.224	Protein CHLOROPLAST IMPORT APPARATUS 2
65	MSTRG.3168	Ca_12588	Ca2	6.745	2.075	putative germin-like protein 2-1

66	MSTRG.3170	Ca_12587	Ca2	6.982	2.063	germin family protein
67	MSTRG.3808	Ca_18069	Ca2	2.616	1.815	ribonuclease 1
68	MSTRG.3097	Ca_20673	Ca2	5.179	1.337	PQQ-dependent membrane bound dehydrogenase, glucose/quinate/shikimate-related
69	MSTRG.3807	Ca_18067	Ca2	2.962	1.266	ribonuclease 1
70	MSTRG.4705	Ca_10210	Ca2	6.434	1.245	cysteine proteinase inhibitor
71	MSTRG.4537	Ca_12453	Ca2	6.701	1.211	ferritin-2, chloroplastic
72	MSTRG.3128	-	Ca2	1.101	1.193	---NA---
73	MSTRG.3309	Ca_10514	Ca2	3.141	1.118	zinc-finger homeodomain protein 9-like
74	MSTRG.4235	Ca_17248	Ca2	7.959	1.099	cytochrome P450 83B1
75	MSTRG.3244	Ca_10582	Ca2	3.497	1.029	senescence-associated carboxylesterase 101 isoform X1
76	MSTRG.3824	Ca_18086	Ca2	2.895	1.023	methyltransferase-like protein 7A isoform X1
77	MSTRG.4400	Ca_14327	Ca2	3.222	-1.046	aspartic proteinase PCS1-like
78	MSTRG.3541	Ca_19151	Ca2	6.266	-1.057	glucan endo-1,3-beta-glucosidase 8
79	MSTRG.3628	Ca_21460	Ca2	4.025	-1.101	DUF1645 family protein
80	MSTRG.3249	Ca_10572	Ca2	4.300	-1.133	Cytochrome P450 82A3
81	MSTRG.4377	Ca_14345	Ca2	7.361	-1.151	senescence-associated protein AAF, chlorolplastic isoform X1
82	MSTRG.3077	Ca_16998	Ca2	4.844	-1.170	heparan-alpha-glucosaminide N-acetyltransferase
83	MSTRG.4475	-	Ca2	3.361	-1.239	haloacid dehalogenase superfamily protein isoform X1
84	MSTRG.3243	Ca_10576	Ca2	2.128	-1.279	zinc finger AN1 domain-containing stress-associated protein 12
85	MSTRG.5011	Ca_09819	Ca2	6.825	-1.292	chlorophyll a-b binding protein 8, chloroplastic
86	MSTRG.4605	Ca_17820	Ca2	6.298	-1.358	E3 ubiquitin-protein ligase COP1
87	MSTRG.4891	Ca_09698	Ca2	1.846	-1.450	transmembrane protein
88	MSTRG.3756	Ca_25885	Ca2	3.429	-1.456	protein NRT1/ PTR FAMILY 4.6
89	MSTRG.4280	Ca_15651	Ca2	4.742	-1.543	probable serine/threonine-protein kinase WNK4
90	MSTRG.4399	Ca_14327	Ca2	1.444	-1.566	---NA---
91	MSTRG.3325	Ca_10502	Ca2	2.468	-1.569	transcription factor MYB90-like
92	MSTRG.3346	Ca_10479	Ca2	2.793	-1.582	DUF4336 domain protein
93	MSTRG.4926	Ca_09731	Ca2	0.555	-1.595	WEB family protein At5g55860-like
94	MSTRG.4261	Ca_17277	Ca2	0.565	-1.692	probable O-methyltransferase 3
95	MSTRG.4779	Ca_15244	Ca2	1.678	-1.698	transmembrane protein, putative
96	MSTRG.3897	Ca_18564	Ca2	3.281	-1.725	ninja-family protein AFP3
97	MSTRG.4228	-	Ca2	2.261	-1.821	receptor-like kinase
98	MSTRG.3491	-	Ca2	0.405	-2.148	transmembrane protein, putative

99	MSTRG.3580	Ca_18121	Ca2	5.920	-2.240	protein DETOXIFICATION 27-like
100	MSTRG.4253	-	Ca2	0.636	-2.587	WRKY family transcription factor
101	MSTRG.3816	Ca_18079	Ca2	0.821	-2.687	dof zinc finger protein
102	MSTRG.4694	Ca_10219	Ca2	-0.149	-2.739	zinc finger protein ZAT2-like
103	MSTRG.4971	Ca_09779	Ca2	7.354	-2.797	chlorophyll a-b binding protein 215, chloroplastic
104	MSTRG.7363	Ca_01113	Ca3	2.562	3.222	dnaJ homolog subfamily B member 6
105	MSTRG.6196	Ca_08294	Ca3	3.996	1.972	chalcone synthase
106	MSTRG.5231	-	Ca3	1.135	1.926	hypothetical protein
107	MSTRG.6891	Ca_12046	Ca3	4.812	1.514	chromodomain-helicase-DNA-binding protein 3-like isoform X1
108	MSTRG.6146	Ca_05995	Ca3	2.558	1.428	CASP-like protein 1F2
109	MSTRG.5939	-	Ca3	1.452	1.228	---NA---
110	MSTRG.5551	Ca_18266	Ca3	1.065	1.217	probable sodium/metabolite cotransporter BASS3, chloroplastic
111	MSTRG.5585	Ca_23345	Ca3	4.058	1.212	protein PHLOEM PROTEIN 2-LIKE A1
112	MSTRG.6977	Ca_00734	Ca3	4.843	1.080	purine-uracil permease NCS1
113	MSTRG.6691	Ca_12198	Ca3	2.728	-1.045	phospholipase A1-Igamma2, chloroplastic-like
114	MSTRG.7493	Ca_01233	Ca3	7.412	-1.083	GDP-mannose 3,5-epimerase 2
115	MSTRG.5644	-	Ca3	3.567	-1.096	conserved Plasmodium protein, unknown function
116	MSTRG.6130	Ca_06008	Ca3	4.093	-1.151	uncharacterized protein LOC101495086
117	MSTRG.6569	Ca_07308	Ca3	2.517	-1.154	lactosylceramide 4-alpha-glycosyltransferase
118	MSTRG.6570	Ca_07309	Ca3	4.154	-1.161	seed maturation protein LEA 4
119	MSTRG.6300	Ca_08192	Ca3	1.987	-1.172	cation/calcium exchanger 2
120	MSTRG.5628	Ca_19616	Ca3	5.974	-1.201	plant/T7H20-70 protein
121	MSTRG.5570	Ca_18297	Ca3	5.103	-1.283	chloroplast envelope quinone oxidoreductase homolog
122	MSTRG.7639	Ca_01358	Ca3	3.177	-1.428	pentatricopeptide repeat-containing protein At4g01400, mitochondrial-like
123	MSTRG.5100	Ca_22148	Ca3	4.064	-1.626	zinc finger protein CONSTANS-LIKE 2
124	MSTRG.6123	Ca_06014	Ca3	3.538	-1.627	protein PLASTID MOVEMENT IMPAIRED 2
125	MSTRG.5924	Ca_06237	Ca3	3.443	-1.632	(+)-neomenthol dehydrogenase
126	MSTRG.7488	Ca_01230	Ca3	6.081	-1.655	probable aldo-keto reductase 1
127	MSTRG.6906	-	Ca3	0.406	-1.709	UDP-glycosyltransferase 73C3-like
128	MSTRG.6450	Ca_07195	Ca3	4.315	-1.834	haloacid dehalogenase-like hydrolase domain-containing protein 3
129	MSTRG.7045	Ca_00794	Ca3	2.900	-1.839	Protein BIC1
130	MSTRG.7623	-	Ca3	2.400	-1.858	putative permease/transmembrane protein
131	MSTRG.6458	Ca_07202	Ca3	4.200	-1.919	uncharacterized protein LOC101515199
132	MSTRG.6340	Ca_08153	Ca3	-1.068	-2.061	---NA---

133	MSTRG.6967	Ca_00727	Ca3	2.691	-2.071	UDP-glycosyltransferase 73C2
134	MSTRG.7362	Ca_01106	Ca3	3.947	-2.077	nicotianamine synthase
135	MSTRG.6904	Ca_23668	Ca3	1.261	-2.079	UDP-glycosyltransferase 73C2
136	MSTRG.6847	-	Ca3	2.523	-2.099	thioredoxin-like protein AAED1, chloroplastic
137	MSTRG.5955	Ca_06198	Ca3	5.027	-2.156	ascorbate transporter, chloroplastic
138	MSTRG.6848	Ca_12007	Ca3	4.272	-2.259	thioredoxin-like protein AAED1, chloroplastic
139	MSTRG.5095	Ca_26371	Ca3	-1.220	-2.471	hypothetical protein VR7878_01751
140	MSTRG.5370	Ca_18807	Ca3	2.984	-2.526	probable aldo-keto reductase 2
141	MSTRG.7640	Ca_01359	Ca3	5.108	-2.584	two-component response regulator-like APRR9 isoform X1
142	MSTRG.5154	Ca_22383	Ca3	1.358	-2.897	cyclic dof factor 2
143	MSTRG.6952	Ca_00712	Ca3	0.189	-3.587	protein NUCLEAR FUSION DEFECTIVE 4-like
144	MSTRG.7647	Ca_01365	Ca3	1.241	-6.813	protein LHY isoform X1
145	MSTRG.7646	Ca_01365	Ca3	4.761	-6.939	protein LHY isoform X1
146	MSTRG.10809	-	Ca4	0.538	3.940	cold regulated protein, putative
147	MSTRG.9297	Ca_05487	Ca4	3.348	2.046	zinc finger protein CONSTANS-LIKE 16
148	MSTRG.8930	Ca_04486	Ca4	1.244	1.789	uncharacterized protein LOC101504477
149	MSTRG.8120	Ca_03798	Ca4	-0.577	1.733	---NA---
150	MSTRG.9479	-	Ca4	-2.043	1.437	chalcone isomerase
151	MSTRG.7887	Ca_07854	Ca4	1.135	1.407	protein disulfide isomerase pTAC5, chloroplastic isoform X1
152	MSTRG.10085	Ca_20019	Ca4	7.332	1.350	peroxidase 5
153	MSTRG.8311	Ca_03609	Ca4	4.982	1.271	galactinol synthase 2
154	MSTRG.9481	Ca_18651	Ca4	8.516	1.219	chalcone isomerase
155	MSTRG.9024	Ca_04579	Ca4	1.889	1.153	DUF1677 family protein
156	MSTRG.9703	Ca_20135	Ca4	2.497	1.135	heat stress transcription factor A-3
157	MSTRG.8504	Ca_08316	Ca4	1.366	1.123	Auxin-binding protein T85
158	MSTRG.10534	Ca_10892	Ca4	6.739	1.088	aspartyl protease AED3-like
159	MSTRG.8919	Ca_04476	Ca4	6.518	1.010	remorin
160	MSTRG.9119	Ca_05658	Ca4	3.453	-1.036	phytosulfokines 3
161	MSTRG.8036	Ca_12171	Ca4	6.714	-1.070	peroxidase 47
162	MSTRG.9187	Ca_05596	Ca4	5.186	-1.078	stress enhanced protein 1, chloroplastic
163	MSTRG.8071	Ca_03845	Ca4	1.798	-1.086	protein yippee-like At4g27745
164	MSTRG.10962	Ca_23012	Ca4	2.398	-1.102	putative transcription factor bZIP family
165	MSTRG.10795	-	Ca4	5.123	-1.112	ethylene-responsive transcription factor RAP2-1
166	MSTRG.7851	Ca_07816	Ca4	2.922	-1.117	heat shock 22 kDa protein, putative

167	MSTRG.10824	Ca_19249	Ca4	3.493	-1.150	uncharacterized protein LOC101511335
168	MSTRG.7766	Ca_07737	Ca4	7.971	-1.163	ABC transporter I family member 21
169	MSTRG.9425	Ca_05367	Ca4	7.146	-1.185	myosin-1
170	MSTRG.8268	Ca_03652	Ca4	4.319	-1.221	F-box protein PP2-B15
171	MSTRG.8138	Ca_03782	Ca4	4.284	-1.235	coatomer protein
172	MSTRG.10971	Ca_23020	Ca4	2.939	-1.237	ABC transporter B family member 13-like
173	MSTRG.10468	Ca_10974	Ca4	5.114	-1.272	protein ACTIVITY OF BC1 COMPLEX KINASE 1, chloroplastic isoform X1
174	MSTRG.8686	Ca_08491	Ca4	7.852	-1.272	aquaporin PIP2-2
175	MSTRG.8368	Ca_03552	Ca4	4.342	-1.292	protein RADIALIS-like 3
176	MSTRG.9128	Ca_05651	Ca4	3.489	-1.298	LIM domain-containing protein WLIM1-like
177	MSTRG.8997	Ca_04552	Ca4	9.764	-1.365	early light-induced protein, chloroplastic
178	MSTRG.10629	Ca_09111	Ca4	-0.288	-1.405	protein GLUTAMINE DUMPER 5
179	MSTRG.8269	-	Ca4	2.237	-1.609	---NA---
180	MSTRG.9726	Ca_14471	Ca4	5.626	-1.645	ABC transporter G family member 22-like isoform X1
181	MSTRG.10363	Ca_14909	Ca4	2.426	-1.773	ultraviolet-B receptor UVR8
182	MSTRG.8246	Ca_03677	Ca4	0.429	-1.802	psbP domain-containing protein 7, chloroplastic
183	MSTRG.10253	Ca_13125	Ca4	4.032	-2.059	chlorophyllide a oxygenase, chloroplastic
184	MSTRG.8469	Ca_03440	Ca4	-1.159	-2.072	nuclear transcription factor Y subunit B-5
185	MSTRG.9444	-	Ca4	1.365	-2.075	RING-H2 finger protein ATL18
186	MSTRG.9021	Ca_04573	Ca4	0.670	-2.097	hypothetical protein MTR_1g103410
187	MSTRG.9874	Ca_21318	Ca4	4.386	-2.214	protein PROTON GRADIENT REGULATION 5, chloroplastic
188	MSTRG.8069	Ca_03847	Ca4	3.431	-2.416	aluminum-activated malate transporter 10
189	MSTRG.8293	Ca_03626	Ca4	1.998	-2.667	nicotianamine synthase
190	MSTRG.9581	Ca_14048	Ca4	2.828	-2.750	protein REVEILLE 8-like isoform X1
191	MSTRG.9066	Ca_04619	Ca4	-2.144	-2.897	---NA---
192	MSTRG.8193	Ca_03727	Ca4	-1.707	-3.086	gibberellin 20 oxidase 2
193	MSTRG.10214	Ca_15106	Ca4	-0.120	-3.549	protein C2-DOMAIN ABA-RELATED 7-like
194	MSTRG.12003	Ca_13416	Ca5	2.270	5.527	protein EARLY FLOWERING 4
195	MSTRG.13274	Ca_07641	Ca5	4.435	4.307	zinc finger protein CONSTANS-LIKE 9
196	MSTRG.12660	Ca_01767	Ca5	0.022	3.903	protein SPA, chloroplastic
197	MSTRG.11768	Ca_15586	Ca5	3.520	3.383	maternal effect embryo arrest protein, putative
198	MSTRG.12860	Ca_01565	Ca5	0.894	3.358	putative receptor protein kinase ZmPK1
199	MSTRG.11788	Ca_15607	Ca5	3.997	2.609	phosphomethylpyrimidine synthase, chloroplastic isoform X2
200	MSTRG.13182	Ca_07542	Ca5	2.522	2.591	alcohol dehydrogenase-like 7

201	MSTRG.12288	Ca_04805	Ca5	6.438	1.558	Monosaccharide-sensing protein 2
202	MSTRG.11399	Ca_17091	Ca5	3.467	1.555	cysteine-rich receptor-like protein kinase 10
203	MSTRG.12802	Ca_01620	Ca5	4.522	1.446	early flowering 3/high response
204	MSTRG.12974	-	Ca5	4.313	1.434	isoamylase 3, chloroplastic isoform X1
205	MSTRG.12516	-	Ca5	3.382	1.395	lachrymatory-factor synthase
206	MSTRG.12135	Ca_16664	Ca5	3.377	1.312	Ribonuclease J
207	MSTRG.13852	Ca_04158	Ca5	2.293	1.272	WAT1-related protein At5g64700-like
208	MSTRG.11775	Ca_15595	Ca5	7.167	1.248	alpha-glucan phosphorylase, H isozyme
209	MSTRG.13385	Ca_11360	Ca5	1.577	1.244	uncharacterized protein LOC101503749 isoform X2
210	MSTRG.12769	Ca_01651	Ca5	3.289	1.152	(S)-coclaurine N-methyltransferase
211	MSTRG.11948	Ca_08906	Ca5	4.778	1.069	probable LRR receptor-like serine/threonine-protein kinase At1g06840
212	MSTRG.12801	Ca_01619	Ca5	5.314	-1.113	zinc finger CCCH domain-containing protein 20-like
213	MSTRG.11947	Ca_08907	Ca5	6.433	-1.134	root phototropism protein 2
214	MSTRG.13155	Ca_07516	Ca5	4.549	-1.171	thiol-disulfide oxidoreductase DCC
215	MSTRG.11632	Ca_18246	Ca5	6.086	-1.207	LON peptidase N-terminal domain and RING finger protein 1 isoform X1
216	MSTRG.13830	-	Ca5	2.045	-1.225	transmembrane protein, putative
217	MSTRG.12610	Ca_01829	Ca5	5.962	-1.249	cryptochrome DASH, chloroplastic/mitochondrial
218	MSTRG.11793	Ca_15611	Ca5	2.634	-1.305	sodium-dependent phosphate transport protein 1, chloroplastic
219	MSTRG.13271	Ca_07638	Ca5	1.374	-1.362	endoglucanase 12
220	MSTRG.11759	Ca_15579	Ca5	5.985	-1.399	chaperonin-like RbcX protein 2, chloroplastic
221	MSTRG.12274	-	Ca5	2.098	-1.447	organ-specific protein P4
222	MSTRG.13556	Ca_03869	Ca5	0.409	-1.460	---NA---
223	MSTRG.11455	Ca_21651	Ca5	5.627	-1.641	plant/F13G24-250 protein
224	MSTRG.11666	Ca_20083	Ca5	3.433	-1.642	senescence regulator
225	MSTRG.11127	Ca_25893	Ca5	8.324	-1.668	serine--glyoxylate aminotransferase
226	MSTRG.11646	Ca_21163	Ca5	3.688	-1.783	fatty acid desaturase 4, chloroplastic
227	MSTRG.12428	Ca_04936	Ca5	2.348	-1.821	mannan endo-1,4-beta-mannosidase 7-like
228	MSTRG.11976	Ca_08881	Ca5	2.922	-1.823	WAT1-related protein At3g02690, chloroplastic
229	MSTRG.12471	-	Ca5	4.244	-1.861	transmembrane protein, putative
230	MSTRG.12999	Ca_01423	Ca5	5.465	-1.867	HVA22-like protein e
231	MSTRG.12450	Ca_04961	Ca5	1.079	-2.006	J domain-containing protein required for chloroplast accumulation response 1 isoform X1
232	MSTRG.13378	Ca_11364	Ca5	-0.588	-2.179	amino acid transporter AVT1H
233	MSTRG.13060	Ca_07420	Ca5	2.658	-2.310	BTB/POZ and TAZ domain-containing protein 1-like
234	MSTRG.13059	-	Ca5	0.918	-2.692	sucrase-like protein

235	MSTRG.13381	-	Ca5	1.357	-3.848	transmembrane protein, putative
236	MSTRG.13809	Ca_04111	Ca5	1.164	-4.137	putative GATA-type transcription activator
237	MSTRG.12074	Ca_13344	Ca5	-0.254	-7.582	WAT1-related protein At4g08290-like
238	MSTRG.15943	Ca_11242	Ca6	1.321	4.550	DUF506 family protein
239	MSTRG.17228	Ca_18903	Ca6	2.267	3.040	lysine-specific demethylase JMJ30
240	MSTRG.17263	Ca_16282	Ca6	3.934	2.992	sterile nodes
241	MSTRG.15669	Ca_06456	Ca6	1.692	2.866	uncharacterized protein LOC101503228 isoform X1
242	MSTRG.14220	Ca_10410	Ca6	5.516	2.241	adagio protein 3
243	MSTRG.14999	Ca_08560	Ca6	2.099	1.905	thiamine thiazole synthase, chloroplastic
244	MSTRG.14344	Ca_05916	Ca6	1.959	1.788	uncharacterized protein LOC101489321
245	MSTRG.17115	Ca_19181	Ca6	2.905	1.740	post-illumination chlorophyll fluorescence increase
246	MSTRG.14112	Ca_10305	Ca6	5.994	1.574	proline transporter 1-like
247	MSTRG.16807	Ca_23255	Ca6	4.498	1.538	putative E3 ubiquitin-protein ligase XBAT31
248	MSTRG.15029	Ca_08529	Ca6	4.060	1.444	subtilisin-like protease SBT3.9 isoform X1
249	MSTRG.17478	Ca_13641	Ca6	2.492	1.403	cytochrome c biogenesis protein CCS1, chloroplastic
250	MSTRG.14249	Ca_10438	Ca6	5.245	1.365	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.4
251	MSTRG.15620	Ca_06411	Ca6	5.842	1.349	CCG-binding protein 1
252	MSTRG.16919	Ca_17742	Ca6	4.307	1.249	zinc finger protein ZPR1-like isoform X2
253	MSTRG.15698	Ca_06485	Ca6	6.801	1.244	Serine/Threonine kinase, plant-type protein, putative
254	MSTRG.15681	-	Ca6	4.983	1.237	PI-PLC X domain-containing protein At5g67130-like
255	MSTRG.17279	-	Ca6	0.051	1.214	alpha-L-fucosidase 2
256	MSTRG.14695	Ca_09649	Ca6	4.049	1.201	RING-H2 finger protein ATL78-like
257	MSTRG.16319	Ca_17486	Ca6	5.928	1.184	alpha carbonic anhydrase 7
258	MSTRG.17217	Ca_18885	Ca6	8.032	1.171	---NA---
259	MSTRG.15447	Ca_22015	Ca6	2.959	1.163	G-type lectin S-receptor-like serine/threonine-protein kinase B120
260	MSTRG.16606	Ca_15777	Ca6	2.530	1.053	serine/threonine-protein kinase-like protein CCR4
261	MSTRG.14717	Ca_09628	Ca6	1.352	1.041	probable WRKY transcription factor 13
262	MSTRG.15572	Ca_06357	Ca6	5.801	1.039	isoflavone synthase
263	MSTRG.17512	Ca_15369	Ca6	10.064	1.004	glycine-rich RNA-binding, abscisic acid-inducible protein-like
264	MSTRG.14404	Ca_05860	Ca6	3.095	-1.056	short-chain dehydrogenase TIC 32, chloroplastic
265	MSTRG.14288	Ca_05968	Ca6	4.583	-1.070	protein sym-1-like
266	MSTRG.16196	Ca_16703	Ca6	8.229	-1.079	probable histone H2B.1
267	MSTRG.15287	Ca_05177	Ca6	5.908	-1.087	stress up-regulated Nod 19 protein
268	MSTRG.14023	Ca_13284	Ca6	5.084	-1.087	nudix hydrolase 18, mitochondrial-like

269	MSTRG.14977	Ca_08576	Ca6	4.354	-1.088	protochlorophyllide-dependent translocon component 52, chloroplastic
270	MSTRG.17455	Ca_13668	Ca6	5.275	-1.090	transmembrane protein 45B
271	MSTRG.15146	Ca_05042	Ca6	0.838	-1.092	probable 9-cis-epoxycarotenoid dioxygenase NCED5, chloroplastic
272	MSTRG.14644	Ca_16944	Ca6	3.762	-1.106	aldehyde dehydrogenase family 3 member H1 isoform X1
273	MSTRG.16568	Ca_15817	Ca6	4.165	-1.110	putative glycerol-3-phosphate transporter 1
274	MSTRG.16567	Ca_15818	Ca6	4.678	-1.120	maltose excess protein 1-like, chloroplastic isoform X1
275	MSTRG.17575	Ca_15429	Ca6	4.996	-1.153	epimerase family protein SDR39U1 homolog, chloroplastic isoform X2
276	MSTRG.14938	Ca_08621	Ca6	6.879	-1.358	tau class glutathione S-transferase
277	MSTRG.14699	Ca_09646	Ca6	2.431	-1.392	probable plastid-lipid-associated protein 7, chloroplastic isoform X1
278	MSTRG.14434	-	Ca6	1.906	-1.446	putative RING-H2 finger protein ATL21B
279	MSTRG.15842	-	Ca6	-0.731	-1.480	putative glycerol-3-phosphate transporter 1
280	MSTRG.17123	Ca_19173	Ca6	2.659	-1.547	Haloalkane dehalogenase 2
281	MSTRG.14246	Ca_10433	Ca6	3.197	-1.602	F-box protein SKIP28
282	MSTRG.17246	Ca_16265	Ca6	1.563	-1.604	UDP-glucose iridoid glucosyltransferase-like
283	MSTRG.15412	Ca_05316	Ca6	5.409	-1.613	K(+) efflux antiporter 3, chloroplastic isoform X1
284	MSTRG.14742	Ca_09604	Ca6	5.474	-1.618	protein ACTIVITY OF BC1 COMPLEX KINASE 8, chloroplastic
285	MSTRG.16186	Ca_16693	Ca6	3.396	-1.635	heat shock cognate 70 kDa protein 2
286	MSTRG.16434	-	Ca6	1.778	-1.653	glucan endo-1,3-beta-glucosidase 14
287	MSTRG.14700	Ca_09644	Ca6	0.628	-1.671	WAT1-related protein At5g64700
288	MSTRG.14418	Ca_05844	Ca6	3.127	-1.698	glutaredoxin domain-containing cysteine-rich protein CG12206
289	MSTRG.16038	Ca_11120	Ca6	5.359	-1.721	calcium-binding EF-hand protein
290	MSTRG.14330	Ca_05930	Ca6	1.372	-1.747	probable protein phosphatase 2C 6
291	MSTRG.16847	Ca_13814	Ca6	5.567	-1.888	heme-binding-like protein At3g10130, chloroplastic
292	MSTRG.17420	Ca_13690	Ca6	6.267	-2.019	B-box zinc finger protein 24
293	MSTRG.16621	Ca_26435	Ca6	2.030	-2.045	NAD(P)H-quinone oxidoreductase subunit T, chloroplastic
294	MSTRG.15852	Ca_16327	Ca6	2.214	-2.076	chaperone protein dnaJ C76, chloroplastic isoform X1
295	MSTRG.16972	-	Ca6	1.994	-2.096	transcription factor DIVARICATA
296	MSTRG.14636	Ca_16936	Ca6	3.479	-2.288	polyketide cyclase/dehydrase and lipid transporter
297	MSTRG.14289	Ca_05967	Ca6	4.008	-2.422	pentatricopeptide repeat-containing protein At5g21222-like
298	MSTRG.17286	Ca_21212	Ca6	3.963	-2.454	protein NRT1/ PTR FAMILY 5.6-like
299	MSTRG.15460	-	Ca6	0.449	-2.509	berberine bridge enzyme-like 17
300	MSTRG.17153	Ca_17524	Ca6	1.397	-2.621	B-box zinc finger protein 32
301	MSTRG.16148	Ca_24166	Ca6	1.173	-3.086	heavy metal-associated isoprenylated plant protein 26-like

302	MSTRG.15353	Ca_05243	Ca6	4.728	-3.461	protein LNK1
303	MSTRG.14076	Ca_13334	Ca6	5.354	-4.979	ultraviolet-B receptor UVR8-like isoform X1
304	MSTRG.20169	Ca_13791	Ca7	3.255	1.735	K(+) efflux antiporter 2, chloroplastic
305	MSTRG.20246	Ca_16441	Ca7	0.718	1.733	BON1-associated-like protein
306	MSTRG.18507	Ca_13196	Ca7	-0.029	1.705	flavonoid 3'-monooxygenase
307	MSTRG.17993	Ca_03109	Ca7	-0.500	1.702	putative pectinesterase/pectinesterase inhibitor 45
308	MSTRG.18933	Ca_09236	Ca7	5.749	1.505	salicylic acid-binding protein 2
309	MSTRG.18540	Ca_13165	Ca7	6.093	1.420	two-component response regulator-like APRR1
310	MSTRG.19034	Ca_09983	Ca7	3.286	1.242	metallothiol transferase FosB-like
311	MSTRG.19511	Ca_19906	Ca7	1.589	1.226	disease resistance protein (CC-NBS-LRR class) family protein
312	MSTRG.17879	Ca_03219	Ca7	4.947	1.194	protein CHLOROPLAST IMPORT APPARATUS 2-like
313	MSTRG.20534	Ca_26358	Ca7	5.138	1.116	dirigent protein 21
314	MSTRG.19125	Ca_09882	Ca7	1.971	1.091	RING-H2 finger protein ATL8-like
315	MSTRG.19192	Ca_15886	Ca7	6.557	1.043	alpha-glucan water dikinase, chloroplastic
316	MSTRG.17722	Ca_03348	Ca7	7.203	-1.054	temperature-induced lipocalin
317	MSTRG.18417	Ca_06624	Ca7	6.668	-1.057	sodium/pyruvate cotransporter BASS2, chloroplastic
318	MSTRG.17814	Ca_03275	Ca7	6.842	-1.079	Zinc finger protein CONSTANS-LIKE 5
319	MSTRG.17721	Ca_03348	Ca7	4.685	-1.090	temperature-induced lipocalin
320	MSTRG.18851	Ca_09317	Ca7	3.843	-1.182	cytochrome P450 81E8-like
321	MSTRG.18199	Ca_06812	Ca7	4.866	-1.236	probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic
322	MSTRG.18354	Ca_06679	Ca7	2.797	-1.248	equilibrative nucleotide transporter 8
323	MSTRG.18078	Ca_03023	Ca7	3.458	-1.269	calcium-binding protein CP1
324	MSTRG.18297	Ca_06730	Ca7	4.158	-1.281	probable anion transporter 6, chloroplastic isoform X1
325	MSTRG.20369	-	Ca7	1.642	-1.285	uncharacterized protein LOC101511185
326	MSTRG.18590	Ca_15322	Ca7	2.455	-1.344	zinc finger protein BRUTUS-like At1g18910 isoform X2
327	MSTRG.19504	-	Ca7	4.212	-1.367	---NA---
328	MSTRG.17691	Ca_03383	Ca7	3.190	-1.455	uncharacterized protein LOC101496027 isoform X1
329	MSTRG.17688	-	Ca7	3.624	-1.477	S-type anion channel SLAH4
330	MSTRG.18026	Ca_03081	Ca7	4.351	-1.509	ABC transporter B family member 11
331	MSTRG.18713	Ca_12773	Ca7	2.974	-1.549	nudix hydrolase 8
332	MSTRG.17811	Ca_03275	Ca7	1.235	-1.554	---NA---
333	MSTRG.17927	Ca_03173	Ca7	3.099	-1.573	putative lactoylglutathione lyase
334	MSTRG.20049	Ca_17633	Ca7	1.646	-1.678	transmembrane protein, putative
335	MSTRG.18548	Ca_13157	Ca7	2.485	-1.678	cyclic dof factor 3

336	MSTRG.18889	Ca_09279	Ca7	5.680	-1.689	zeaxanthin epoxidase, chloroplastic-like
337	MSTRG.19604	Ca_18940	Ca7	1.954	-1.864	PHD transcription factor
338	MSTRG.17653	-	Ca7	3.080	-2.137	tonoplast dicarboxylate transporter
339	MSTRG.19243	Ca_15837	Ca7	0.660	-2.340	protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
340	MSTRG.18769	Ca_12830	Ca7	5.046	-2.594	protein NRT1/ PTR FAMILY 7.3-like
341	MSTRG.18702	-	Ca7	-2.974	-3.055	---NA---
342	MSTRG.18066	Ca_03041	Ca7	2.987	-3.535	cell wall / vacuolar inhibitor of fructosidase 1-like
343	MSTRG.18067	Ca_03040	Ca7	-0.230	-3.563	cell wall / vacuolar inhibitor of fructosidase 1-like
344	MSTRG.20363	Ca_20210	Ca7	3.169	-5.447	protein LNK3
345	MSTRG.20764	Ca_02420	Ca8	8.640	1.989	thaumatin-like protein 1
346	MSTRG.20707	Ca_15040	Ca8	3.252	1.793	GDSL esterase/lipase At4g10955-like
347	MSTRG.21079	Ca_02105	Ca8	3.321	1.757	thioredoxin-like protein HCF164, chloroplastic
348	MSTRG.21599	Ca_18426	Ca8	2.186	1.674	probable carboxylesterase 18
349	MSTRG.20880	Ca_02300	Ca8	4.492	1.481	beta-amylase 3, chloroplastic
350	MSTRG.20550	Ca_11928	Ca8	4.670	1.364	protein CHROMATIN REMODELING 25
351	MSTRG.21713	Ca_23842	Ca8	4.247	1.071	endosomal targeting BRO1-like domain protein
352	MSTRG.20551	Ca_11927	Ca8	5.071	1.037	O-acyltransferase WSD1-like
353	MSTRG.21390	Ca_10648	Ca8	5.397	-1.012	pectin acetylesterase 8-like isoform X1
354	MSTRG.20807	Ca_02377	Ca8	5.172	-1.059	deoxyribodipyrimidine photo-lyase
355	MSTRG.21369	Ca_10666	Ca8	3.822	-1.115	abscisic acid 8'-hydroxylase 1
356	MSTRG.20935	Ca_02242	Ca8	1.944	-1.219	protein PHLOEM PROTEIN 2-LIKE A10
357	MSTRG.20740	-	Ca8	-0.168	-1.266	Putative ribonuclease H protein
358	MSTRG.21029	Ca_02150	Ca8	3.907	-1.310	zeaxanthin epoxidase
359	MSTRG.20766	Ca_02422	Ca8	1.450	-1.348	remorin-like isoform X1
360	MSTRG.21105	Ca_02080	Ca8	1.342	-1.416	calcium uniporter protein 2, mitochondrial-like
361	MSTRG.21859	Ca_12980	Ca8	2.679	-1.439	probable sulfate transporter 3.5
362	MSTRG.21551	Ca_11546	Ca8	5.127	-1.687	probable mannitol dehydrogenase
363	MSTRG.21944	Ca_15504	Ca8	4.281	-1.828	uncharacterized protein LOC101493710
364	MSTRG.21200	Ca_01985	Ca8	5.241	-1.894	B-box zinc finger protein 18-like
365	MSTRG.21552	Ca_11547	Ca8	0.122	-2.170	probable mannitol dehydrogenase
366	MSTRG.20901	Ca_02279	Ca8	3.812	-3.389	protein NRT1/ PTR FAMILY 7.3
367	MSTRG.21832	Ca_12999	Ca8	0.180	-3.495	dehydrin
368	MSTRG.21987	Ca_15550	Ca8	-1.666	-6.294	sodium transporter HKT1-like
369	MSTRG.22026	-	scaffold1006	5.048	-1.742	beta-amylase 1, chloroplastic

370	MSTRG.22028	-	scaffold1006	2.576	-3.916	protein REVEILLE 7-like
371	MSTRG.22113	Ca_17199	scaffold1047	4.670	4.654	putative phospholipase A(2)
372	MSTRG.22234	-	scaffold109_1	2.362	-1.630	protein phosphatase 2C 50 isoform X1
373	MSTRG.22274	Ca_24644	scaffold1115	4.583	-1.923	uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic-like
374	MSTRG.22399	Ca_24664	scaffold1202	6.573	-1.138	inositol transporter 1-like
375	MSTRG.22424	Ca_24703	scaffold123	3.544	1.180	flavonol synthase/flavanone 3-hydroxylase
376	MSTRG.22462	Ca_21449	scaffold128	7.865	2.452	germin-like protein subfamily 1 member 7
377	MSTRG.22493	-	scaffold1301_1	4.306	-2.568	heavy metal-associated isoprenylated plant protein 24
378	MSTRG.22556	-	scaffold1324	1.659	3.480	Protein Rev like
379	MSTRG.22704	-	scaffold1348_1	6.253	1.448	cytochrome P450 71A1-like
380	MSTRG.22744	Ca_21997	scaffold1351	5.940	1.061	alpha carbonic anhydrase 7-like
381	MSTRG.22809	Ca_26980	scaffold1419	2.942	-1.124	GDP-mannose 3,5-epimerase 2
382	MSTRG.22811	-	scaffold1419	2.804	-1.162	GDP-mannose 3,5-epimerase 2
383	MSTRG.22815	Ca_26982	scaffold1419	2.959	-1.172	granule-bound starch synthase 1, chloroplastic/amyloplastic-like
384	MSTRG.22870	Ca_24090	scaffold1504	1.060	1.863	cysteine/histidine-rich C1 domain protein
385	MSTRG.22925	Ca_21071	scaffold157	2.777	1.614	peroxisomal nicotinamide adenine dinucleotide carrier-like
386	MSTRG.23319	-	scaffold1981	-2.664	-3.245	---NA---
387	MSTRG.23346	Ca_26673	scaffold1991	5.428	-1.996	chromosome condensation regulator RCC1 repeat protein
388	MSTRG.23515	Ca_25197	scaffold227	3.125	-1.667	glutaredoxin domain-containing cysteine-rich protein CG12206
389	MSTRG.23527	-	scaffold2330	4.486	1.271	transmembrane protein, putative
390	MSTRG.23615	Ca_22270	scaffold242	4.287	1.380	remorin 4.1
391	MSTRG.23624	Ca_27038	scaffold250	4.446	-1.414	peptide methionine sulfoxide reductase B1, chloroplastic
392	MSTRG.23790	Ca_20596	scaffold284	2.329	-1.250	nudix hydrolase 1
393	MSTRG.23792	Ca_20600	scaffold284	7.728	-1.964	nitrate reductase [NADH] 2
394	MSTRG.23793	-	scaffold284	-3.570	-4.879	pentatricopeptide repeat-containing protein At1g62590-like
395	MSTRG.23821	Ca_19826	scaffold290	7.346	-2.137	magnesium-chelatase subunit ChlH, chloroplastic
396	MSTRG.24036	Ca_25757	scaffold332	3.440	-1.112	transmembrane protein, putative
397	MSTRG.24316	Ca_18978	scaffold40	4.149	-1.022	phospholipase A2
398	MSTRG.24384	Ca_26396	scaffold419	4.222	1.261	Putative disease resistance protein
399	MSTRG.24399	-	scaffold420	1.498	1.710	glycine-rich RNA-binding protein GRP1A
400	MSTRG.24433	-	scaffold421_1	-1.749	1.936	transmembrane protein, putative
401	MSTRG.24499	Ca_22618	scaffold451	2.018	-1.488	transcription factor HY5-like isoform X1
402	MSTRG.24664	-	scaffold5226	0.526	-2.463	protein FAR-RED IMPAIRED RESPONSE 1-like

403	MSTRG.24732	Ca_27303	scaffold5389	0.576	2.848	lysine-specific demethylase JMJ30
404	MSTRG.24883	-	scaffold599	-1.611	-3.717	protein TAPETUM DETERMINANT 1
405	MSTRG.24918	Ca_27770	scaffold627	4.680	-3.790	protein LNK2 isoform X1
406	MSTRG.25131	Ca_25929	scaffold753	1.650	-2.614	cyclic dof factor 3
407	MSTRG.25205	-	scaffold809	2.083	-1.570	hypothetical protein L195_g052424
408	MSTRG.25248	Ca_22418	scaffold845	4.110	-1.454	granule-bound starch synthase 1, chloroplastic/amyloplastic-like
409	MSTRG.25352	Ca_22184	scaffold88	-0.811	-3.519	Monoglyceride lipase
410	MSTRG.25441	-	scaffold913	-2.971	-1.149	late embryogenesis abundant hydroxyproline-rich glycoprotein
411	MSTRG.25579	Ca_21394	scaffold98	5.866	1.028	putative pectinesterase
412	MSTRG.25571	-	scaffold98	-0.593	-2.046	---NA---

Supplementary Table 3: PRR resistance genes in PRR moderately resistant genotype Yorker differently expressed under inoculation (Yor-I)

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)	Description of the gene
1	MSTRG.147	Ca_27893	C11165044	3.413	-3.319	zinc finger protein CONSTANS-LIKE 2-like
2	MSTRG.157	Ca_28203	C11166868	2.638	1.442	probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
3	MSTRG.165	Ca_27557	C11172910	4.534	-2.643	tonoplast dicarboxylate transporter
4	MSTRG.171	Ca_27440	C11176802	4.725	1.128	magnesium-chelatase subunit ChlD, chloroplastic isoform X2
5	MSTRG.842	Ca_00665	Ca1	-1.244	5.016	chaperonin-like RBCX protein 1, chloroplastic
6	MSTRG.1888	Ca_06938	Ca1	-1.487	4.818	organic cation/carnitine transporter 4
7	MSTRG.2107	-	Ca1	-0.696	2.970	---NA---
8	MSTRG.406	Ca_00201	Ca1	5.665	2.563	sulfite exporter TauE/SafE family protein 2
9	MSTRG.1231	Ca_02818	Ca1	3.436	2.474	dynein light chain 1, cytoplasmic-like
10	MSTRG.1230	Ca_02819	Ca1	6.338	1.732	late embryogenesis abundant protein
11	MSTRG.367	Ca_00160	Ca1	2.525	1.619	costars family protein
12	MSTRG.2981	-	Ca1	-2.358	1.536	---NA---
13	MSTRG.1994	Ca_14786	Ca1	4.141	1.536	keratin, type I cytoskeletal 9
14	MSTRG.2966	Ca_12936	Ca1	4.006	1.519	protein trichome birefringence-like 41
15	MSTRG.3005	Ca_12890	Ca1	2.438	1.495	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10
16	MSTRG.1880	Ca_06947	Ca1	4.850	1.406	50S ribosomal protein L24, chloroplastic
17	MSTRG.2339	Ca_20295	Ca1	1.993	1.301	protein SRG1
18	MSTRG.1992	Ca_14787	Ca1	2.115	1.252	cAMP-regulated phosphoprotein-like protein
19	MSTRG.1993	-	Ca1	-0.752	1.251	ribonuclease H
20	MSTRG.1792	Ca_07045	Ca1	1.914	1.225	fatty acyl-CoA reductase 3
21	MSTRG.605	Ca_00398	Ca1	2.402	1.198	plant cysteine oxidase 4-like
22	MSTRG.623	Ca_00419	Ca1	4.030	1.195	DUF1685 family protein
23	MSTRG.2974	Ca_12925	Ca1	2.806	1.194	BES1/BZR1 homolog protein 4
24	MSTRG.535	Ca_00331	Ca1	3.244	1.183	protein E6
25	MSTRG.1075	Ca_08071	Ca1	2.526	1.172	hypothetical protein MtrunA17_Chr2g0293951
26	MSTRG.2639	Ca_13942	Ca1	6.523	1.140	non-specific lipid-transfer protein 8
27	MSTRG.2080	Ca_17380	Ca1	2.835	1.112	protein PLASTID TRANSCRIPTIONALLY ACTIVE 14 isoform X1
28	MSTRG.507	Ca_00303	Ca1	2.835	1.088	E3 ubiquitin-protein ligase RMA1H1-like
29	MSTRG.2699	Ca_18470	Ca1	3.304	1.032	fatty-acid-binding protein 3, chloroplastic
30	MSTRG.673	Ca_00480	Ca1	2.084	-1.002	protein kinase PINOID-like
31	MSTRG.1614	Ca_14080	Ca1	3.417	-1.007	uncharacterized serine-rich protein C1E8.05
32	MSTRG.548	Ca_00344	Ca1	2.490	-1.058	NAC domain-containing protein 73-like
33	MSTRG.2108	Ca_17351	Ca1	4.429	-1.095	ankyrin repeat-containing protein NPR4-like isoform X2
34	MSTRG.1168	Ca_02879	Ca1	4.970	-1.100	probable polygalacturonase At3g15720
35	MSTRG.613	Ca_00408	Ca1	2.864	-1.239	RING/FYVE/PHD zinc finger protein
36	MSTRG.2726	Ca_23112	Ca1	8.159	-1.380	probable glutathione S-transferase
37	MSTRG.497	Ca_00295	Ca1	1.689	-1.392	dof zinc finger protein DOF1.4
38	MSTRG.774	Ca_00589	Ca1	3.343	-1.407	transmembrane protein 45A-like

39	MSTRG.1928	Ca_06901	Ca1	0.699	-1.446	NAC transcription factor 56
40	MSTRG.324	Ca_00127	Ca1	6.008	-1.464	protein LNK1-like isoform X4
41	MSTRG.1741	-	Ca1	3.161	-1.473	protein FAF-like, chloroplastic
42	MSTRG.1651	Ca_14118	Ca1	3.913	-1.473	coumaroyl-CoA:anthocyanidin 3-O-glucoside-6"-O-coumaroyltransferase 1-like
43	MSTRG.2321	Ca_18618	Ca1	0.714	-1.482	chloroplast envelope quinone oxidoreductase homolog
44	MSTRG.513	Ca_00310	Ca1	2.493	-1.502	DUF506 family protein
45	MSTRG.2739	Ca_25800	Ca1	0.965	-1.554	9-cis-epoxycarotenoid dioxygenase
46	MSTRG.481	Ca_00278	Ca1	3.878	-1.682	polyphenol oxidase A1, chloroplastic
47	MSTRG.2228	Ca_19300	Ca1	0.856	-1.701	---NA---
48	MSTRG.1395	Ca_02643	Ca1	3.683	-1.755	aluminum-activated citrate transporter
49	MSTRG.1070	Ca_08061	Ca1	1.875	-1.791	polygalacturonase At1g48100
50	MSTRG.430	-	Ca1	-1.065	-1.885	B-box domain protein 31-like
51	MSTRG.2521	-	Ca1	0.388	-1.896	ribonuclease H
52	MSTRG.1607	-	Ca1	3.449	-1.987	proton pump interactor, putative
53	MSTRG.1085	Ca_08081	Ca1	0.059	-2.197	cell wall / vacuolar inhibitor of fructosidase 1-like
54	MSTRG.453	Ca_00247	Ca1	-0.092	-2.289	DUF4408 domain protein
55	MSTRG.1665	Ca_14127	Ca1	3.465	-2.382	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130
56	MSTRG.1345	Ca_02689	Ca1	6.327	-3.359	salt tolerance protein
57	MSTRG.1344	Ca_02690	Ca1	-0.527	-4.347	protein STRICTOSIDINE SYNTHASE-LIKE 13
58	MSTRG.1684	-	Ca1	-0.180	-4.445	B-box domain protein 30
59	MSTRG.4808	Ca_15276	Ca2	-1.149	8.686	Small heat shock protein C2
60	MSTRG.4235	Ca_17248	Ca2	7.959	2.846	cytochrome P450 83B1
61	MSTRG.4380	Ca_14343	Ca2	4.173	2.157	GDSL esterase/lipase At5g37690
62	MSTRG.3390	-	Ca2	3.679	2.046	copper transport protein CCH-like
63	MSTRG.4557	Ca_12430	Ca2	5.336	1.804	putative sodium-coupled neutral amino acid transporter 10
64	MSTRG.4781	-	Ca2	1.791	1.561	transmembrane protein, putative
65	MSTRG.4565	Ca_12422	Ca2	6.607	1.440	peroxidase P7
66	MSTRG.4754	Ca_10155	Ca2	2.404	1.436	oxygen-evolving enhancer protein 2, chloroplastic
67	MSTRG.4783	Ca_15248	Ca2	0.418	1.425	probable sucrose-phosphate synthase 2
68	MSTRG.4176	Ca_14257	Ca2	4.833	1.385	cytochrome P450 86A1
69	MSTRG.3726	Ca_17586	Ca2	2.970	1.384	glutathione S-transferase U17-like
70	MSTRG.3093	Ca_20670	Ca2	4.836	1.354	O-acyltransferase WSD1
71	MSTRG.3403	-	Ca2	2.411	1.319	serine carboxypeptidase-like 25
72	MSTRG.3280	-	Ca2	4.302	1.299	AAA-ATPase ASD, mitochondrial-like
73	MSTRG.3128	-	Ca2	1.101	1.244	---NA---
74	MSTRG.4864	Ca_16864	Ca2	4.159	1.209	trigger factor-like protein TIG, Chloroplastic
75	MSTRG.3266	-	Ca2	0.050	1.179	CLAVATA3/ESR (CLE)-related protein 25
76	MSTRG.3808	Ca_18069	Ca2	2.616	1.165	ribonuclease 1
77	MSTRG.3990	Ca_15978	Ca2	4.678	1.085	peroxidase 11
78	MSTRG.4132	Ca_21659	Ca2	2.500	1.064	probable inactive receptor kinase At5g58300
79	MSTRG.3094	Ca_20671	Ca2	4.630	1.051	O-acyltransferase WSD1

80	MSTRG.3512	Ca_20936	Ca2	6.644	1.040	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
81	MSTRG.4537	Ca_12453	Ca2	6.701	1.024	ferritin-2, chloroplastic
82	MSTRG.4358	Ca_14365	Ca2	4.039	1.013	probable fructokinase-6, chloroplastic
83	MSTRG.3109	Ca_20695	Ca2	2.271	1.009	KDPG and KHG aldolase
84	MSTRG.3715	Ca_17597	Ca2	4.849	-1.004	transcription factor MYB1R1
85	MSTRG.3641	Ca_22315	Ca2	2.332	-1.006	U-box domain-containing protein 19-like
86	MSTRG.4343	Ca_14379	Ca2	6.138	-1.020	Universal stress protein A-like protein
87	MSTRG.3133	Ca_12622	Ca2	4.978	-1.080	---NA---
88	MSTRG.3325	Ca_10502	Ca2	2.468	-1.097	transcription factor MYB90-like
89	MSTRG.3628	Ca_21460	Ca2	4.025	-1.158	DUF1645 family protein
90	MSTRG.4605	Ca_17820	Ca2	6.298	-1.218	E3 ubiquitin-protein ligase COP1
91	MSTRG.3897	Ca_18564	Ca2	3.281	-1.222	ninja-family protein AFP3
92	MSTRG.3164	Ca_12593	Ca2	0.654	-1.265	U-box domain-containing protein 6
93	MSTRG.4086	Ca_14976	Ca2	4.082	-1.310	uncharacterized protein LOC101504435
94	MSTRG.4779	Ca_15244	Ca2	1.678	-1.322	transmembrane protein, putative
95	MSTRG.4891	Ca_09698	Ca2	1.846	-1.332	transmembrane protein
96	MSTRG.3243	Ca_10576	Ca2	2.128	-1.336	zinc finger AN1 domain-containing stress-associated protein 12
97	MSTRG.4488	Ca_12504	Ca2	1.597	-1.400	WUSCHEL-related homeobox 5
98	MSTRG.3545	Ca_19144	Ca2	4.439	-1.425	NAC domain-containing protein 87
99	MSTRG.3346	Ca_10479	Ca2	2.793	-1.567	DUF4336 domain protein
100	MSTRG.3542	Ca_19147	Ca2	1.899	-1.569	myb-related protein 2-like isoform X1
101	MSTRG.3491	-	Ca2	0.405	-1.746	transmembrane protein, putative
102	MSTRG.3580	Ca_18121	Ca2	5.920	-1.811	protein DETOXIFICATION 27-like
103	MSTRG.4104	Ca_14956	Ca2	2.338	-2.040	MADS-box transcription factor 23-like isoform X3
104	MSTRG.4253	-	Ca2	0.636	-2.515	WRKY family transcription factor
105	MSTRG.3816	Ca_18079	Ca2	0.821	-2.533	dof zinc finger protein
106	MSTRG.3199	Ca_12556	Ca2	1.378	-2.684	2-methylene-furan-3-one reductase-like
107	MSTRG.3134	Ca_12619	Ca2	-4.201	-7.252	putative glutamine amidotransferase GAT1_2.1
108	MSTRG.5151	-	Ca3	-3.521	5.218	cell morphogenesis protein PAG1 isoform X2
109	MSTRG.5230	Ca_24830	Ca3	1.013	5.105	probable disease resistance protein At4g27220
110	MSTRG.7451	Ca_01197	Ca3	-0.981	4.622	protein BONZAI 3
111	MSTRG.7363	Ca_01113	Ca3	2.562	2.979	dnaJ homolog subfamily B member 6
112	MSTRG.5231	-	Ca3	1.135	2.759	hypothetical protein
113	MSTRG.5281	Ca_16514	Ca3	3.081	2.500	basic leucine zipper 43
114	MSTRG.5913	Ca_06245	Ca3	3.914	2.446	SPX domain-containing membrane protein At4g22990 isoform X1
115	MSTRG.6589	Ca_07325	Ca3	3.058	2.389	thioredoxin-like 3-1, chloroplastic
116	MSTRG.7563	Ca_01292	Ca3	3.693	2.379	GDSL esterase/lipase At4g01130 isoform X1
117	MSTRG.5376	-	Ca3	0.506	2.175	protein LAZY 1 isoform X1
118	MSTRG.7326	-	Ca3	5.271	1.931	protein NRT1/ PTR FAMILY 4.6-like
119	MSTRG.6146	Ca_05995	Ca3	2.558	1.764	CASP-like protein 1F2
120	MSTRG.6280	Ca_08212	Ca3	8.325	1.759	protein SRC1

121	MSTRG.6891	Ca_12046	Ca3	4.812	1.539	chromodomain-helicase-DNA-binding protein 3-like isoform X1
122	MSTRG.6176	Ca_23888	Ca3	5.067	1.440	light-regulated protein
123	MSTRG.5229	Ca_24829	Ca3	4.088	1.432	putative leucine-rich repeat domain, L domain-containing protein
124	MSTRG.6901	Ca_23676	Ca3	4.385	1.386	CASP-like protein 2D1
125	MSTRG.6385	Ca_08104	Ca3	3.029	1.274	psbP domain-containing protein 6, chloroplastic
126	MSTRG.5991	Ca_06163	Ca3	2.943	1.266	probable WRKY transcription factor 43
127	MSTRG.6196	Ca_08294	Ca3	3.996	1.222	chalcone synthase
128	MSTRG.6655	Ca_07390	Ca3	1.756	1.153	plant/T24G3-80 protein
129	MSTRG.5676	Ca_19324	Ca3	2.876	1.140	transmembrane protein, putative
130	MSTRG.6800	Ca_11962	Ca3	5.410	1.078	cation/H(+) antiporter 20
131	MSTRG.6667	-	Ca3	4.498	1.067	Lipid transfer protein
132	MSTRG.6809	Ca_11977	Ca3	4.277	1.039	uncharacterized protein LOC101499143
133	MSTRG.5980	Ca_06175	Ca3	5.078	1.031	50S ribosomal protein L5, chloroplastic
134	MSTRG.7250	Ca_00998	Ca3	6.077	1.029	probable beta-D-xylosidase 2
135	MSTRG.7418	Ca_01160	Ca3	4.316	1.023	DNA polymerase zeta catalytic subunit
136	MSTRG.6212	Ca_08280	Ca3	3.685	1.022	disease resistance gene, putative
137	MSTRG.5499	Ca_22495	Ca3	4.764	-1.005	hydroquinone glucosyltransferase-like
138	MSTRG.6130	Ca_06008	Ca3	4.093	-1.012	uncharacterized protein LOC101495086
139	MSTRG.5475	Ca_23303	Ca3	5.967	-1.017	light-harvesting complex-like protein OHP1, chloroplastic
140	MSTRG.6690	Ca_12201	Ca3	3.141	-1.054	magnesium transporter MRS2-I-like isoform X1
141	MSTRG.5279	Ca_16520	Ca3	8.179	-1.144	probable sodium-coupled neutral amino acid transporter 6
142	MSTRG.7174	Ca_00930	Ca3	1.389	-1.146	monothiol glutaredoxin-S11-like
143	MSTRG.6569	Ca_07308	Ca3	2.517	-1.180	lactosylceramide 4-alpha-glycosyltransferase
144	MSTRG.7639	Ca_01358	Ca3	3.177	-1.197	pentatricopeptide repeat-containing protein At4g01400, mitochondrial-like
145	MSTRG.6298	Ca_08197	Ca3	6.693	-1.200	cationic amino acid transporter 2, vacuolar
146	MSTRG.6002	Ca_06155	Ca3	-0.053	-1.212	protein MAIN-LIKE 1-like
147	MSTRG.7182	Ca_00938	Ca3	5.323	-1.233	spermatogenesis-associated protein 20
148	MSTRG.6921	Ca_20876	Ca3	4.821	-1.237	protein BIC1
149	MSTRG.5724	Ca_09400	Ca3	2.358	-1.255	Putative Myb family transcription factor
150	MSTRG.5100	Ca_22148	Ca3	4.064	-1.328	zinc finger protein CONSTANS-LIKE 2
151	MSTRG.7045	Ca_00794	Ca3	2.900	-1.341	Protein BIC1
152	MSTRG.6450	Ca_07195	Ca3	4.315	-1.371	haloacid dehalogenase-like hydrolase domain-containing protein 3
153	MSTRG.6697	Ca_12208	Ca3	4.359	-1.405	cytochrome P450 94A1-like
154	MSTRG.7307	Ca_01056	Ca3	1.599	-1.481	uncharacterized protein LOC101492848
155	MSTRG.7361	Ca_01106	Ca3	5.971	-1.501	nicotianamine synthase
156	MSTRG.6693	Ca_12204	Ca3	3.752	-1.501	PRA1 family protein F2-like
157	MSTRG.7128	Ca_00882	Ca3	3.017	-1.506	ABC transporter G family member 22 isoform X1
158	MSTRG.7302	Ca_01051	Ca3	4.373	-1.575	chitinase 10
159	MSTRG.5924	Ca_06237	Ca3	3.443	-1.594	(+)-neomenthol dehydrogenase
160	MSTRG.5570	Ca_18297	Ca3	5.103	-1.619	chloroplast envelope quinone oxidoreductase homolog

161	MSTRG.5955	Ca_06198	Ca3	5.027	-1.776	ascorbate transporter, chloroplastic
162	MSTRG.6458	Ca_07202	Ca3	4.200	-1.932	uncharacterized protein LOC101515199
163	MSTRG.6788	Ca_12296	Ca3	-0.554	-2.001	---NA---
164	MSTRG.7362	Ca_01106	Ca3	3.947	-2.017	nicotianamine synthase
165	MSTRG.6847	-	Ca3	2.523	-2.026	thioredoxin-like protein AAED1, chloroplastic
166	MSTRG.6848	Ca_12007	Ca3	4.272	-2.115	thioredoxin-like protein AAED1, chloroplastic
167	MSTRG.6015	Ca_06140	Ca3	-0.669	-2.395	auxin efflux carrier component 5
168	MSTRG.5819	Ca_09495	Ca3	2.203	-2.456	probable WRKY transcription factor 70
169	MSTRG.5370	Ca_18807	Ca3	2.984	-2.638	probable aldo-keto reductase 2
170	MSTRG.7640	Ca_01359	Ca3	5.108	-3.151	two-component response regulator-like APRR9 isoform X1
171	MSTRG.5154	Ca_22383	Ca3	1.358	-3.430	cyclic dof factor 2
172	MSTRG.6094	-	Ca3	-3.080	-6.312	flavanone 3-dioxygenase 3-like
173	MSTRG.7646	Ca_01365	Ca3	4.761	-6.714	protein LHY isoform X1
174	MSTRG.7647	Ca_01365	Ca3	1.241	-8.511	protein LHY isoform X1
175	MSTRG.9054	-	Ca4	-0.631	3.540	---NA---
176	MSTRG.10760	Ca_18369	Ca4	4.745	2.390	beta-galactosidase-like isoform X1
177	MSTRG.10809	-	Ca4	0.538	1.866	cold regulated protein, putative
178	MSTRG.7678	Ca_07655	Ca4	0.758	1.846	probable membrane-associated kinase regulator 4
179	MSTRG.8535	Ca_08345	Ca4	3.358	1.827	transcription factor TGA4
180	MSTRG.8112	Ca_03805	Ca4	1.287	1.780	ammonium transporter 1 member 2
181	MSTRG.8410	Ca_03507	Ca4	-0.407	1.702	universal stress protein A-like protein
182	MSTRG.9229	Ca_05557	Ca4	3.959	1.636	protein DETOXIFICATION 12
183	MSTRG.10085	Ca_20019	Ca4	7.332	1.620	peroxidase 5
184	MSTRG.8178	-	Ca4	-1.033	1.567	ribonuclease H
185	MSTRG.10420	Ca_11021	Ca4	2.865	1.557	protein CUP-SHAPED COTYLEDON 1-like
186	MSTRG.9243	Ca_05546	Ca4	1.896	1.389	putative zinc finger protein At1g68190 isoform X1
187	MSTRG.8820	Ca_04381	Ca4	7.804	1.384	abscisic stress-ripening protein 1-like
188	MSTRG.8504	Ca_08316	Ca4	1.366	1.350	Auxin-binding protein T85
189	MSTRG.8311	Ca_03609	Ca4	4.982	1.343	galactinol synthase 2
190	MSTRG.8273	Ca_03649	Ca4	2.254	1.339	probable protein phosphatase 2C 34
191	MSTRG.7877	Ca_07845	Ca4	2.052	1.333	adenylate isopentenyltransferase 3, chloroplastic
192	MSTRG.8720	Ca_04293	Ca4	4.513	1.330	---NA---
193	MSTRG.10383	Ca_14886	Ca4	2.372	1.317	metal-nicotianamine transporter YSL3
194	MSTRG.9855	Ca_20441	Ca4	3.876	1.291	transmembrane protein, putative
195	MSTRG.10381	Ca_14887	Ca4	3.726	1.290	protein PEP-RELATED DEVELOPMENT ARRESTED 1, chloroplastic
196	MSTRG.10238	Ca_13141	Ca4	1.793	1.240	DUF3326 family protein
197	MSTRG.10534	Ca_10892	Ca4	6.739	1.237	aspartyl protease AED3-like
198	MSTRG.8365	Ca_03556	Ca4	5.360	1.187	protein translocase subunit SecA, chloroplastic
199	MSTRG.8285	-	Ca4	1.171	1.167	uncharacterized protein LOC101513260
200	MSTRG.8643	Ca_08448	Ca4	2.715	1.154	unknown protein, partial
201	MSTRG.8109	Ca_03808	Ca4	5.504	1.129	probable leucine-rich repeat receptor-like protein kinase At5g63930

202	MSTRG.8083	Ca_03838	Ca4	3.827	1.086	probable lysophospholipase BODYGUARD 3
203	MSTRG.10147	Ca_14818	Ca4	6.117	1.068	long chain acyl-CoA synthetase 2-like
204	MSTRG.8516	Ca_08326	Ca4	1.100	1.062	probable glutathione S-transferase
205	MSTRG.8482	Ca_03426	Ca4	4.607	1.060	protease Do-like 2, chloroplastic isoform X1
206	MSTRG.9206	Ca_05579	Ca4	4.688	1.034	ABC transporter G family member 7
207	MSTRG.7805	Ca_07770	Ca4	3.381	1.019	cytochrome P450 94A2-like
208	MSTRG.8932	Ca_04488	Ca4	2.483	-1.010	heat stress transcription factor B-2a-like
209	MSTRG.9119	Ca_05658	Ca4	3.453	-1.044	phytosulfokines 3
210	MSTRG.8398	Ca_03519	Ca4	-0.171	-1.088	plant invertase/pectin methylesterase inhibitor
211	MSTRG.7766	Ca_07737	Ca4	7.971	-1.091	ABC transporter I family member 21
212	MSTRG.10006	Ca_15466	Ca4	5.495	-1.121	protein fluG
213	MSTRG.10363	Ca_14909	Ca4	2.426	-1.145	ultraviolet-B receptor UVR8
214	MSTRG.9072	Ca_04624	Ca4	2.080	-1.161	protein FANTASTIC FOUR 3
215	MSTRG.10017	Ca_15483	Ca4	4.653	-1.212	CBL-interacting serine/threonine-protein kinase 4-like
216	MSTRG.9425	Ca_05367	Ca4	7.146	-1.230	myosin-1
217	MSTRG.7851	Ca_07816	Ca4	2.922	-1.236	heat shock 22 kDa protein, putative
218	MSTRG.9933	-	Ca4	2.111	-1.245	uncharacterized protein LOC113784405
219	MSTRG.10718	Ca_09200	Ca4	2.624	-1.280	transcription factor RAX2-like
220	MSTRG.9020	-	Ca4	0.853	-1.283	hypothetical protein MTR_1g103410
221	MSTRG.9726	Ca_14471	Ca4	5.626	-1.286	ABC transporter G family member 22-like isoform X1
222	MSTRG.9429	Ca_05361	Ca4	5.223	-1.314	GEM-like protein 4
223	MSTRG.9021	Ca_04573	Ca4	0.670	-1.340	hypothetical protein MTR_1g103410
224	MSTRG.10672	Ca_09156	Ca4	3.632	-1.368	glutaredoxin-C6
225	MSTRG.8588	Ca_08397	Ca4	3.438	-1.369	geraniol 8-hydroxylase-like
226	MSTRG.10684	Ca_09166	Ca4	2.931	-1.375	zinc transporter 4, chloroplastic-like
227	MSTRG.8377	Ca_03541	Ca4	2.245	-1.393	polygalacturonase At1g48100
228	MSTRG.10321	Ca_13061	Ca4	3.404	-1.455	rust resistance kinase Lr10-like
229	MSTRG.8589	Ca_08398	Ca4	3.295	-1.458	geraniol 8-hydroxylase-like
230	MSTRG.8997	Ca_04552	Ca4	9.764	-1.477	early light-induced protein, chloroplastic
231	MSTRG.9174	Ca_05608	Ca4	5.636	-1.512	putative UDP-glucose glucosyltransferase
232	MSTRG.8138	Ca_03782	Ca4	4.284	-1.624	coatomer protein
233	MSTRG.10525	Ca_10900	Ca4	0.342	-1.640	Sigma factor binding protein 1, chloroplastic
234	MSTRG.10215	Ca_15105	Ca4	3.523	-1.752	MLP-like protein 328
235	MSTRG.8927	-	Ca4	1.822	-1.772	Clavata3/ESR (CLE) gene family member MtCLE05
236	MSTRG.8692	-	Ca4	2.342	-1.778	hypothetical protein POPTR_010G221266
237	MSTRG.9581	Ca_14048	Ca4	2.828	-1.800	protein REVEILLE 8-like isoform X1
238	MSTRG.8571	Ca_08377	Ca4	1.627	-1.964	---NA---
239	MSTRG.10735	-	Ca4	2.986	-2.018	uncharacterized protein LOC101497077
240	MSTRG.10971	Ca_23020	Ca4	2.939	-2.060	ABC transporter B family member 13-like
241	MSTRG.9444	-	Ca4	1.365	-2.078	RING-H2 finger protein ATL18
242	MSTRG.9719	-	Ca4	-0.351	-2.116	Copia protein

243	MSTRG.9166	Ca_05616	Ca4	4.239	-2.125	uncharacterized protein LOC101504693
244	MSTRG.9874	Ca_21318	Ca4	4.386	-2.223	protein PROTON GRADIENT REGULATION 5, chloroplastic
245	MSTRG.10253	Ca_13125	Ca4	4.032	-2.327	chlorophyllide a oxygenase, chloroplastic
246	MSTRG.9593	-	Ca4	-0.620	-2.337	protamine P1 family protein
247	MSTRG.10463	Ca_10980	Ca4	1.872	-2.400	plasma membrane ATPase 4
248	MSTRG.10740	-	Ca4	-2.137	-4.120	---NA---
249	MSTRG.10214	Ca_15106	Ca4	-0.120	-6.363	protein C2-DOMAIN ABA-RELATED 7-like
250	MSTRG.12003	Ca_13416	Ca5	2.270	5.754	protein EARLY FLOWERING 4
251	MSTRG.12660	Ca_01767	Ca5	0.022	5.215	protein SPA, chloroplastic
252	MSTRG.11768	Ca_15586	Ca5	3.520	5.161	maternal effect embryo arrest protein, putative
253	MSTRG.13274	Ca_07641	Ca5	4.435	4.107	zinc finger protein CONSTANS-LIKE 9
254	MSTRG.12874	Ca_01550	Ca5	-1.406	3.915	transcription factor HEC2-like
255	MSTRG.12860	Ca_01565	Ca5	0.894	3.180	putative receptor protein kinase ZmPK1
256	MSTRG.11788	Ca_15607	Ca5	3.997	2.566	phosphomethylpyrimidine synthase, chloroplastic isoform X2
257	MSTRG.13182	Ca_07542	Ca5	2.522	2.326	alcohol dehydrogenase-like 7
258	MSTRG.13310	Ca_19234	Ca5	0.900	2.199	nudix hydrolase 2
259	MSTRG.12976	Ca_01445	Ca5	4.133	2.022	alcohol dehydrogenase-like 2
260	MSTRG.12272	Ca_04788	Ca5	9.065	2.010	specific tissue protein
261	MSTRG.11831	Ca_09038	Ca5	3.697	1.910	internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial
262	MSTRG.12847	Ca_01577	Ca5	-0.246	1.801	Tetratricopeptide repeat protein 1
263	MSTRG.12730	Ca_01693	Ca5	2.606	1.626	protein GLUTAMINE DUMPER 5
264	MSTRG.13266	Ca_07635	Ca5	5.830	1.508	subtilisin-like protease SBT5.3
265	MSTRG.11960	Ca_08894	Ca5	3.956	1.483	putative magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase
266	MSTRG.12974	-	Ca5	4.313	1.470	isoamylase 3, chloroplastic isoform X1
267	MSTRG.13357	Ca_11390	Ca5	0.051	1.415	probable xyloglucan galactosyltransferase GT14
268	MSTRG.12128	Ca_16657	Ca5	7.404	1.360	putative inactive purple acid phosphatase 27
269	MSTRG.12135	Ca_16664	Ca5	3.377	1.341	Ribonuclease J
270	MSTRG.11266	-	Ca5	0.546	1.314	cytosolic sulfotransferase 15-like
271	MSTRG.11201	Ca_18739	Ca5	1.170	1.303	putative transcription factor B3-Domain family
272	MSTRG.12802	Ca_01620	Ca5	4.522	1.254	early flowering 3/high response
273	MSTRG.11977	Ca_08877	Ca5	0.238	1.233	uncharacterized protein LOC101494805
274	MSTRG.11775	Ca_15595	Ca5	7.167	1.228	alpha-glucan phosphorylase, H isozyme
275	MSTRG.11159	Ca_20740	Ca5	1.520	1.183	transmembrane protein, putative
276	MSTRG.12024	Ca_13399	Ca5	4.252	1.178	UTP--glucose-1-phosphate uridylyltransferase 3, chloroplastic
277	MSTRG.13344	Ca_11406	Ca5	4.669	1.158	cysteine desulfurase 1, chloroplastic
278	MSTRG.12265	Ca_04782	Ca5	3.461	1.105	probable receptor-like serine/threonine-protein kinase At4g34500
279	MSTRG.13061	Ca_07421	Ca5	5.795	1.056	probable pectate lyase 5
280	MSTRG.12288	Ca_04805	Ca5	6.438	1.024	Monosaccharide-sensing protein 2
281	MSTRG.11790	Ca_15610	Ca5	5.528	1.010	cytochrome P450 86A1
282	MSTRG.13683	Ca_03988	Ca5	1.715	-1.002	RING-H2 finger protein ATL65

283	MSTRG.13161	Ca_07521	Ca5	4.062	-1.010	UVI1, putative
284	MSTRG.11741	Ca_17668	Ca5	4.743	-1.018	Subtilisin-like protease SBT5.4
285	MSTRG.11782	Ca_15601	Ca5	3.374	-1.029	protein NRT1/ PTR FAMILY 8.1-like
286	MSTRG.13524	Ca_12665	Ca5	1.844	-1.077	uncharacterized protein At4g08330, chloroplastic-like
287	MSTRG.13614	Ca_03916	Ca5	6.504	-1.090	F-box protein SKP2A-like
288	MSTRG.11127	Ca_25893	Ca5	8.324	-1.121	serine--glyoxylate aminotransferase
289	MSTRG.12132	Ca_16662	Ca5	1.951	-1.147	calcium-binding protein CML38
290	MSTRG.13764	Ca_04067	Ca5	3.466	-1.156	heavy metal-associated isoprenylated plant protein 9
291	MSTRG.11632	Ca_18246	Ca5	6.086	-1.159	LON peptidase N-terminal domain and RING finger protein 1 isoform X1
292	MSTRG.12106	Ca_16633	Ca5	4.033	-1.173	probable trehalose-phosphate phosphatase J
293	MSTRG.12094	Ca_16620	Ca5	4.848	-1.185	sulfate transporter 1.3
294	MSTRG.13844	Ca_04147	Ca5	3.394	-1.241	ethylene-responsive transcription factor ERF110
295	MSTRG.13155	Ca_07516	Ca5	4.549	-1.253	thiol-disulfide oxidoreductase DCC
296	MSTRG.11947	Ca_08907	Ca5	6.433	-1.304	root phototropism protein 2
297	MSTRG.13857	Ca_04163	Ca5	1.108	-1.315	---NA---
298	MSTRG.12610	Ca_01829	Ca5	5.962	-1.318	cryptochrome DASH, chloroplastic/mitochondrial
299	MSTRG.11976	Ca_08881	Ca5	2.922	-1.373	WAT1-related protein At3g02690, chloroplastic
300	MSTRG.13647	Ca_03953	Ca5	6.497	-1.399	RNA polymerase sigma factor sigE, chloroplastic/mitochondrial
301	MSTRG.11759	Ca_15579	Ca5	5.985	-1.411	chaperonin-like RbcX protein 2, chloroplastic
302	MSTRG.11455	Ca_21651	Ca5	5.627	-1.417	plant/F13G24-250 protein
303	MSTRG.11988	Ca_13431	Ca5	5.163	-1.430	cysteine-rich receptor-like protein kinase 2
304	MSTRG.13773	Ca_04080	Ca5	4.975	-1.450	protein RESPONSE TO LOW SULFUR 2-like
305	MSTRG.11283	Ca_23782	Ca5	3.247	-1.467	pectinesterase/pectinesterase inhibitor
306	MSTRG.11793	Ca_15611	Ca5	2.634	-1.496	sodium-dependent phosphate transport protein 1, chloroplastic
307	MSTRG.12801	Ca_01619	Ca5	5.314	-1.537	zinc finger CCCH domain-containing protein 20-like
308	MSTRG.11646	Ca_21163	Ca5	3.688	-1.603	fatty acid desaturase 4, chloroplastic
309	MSTRG.12539	Ca_01898	Ca5	2.386	-1.760	bark storage protein A-like
310	MSTRG.13060	Ca_07420	Ca5	2.658	-2.051	BTB/POZ and TAZ domain-containing protein 1-like
311	MSTRG.12827	Ca_01600	Ca5	1.350	-2.065	uncharacterized protein LOC101498288 isoform X2
312	MSTRG.13518	-	Ca5	3.954	-2.300	hypothetical protein MTR_3g087890
313	MSTRG.13059	-	Ca5	0.918	-2.921	sucrase-like protein
314	MSTRG.13381	-	Ca5	1.357	-3.161	transmembrane protein, putative
315	MSTRG.13809	Ca_04111	Ca5	1.164	-4.149	putative GATA-type transcription activator
316	MSTRG.12177	-	Ca5	-3.398	-5.302	---NA---
317	MSTRG.12074	Ca_13344	Ca5	-0.254	-9.406	WAT1-related protein At4g08290-like
318	MSTRG.16572	-	Ca6	-3.198	5.309	uncharacterized protein LOC105852351
319	MSTRG.17228	Ca_18903	Ca6	2.267	2.892	lysine-specific demethylase JMJ30
320	MSTRG.17263	Ca_16282	Ca6	3.934	2.769	sterile nodes
321	MSTRG.17478	Ca_13641	Ca6	2.492	1.990	cytochrome c biogenesis protein CCS1, chloroplastic
322	MSTRG.17115	Ca_19181	Ca6	2.905	1.965	post-illumination chlorophyll fluorescence increase
323	MSTRG.16533	Ca_24447	Ca6	2.601	1.896	aquaporin SIP1-2

324	MSTRG.15669	Ca_06456	Ca6	1.692	1.771	uncharacterized protein LOC101503228 isoform X1
325	MSTRG.15565	Ca_06354	Ca6	1.517	1.666	putative methyltransferase
326	MSTRG.14564	Ca_05699	Ca6	5.723	1.659	bidirectional sugar transporter SWEET14-like
327	MSTRG.15580	Ca_06369	Ca6	3.445	1.593	GDSL esterase/lipase At5g45960
328	MSTRG.15029	Ca_08529	Ca6	4.060	1.564	subtilisin-like protease SBT3.9 isoform X1
329	MSTRG.16348	Ca_17463	Ca6	8.536	1.399	xyloglucan endotransglucosylase/hydrolase protein 31
330	MSTRG.15698	Ca_06485	Ca6	6.801	1.381	Serine/Threonine kinase, plant-type protein, putative
331	MSTRG.14344	Ca_05916	Ca6	1.959	1.357	uncharacterized protein LOC101489321
332	MSTRG.15017	Ca_08538	Ca6	4.459	1.345	serine hydroxylmethyltransferase
333	MSTRG.14448	Ca_05820	Ca6	7.722	1.332	endoglucanase 6
334	MSTRG.15907	Ca_11281	Ca6	0.320	1.279	UDP-glycosyltransferase 79B30
335	MSTRG.16902	Ca_13878	Ca6	4.692	1.275	30S ribosomal protein S10, chloroplastic
336	MSTRG.14898	Ca_08667	Ca6	3.286	1.242	homeobox-leucine zipper protein ATHB-14
337	MSTRG.14824	Ca_16780	Ca6	3.839	1.239	chloroplast sensor kinase, chloroplastic
338	MSTRG.15475	Ca_19667	Ca6	3.291	1.206	PAP-specific phosphatase HAL2-like
339	MSTRG.15803	Ca_16377	Ca6	3.743	1.205	putative expansin/Lol pI
340	MSTRG.16324	Ca_17482	Ca6	1.531	1.195	BEL1-like homeodomain protein 8
341	MSTRG.15797	Ca_06580	Ca6	6.760	1.185	VWA domain-containing protein
342	MSTRG.15695	Ca_06482	Ca6	2.895	1.183	scopoletin glucosyltransferase
343	MSTRG.16584	Ca_15804	Ca6	1.795	1.176	polygalacturonase QRT2-like
344	MSTRG.15070	Ca_20483	Ca6	4.836	1.170	lipoxygenase 6, chloroplastic
345	MSTRG.16769	Ca_23155	Ca6	1.945	1.146	plant/F9H3-4 protein
346	MSTRG.16605	Ca_15778	Ca6	2.830	1.118	receptor protein-tyrosine kinase CEPR2
347	MSTRG.15718	Ca_06502	Ca6	2.744	1.112	transcription termination factor MTERF6, chloroplastic/mitochondrial
348	MSTRG.14415	Ca_05847	Ca6	4.116	1.101	30S ribosomal protein S6 alpha, chloroplastic
349	MSTRG.14220	Ca_10410	Ca6	5.516	1.090	adagio protein 3
350	MSTRG.15573	Ca_06357	Ca6	3.251	1.088	isoflavone synthase
351	MSTRG.15794	Ca_06579	Ca6	8.548	1.086	nodulin-related protein 1-like
352	MSTRG.15793	Ca_06579	Ca6	6.090	1.081	nodulin-related protein 1-like
353	MSTRG.14112	Ca_10305	Ca6	5.994	1.070	proline transporter 1-like
354	MSTRG.16480	Ca_15199	Ca6	4.592	1.068	protein FAF-like, chloroplastic
355	MSTRG.14249	Ca_10438	Ca6	5.245	1.057	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.4
356	MSTRG.15768	Ca_06554	Ca6	3.876	1.048	putative NusB antitermination factor
357	MSTRG.14695	Ca_09649	Ca6	4.049	1.042	RING-H2 finger protein ATL78-like
358	MSTRG.17575	Ca_15429	Ca6	4.996	-1.008	epimerase family protein SDR39U1 homolog, chloroplastic isoform X2
359	MSTRG.16101	Ca_11062	Ca6	3.998	-1.041	DUF3067 family protein
360	MSTRG.15028	Ca_08527	Ca6	3.069	-1.100	crocetin glucosyltransferase, chloroplastic
361	MSTRG.15781	Ca_06567	Ca6	2.160	-1.106	Glucan endo-1,3-beta-glucosidase-like protein
362	MSTRG.16400	Ca_16452	Ca6	3.064	-1.125	probable 2-carboxy-D-arabinitol-1-phosphatase
363	MSTRG.15287	Ca_05177	Ca6	5.908	-1.135	stress up-regulated Nod 19 protein

364	MSTRG.14339	Ca_05922	Ca6	5.256	-1.180	probable pectinesterase 53
365	MSTRG.16847	Ca_13814	Ca6	5.567	-1.239	heme-binding-like protein At3g10130, chloroplastic
366	MSTRG.17247	Ca_16266	Ca6	0.945	-1.241	copper transporter 6-like
367	MSTRG.13984	Ca_13249	Ca6	3.955	-1.245	uncharacterized serine-rich protein C215.13
368	MSTRG.14811	Ca_09539	Ca6	3.584	-1.273	Avr9/Cf-9 rapidly elicited protein, putative
369	MSTRG.14404	Ca_05860	Ca6	3.095	-1.278	short-chain dehydrogenase TIC 32, chloroplastic
370	MSTRG.16569	-	Ca6	0.358	-1.334	---NA---
371	MSTRG.15751	Ca_06533	Ca6	4.889	-1.345	probable inorganic phosphate transporter 1-9
372	MSTRG.14418	Ca_05844	Ca6	3.127	-1.382	glutaredoxin domain-containing cysteine-rich protein CG12206
373	MSTRG.14938	Ca_08621	Ca6	6.879	-1.392	tau class glutathione S-transferase
374	MSTRG.17286	Ca_21212	Ca6	3.963	-1.463	protein NRT1/ PTR FAMILY 5.6-like
375	MSTRG.14742	Ca_09604	Ca6	5.474	-1.463	protein ACTIVITY OF BC1 COMPLEX KINASE 8, chloroplastic
376	MSTRG.14147	Ca_10331	Ca6	3.544	-1.539	NF-X1-type zinc finger protein NFXL1
377	MSTRG.15412	Ca_05316	Ca6	5.409	-1.558	K(+) efflux antiporter 3, chloroplastic isoform X1
378	MSTRG.16273	Ca_14581	Ca6	5.832	-1.578	probable glutathione S-transferase
379	MSTRG.16568	Ca_15817	Ca6	4.165	-1.579	putative glycerol-3-phosphate transporter 1
380	MSTRG.14735	Ca_09609	Ca6	4.092	-1.639	stress enhanced protein 2, chloroplastic
381	MSTRG.15932	Ca_11257	Ca6	1.839	-1.666	uncharacterized protein LOC101503424
382	MSTRG.14365	Ca_05895	Ca6	0.888	-1.765	1-aminocyclopropane-1-carboxylate synthase 7
383	MSTRG.16621	Ca_26435	Ca6	2.030	-1.790	NAD(P)H-quinone oxidoreductase subunit T, chloroplastic
384	MSTRG.16972	-	Ca6	1.994	-1.843	transcription factor DIVARICATA
385	MSTRG.14434	-	Ca6	1.906	-1.869	putative RING-H2 finger protein ATL21B
386	MSTRG.16234	-	Ca6	3.679	-1.870	hypothetical protein MTR_4g061300
387	MSTRG.14636	Ca_16936	Ca6	3.479	-1.874	polyketide cyclase/dehydrase and lipid transporter
388	MSTRG.14246	Ca_10433	Ca6	3.197	-1.902	F-box protein SKIP28
389	MSTRG.16434	-	Ca6	1.778	-1.908	glucan endo-1,3-beta-glucosidase 14
390	MSTRG.17420	Ca_13690	Ca6	6.267	-2.007	B-box zinc finger protein 24
391	MSTRG.15589	Ca_06379	Ca6	0.073	-2.147	flagellar basal body L-ring protein
392	MSTRG.14289	Ca_05967	Ca6	4.008	-2.152	pentatricopeptide repeat-containing protein At5g21222-like
393	MSTRG.14330	Ca_05930	Ca6	1.372	-2.599	probable protein phosphatase 2C 6
394	MSTRG.17153	Ca_17524	Ca6	1.397	-2.697	B-box zinc finger protein 32
395	MSTRG.15852	Ca_16327	Ca6	2.214	-3.275	chaperone protein dnaJ C76, chloroplastic isoform X1
396	MSTRG.15353	Ca_05243	Ca6	4.728	-3.297	protein LNK1
397	MSTRG.14076	Ca_13334	Ca6	5.354	-4.936	ultraviolet-B receptor UVR8-like isoform X1
398	MSTRG.18374	Ca_06660	Ca7	2.197	2.447	protein NRT1/ PTR FAMILY 6.2
399	MSTRG.20225	Ca_16414	Ca7	2.600	2.127	UDP-glycosyltransferase 1
400	MSTRG.18641	Ca_17318	Ca7	0.790	2.096	WAT1-related protein At3g28050-like
401	MSTRG.19206	Ca_15872	Ca7	-0.770	2.034	protein PHYLLO, chloroplastic isoform X1
402	MSTRG.18704	Ca_12765	Ca7	-0.103	1.899	ethylene-responsive transcription factor ERF038-like
403	MSTRG.20169	Ca_13791	Ca7	3.255	1.691	K(+) efflux antiporter 2, chloroplastic
404	MSTRG.18933	Ca_09236	Ca7	5.749	1.659	salicylic acid-binding protein 2

405	MSTRG.19043	Ca_09975	Ca7	2.733	1.541	transmembrane protein, putative
406	MSTRG.18550	Ca_13155	Ca7	5.855	1.502	GDSL esterase/lipase At1g74460-like
407	MSTRG.20407	Ca_21371	Ca7	3.737	1.442	protein YLS3-like
408	MSTRG.19314	Ca_12345	Ca7	3.791	1.379	E3 ubiquitin-protein ligase WAVH1-like
409	MSTRG.18763	Ca_12825	Ca7	5.066	1.333	two-component response regulator-like APRR2
410	MSTRG.18351	Ca_06683	Ca7	3.601	1.293	thylakoid lumenal 16.5 kDa protein, chloroplastic
411	MSTRG.18827	Ca_09343	Ca7	4.688	1.266	acetamidase/formamidase, putative
412	MSTRG.19389	-	Ca7	1.107	1.242	probable protein phosphatase 2C 39 isoform X3
413	MSTRG.19203	Ca_15876	Ca7	2.689	1.193	protein PHYLLO, chloroplastic isoform X1
414	MSTRG.19826	Ca_10081	Ca7	4.396	1.166	receptor-like serine/threonine-protein kinase ALE2 isoform X1
415	MSTRG.18540	Ca_13165	Ca7	6.093	1.140	two-component response regulator-like APRR1
416	MSTRG.19125	Ca_09882	Ca7	1.971	1.120	RING-H2 finger protein ATL8-like
417	MSTRG.19022	Ca_23046	Ca7	3.279	1.119	3-epi-6-deoxocathasterone 23-monooxygenase
418	MSTRG.20136	Ca_13741	Ca7	3.484	1.107	ascorbate transporter, chloroplastic
419	MSTRG.19088	Ca_09932	Ca7	3.597	1.085	UPF0548 protein At2g17695
420	MSTRG.17682	Ca_03389	Ca7	3.014	1.063	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.7
421	MSTRG.18078	Ca_03023	Ca7	3.458	-1.004	calcium-binding protein CP1
422	MSTRG.17814	Ca_03275	Ca7	6.842	-1.012	Zinc finger protein CONSTANS-LIKE 5
423	MSTRG.18666	Ca_17294	Ca7	3.387	-1.066	triose phosphate/phosphate translocator, non-green plastid, chloroplastic
424	MSTRG.17927	Ca_03173	Ca7	3.099	-1.074	putative lactoylglutathione lyase
425	MSTRG.18745	Ca_12808	Ca7	6.871	-1.099	beta-amylase 3, chloroplastic
426	MSTRG.20394	Ca_25031	Ca7	2.862	-1.108	cysteine-rich receptor-like protein kinase 10
427	MSTRG.19050	Ca_09968	Ca7	3.986	-1.125	chaperone protein dnaJ 11, chloroplastic
428	MSTRG.19803	Ca_10103	Ca7	4.560	-1.131	inorganic pyrophosphatase 2
429	MSTRG.17660	Ca_03409	Ca7	1.244	-1.201	DUF506 family protein
430	MSTRG.20361	-	Ca7	2.222	-1.224	cysteine-rich receptor-like protein kinase
431	MSTRG.18713	Ca_12773	Ca7	2.974	-1.226	nudix hydrolase 8
432	MSTRG.18366	Ca_06668	Ca7	-0.631	-1.227	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK1
433	MSTRG.17943	Ca_03159	Ca7	0.959	-1.230	protein BIG GRAIN 1-like A
434	MSTRG.17709	Ca_03364	Ca7	1.309	-1.256	cullin-like protein
435	MSTRG.18851	Ca_09317	Ca7	3.843	-1.308	cytochrome P450 81E8-like
436	MSTRG.18732	Ca_12796	Ca7	5.695	-1.383	cationic amino acid transporter 6, chloroplastic-like
437	MSTRG.19243	Ca_15837	Ca7	0.660	-1.417	protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
438	MSTRG.18650	Ca_17309	Ca7	2.818	-1.478	U-box domain-containing protein 19-like
439	MSTRG.19504	-	Ca7	4.212	-1.505	---NA---
440	MSTRG.20162	Ca_13779	Ca7	0.116	-1.611	transcription factor MYB41-like
441	MSTRG.18889	Ca_09279	Ca7	5.680	-1.658	zeaxanthin epoxidase, chloroplastic-like
442	MSTRG.18548	Ca_13157	Ca7	2.485	-1.797	cyclic dof factor 3
443	MSTRG.17916	Ca_03183	Ca7	0.095	-1.799	heat stress transcription factor A-2
444	MSTRG.20400	-	Ca7	-1.139	-2.005	---NA---

445	MSTRG.18354	Ca_06679	Ca7	2.797	-2.116	equilibrative nucleotide transporter 8
446	MSTRG.20500	-	Ca7	-0.656	-2.122	F-box/FBD/LRR-repeat protein At1g13570-like
447	MSTRG.17653	-	Ca7	3.080	-2.556	tonoplast dicarboxylate transporter
448	MSTRG.19669	-	Ca7	-0.088	-2.742	gag-pol polyprotein
449	MSTRG.19570	-	Ca7	-0.180	-2.859	Clavata3/ESR (CLE) gene family member
450	MSTRG.18066	Ca_03041	Ca7	2.987	-2.922	cell wall / vacuolar inhibitor of fructosidase 1-like
451	MSTRG.18067	Ca_03040	Ca7	-0.230	-3.892	cell wall / vacuolar inhibitor of fructosidase 1-like
452	MSTRG.20363	Ca_20210	Ca7	3.169	-5.445	protein LNK3
453	MSTRG.21800	Ca_13026	Ca8	1.680	2.588	protein SAR DEFICIENT 1-like
454	MSTRG.20939	Ca_02239	Ca8	1.728	1.918	VQ motif-containing protein 29-like
455	MSTRG.21599	Ca_18426	Ca8	2.186	1.535	probable carboxylesterase 18
456	MSTRG.21079	Ca_02105	Ca8	3.321	1.359	thioredoxin-like protein HCF164, chloroplastic
457	MSTRG.20550	Ca_11928	Ca8	4.670	1.067	protein CHROMATIN REMODELING 25
458	MSTRG.21713	Ca_23842	Ca8	4.247	1.044	endosomal targeting BRO1-like domain protein
459	MSTRG.20935	Ca_02242	Ca8	1.944	-1.041	protein PHLOEM PROTEIN 2-LIKE A10
460	MSTRG.21105	Ca_02080	Ca8	1.342	-1.194	calcium uniporter protein 2, mitochondrial-like
461	MSTRG.20622	Ca_11865	Ca8	1.627	-1.224	heat shock 22 kDa protein
462	MSTRG.20807	Ca_02377	Ca8	5.172	-1.259	deoxyribodipyrimidine photo-lyase
463	MSTRG.21043	Ca_02137	Ca8	6.402	-1.272	patatin-like protein 1
464	MSTRG.21650	Ca_16840	Ca8	4.743	-1.353	protein PLASTID MOVEMENT IMPAIRED 1-like
465	MSTRG.21864	Ca_12975	Ca8	2.896	-1.508	multiprotein-bridging factor 1c
466	MSTRG.21200	Ca_01985	Ca8	5.241	-1.562	B-box zinc finger protein 18-like
467	MSTRG.20906	Ca_02274	Ca8	1.585	-1.638	NAC domain-containing protein 71
468	MSTRG.21585	Ca_18413	Ca8	4.882	-1.666	kunitz-type trypsin inhibitor-like 2 protein
469	MSTRG.21862	Ca_12972	Ca8	1.003	-1.839	Aldehyde dehydrogenase family 2 member C4
470	MSTRG.21551	Ca_11546	Ca8	5.127	-1.906	probable mannitol dehydrogenase
471	MSTRG.21987	Ca_15550	Ca8	-1.666	-2.811	sodium transporter HKT1-like
472	MSTRG.22026	-	scaffold1006	5.048	-1.834	beta-amylase 1, chloroplastic
473	MSTRG.22028	-	scaffold1006	2.576	-3.947	protein REVEILLE 7-like
474	MSTRG.22113	Ca_17199	scaffold1047	4.670	3.497	putative phospholipase A(2)
475	MSTRG.22149	-	scaffold1052	-2.764	-6.383	plant/F25P12-18 protein
476	MSTRG.22274	Ca_24644	scaffold1115	4.583	-1.713	uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic-like
477	MSTRG.22315	Ca_26892	scaffold1152	3.639	1.694	30S ribosomal protein 2, chloroplastic
478	MSTRG.22420	-	scaffold1226	-1.346	-3.177	sensor histidine kinase
479	MSTRG.22493	-	scaffold1301_1	4.306	-1.594	heavy metal-associated isoprenylated plant protein 24
480	MSTRG.22556	-	scaffold1324	1.659	2.305	Protein Rev like
481	MSTRG.22570	Ca_19786	scaffold1324	2.839	1.015	protein IQ-DOMAIN 14-like
482	MSTRG.22565	Ca_19779	scaffold1324	1.591	-1.251	Ulp1 protease family, carboxy-terminal domain protein
483	MSTRG.22590	Ca_22590	scaffold134	3.541	-1.134	G-type lectin S-receptor-like serine/threonine-protein kinase
484	MSTRG.22691	-	scaffold1348_1	4.451	1.505	probable pectate lyase 18
485	MSTRG.22700	-	scaffold1348_1	6.547	1.030	28 kDa ribonucleoprotein, chloroplastic

486	MSTRG.22792	-	scaffold1417	1.071	1.391	hypothetical protein GLYMA_19G093700
487	MSTRG.22870	Ca_24090	scaffold1504	1.060	3.228	cysteine/histidine-rich C1 domain protein
488	MSTRG.22904	Ca_23862	scaffold1545	3.254	1.432	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 7-like
489	MSTRG.22919	Ca_21064	scaffold157	6.635	1.264	isoliquiritigenin 2'-O-methyltransferase-like
490	MSTRG.22925	Ca_21071	scaffold157	2.777	1.076	peroxisomal nicotinamide adenine dinucleotide carrier-like
491	MSTRG.23027	Ca_24155	scaffold167	4.895	-1.004	M48 family peptidase
492	MSTRG.23022	Ca_24156	scaffold167	-0.539	-2.211	sulfite oxidase
493	MSTRG.23066	Ca_25723	scaffold1710	1.933	1.050	LysM domain containing protein
494	MSTRG.23098	Ca_21709	scaffold174	2.099	-1.591	carboxyl-terminal-processing peptidase 3, chloroplastic
495	MSTRG.23264	-	scaffold193	-0.144	-4.902	DUF688 family protein
496	MSTRG.23346	Ca_26673	scaffold1991	5.428	-1.536	chromosome condensation regulator RCC1 repeat protein
497	MSTRG.23345	Ca_24935	scaffold2	-2.589	-6.070	protein transport Sec1a
498	MSTRG.23402	-	scaffold206	3.516	-2.316	uncharacterized protein LOC106766073
499	MSTRG.23515	Ca_25197	scaffold227	3.125	-1.373	glutaredoxin domain-containing cysteine-rich protein CG12206
500	MSTRG.23527	-	scaffold2330	4.486	1.028	transmembrane protein, putative
501	MSTRG.23536	Ca_26079	scaffold235	5.805	-1.921	probable trehalose-phosphate phosphatase C
502	MSTRG.23584	Ca_25578	scaffold2386	-0.007	-2.100	flagellar basal body L-ring protein
503	MSTRG.23615	Ca_22270	scaffold242	4.287	1.269	remorin 4.1
504	MSTRG.23624	Ca_27038	scaffold250	4.446	-1.182	peptide methionine sulfoxide reductase B1, chloroplastic
505	MSTRG.23644	-	scaffold2560	0.862	-1.016	UDP-glycosyltransferase 74B1
506	MSTRG.23677	-	scaffold26	2.355	-1.144	UDP-glycosyltransferase 1
507	MSTRG.23713	-	scaffold2711	-1.220	-1.398	---NA---
508	MSTRG.23758	Ca_24404	scaffold2763	7.322	1.094	isoliquiritigenin 2'-O-methyltransferase-like
509	MSTRG.23812	Ca_25387	scaffold287	0.409	-1.152	probable serine/threonine-protein kinase WNK7 isoform X1
510	MSTRG.23839	-	scaffold290	0.235	1.242	hypothetical protein TSUD_335750
511	MSTRG.23821	Ca_19826	scaffold290	7.346	-1.901	magnesium-chelatase subunit ChlH, chloroplastic
512	MSTRG.23907	Ca_25903	scaffold305	5.714	1.261	glycerol-3-phosphate 2-O-acyltransferase 6
513	MSTRG.24182	Ca_25858	scaffold36	4.409	1.349	triacylglycerol lipase 2
514	MSTRG.24252	Ca_27662	scaffold3865	6.474	-1.032	probable sulfate transporter 4.2
515	MSTRG.24384	Ca_26396	scaffold419	4.222	1.846	Putative disease resistance protein
516	MSTRG.24399	-	scaffold420	1.498	1.587	glycine-rich RNA-binding protein GRP1A
517	MSTRG.24499	Ca_22618	scaffold451	2.018	-1.717	transcription factor HY5-like isoform X1
518	MSTRG.24664	-	scaffold5226	0.526	-2.711	protein FAR-RED IMPAIRED RESPONSE 1-like
519	MSTRG.24669	Ca_26392	scaffold527	2.540	-1.214	thiamine pyrophosphate-binding protein
520	MSTRG.24723	Ca_23286	scaffold537	5.549	1.601	expansin-B3
521	MSTRG.24732	Ca_27303	scaffold5389	0.576	3.252	lysine-specific demethylase JMJ30
522	MSTRG.24918	Ca_27770	scaffold627	4.680	-3.123	protein LNK2 isoform X1
523	MSTRG.24970	Ca_27555	scaffold6458	0.764	1.946	nudix hydrolase 2
524	MSTRG.24968	-	scaffold6458	1.827	-2.998	digestive organ expansion factor-like protein
525	MSTRG.25057	Ca_27281	scaffold707	-0.670	1.649	cytosolic sulfotransferase 15-like
526	MSTRG.25131	Ca_25929	scaffold753	1.650	-3.300	cyclic dof factor 3

527	MSTRG.25171	-	scaffold787	-0.245	-2.772	putative copia-type protein
528	MSTRG.25205	-	scaffold809	2.083	-2.483	hypothetical protein L195_g052424
529	MSTRG.25232	-	scaffold812	6.462	-1.065	---NA---
530	MSTRG.25327	Ca_26775	scaffold875	4.666	-1.090	DNA-binding protein SMUBP-2
531	MSTRG.25345	Ca_22178	scaffold88	4.758	2.167	methylecgonone reductase-like
532	MSTRG.25408	-	scaffold895	1.788	-1.296	glycoside hydrolase family 1 protein

Supplementary Table 4: PRR resistance genes in PRR susceptible genotype Rupali differently expressed under inoculation (Rup-I)

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)	Description of the gene
1	MSTRG.78	Ca_27990	C11107558	-4.665	-8.140	protein CURVATURE THYLAKOID 1B, chloroplastic-like
2	MSTRG.121	Ca_27865	C11151940	-1.737	-3.409	UPF0098 protein MTH-273
3	MSTRG.146	Ca_28056	C11164954	2.670	-1.047	protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB4, chloroplastic
4	MSTRG.147	Ca_27893	C11165044	3.413	-2.614	zinc finger protein CONSTANS-LIKE 2-like
5	MSTRG.156	-	C11165890	-2.650	-8.908	late embryogenesis abundant protein 2
6	MSTRG.157	Ca_28203	C11166868	2.638	2.431	probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
7	MSTRG.165	Ca_27557	C11172910	4.534	-1.457	tonoplast dicarboxylate transporter
8	MSTRG.174	Ca_28257	C11177172	4.151	1.081	uncharacterized protein At3g06530-like
9	MSTRG.2555	-	Ca1	0.600	4.735	nucleosome assembly protein 1-like 3
10	MSTRG.958	-	Ca1	-0.889	2.765	PKS-NRPS hybrid synthetase CHGG_01239-like
11	MSTRG.842	Ca_00665	Ca1	-1.244	2.530	chaperonin-like RBCX protein 1, chloroplastic
12	MSTRG.2339	Ca_20295	Ca1	1.993	2.390	protein SRG1
13	MSTRG.2981	-	Ca1	-2.358	2.386	---NA---
14	MSTRG.322	Ca_00125	Ca1	3.377	2.350	cationic peroxidase 2-like
15	MSTRG.1281	Ca_02766	Ca1	3.525	2.319	probable LRR receptor-like serine/threonine-protein kinase At1g05700
16	MSTRG.1304	Ca_02737	Ca1	3.522	2.134	beta-fructofuranosidase, cell wall isozyme
17	MSTRG.1120	Ca_02925	Ca1	2.011	2.078	probable WRKY transcription factor 40
18	MSTRG.2014	Ca_14771	Ca1	0.225	2.032	pathogenesis-related protein STH-2-like
19	MSTRG.1280	Ca_02765	Ca1	3.302	1.987	putative transcription factor WD40-like family
20	MSTRG.2662	Ca_18440	Ca1	1.966	1.846	VQ motif-containing protein 1-like
21	MSTRG.563	Ca_00359	Ca1	1.263	1.807	pathogenesis-related genes transcriptional activator PTI5-like
22	MSTRG.2745	Ca_22515	Ca1	3.553	1.760	protein GRIM REAPER
23	MSTRG.3006	-	Ca1	9.041	1.736	epidermis-specific secreted glycoprotein EP1
24	MSTRG.1391	Ca_02649	Ca1	3.755	1.694	ADP,ATP carrier protein, mitochondrial
25	MSTRG.564	Ca_00360	Ca1	-2.635	1.670	uncharacterized protein LOC101506742
26	MSTRG.377	-	Ca1	2.047	1.666	oligopeptide transporter 4
27	MSTRG.1981	Ca_22779	Ca1	7.814	1.652	glucan endo-1,3-beta-glucosidase, basic isoform
28	MSTRG.569	Ca_00363	Ca1	4.734	1.565	glutamate receptor 2.7-like
29	MSTRG.690	Ca_00497	Ca1	1.943	1.539	gibberellin 2-beta-dioxygenase
30	MSTRG.997	Ca_07988	Ca1	5.582	1.528	peroxidase 15
31	MSTRG.2325	Ca_20281	Ca1	4.013	1.493	peroxidase 7-like
32	MSTRG.376	Ca_00171	Ca1	5.530	1.481	oligopeptide transporter 4-like
33	MSTRG.2197	Ca_20616	Ca1	4.138	1.427	putative transcription factor bHLH041
34	MSTRG.1273	Ca_02773	Ca1	1.451	1.394	GDSL esterase/lipase APG
35	MSTRG.2278	Ca_18303	Ca1	1.406	1.376	uncharacterized protein LOC101488468
36	MSTRG.2724	Ca_23111	Ca1	2.395	1.364	probable glutathione S-transferase
37	MSTRG.1237	Ca_02810	Ca1	6.446	1.330	protein PLANT CADMIUM RESISTANCE 8
38	MSTRG.1724	Ca_07110	Ca1	5.671	1.299	cellulose synthase-like protein H1
39	MSTRG.258	Ca_00063	Ca1	5.266	1.266	probable receptor-like protein kinase At1g11050
40	MSTRG.2074	Ca_17387	Ca1	8.254	1.217	isoflavone 3'-hydroxylase
41	MSTRG.428	Ca_00219	Ca1	5.466	1.191	receptor-like serine/threonine-protein kinase SD1-8

42	MSTRG.1837	Ca_06993	Ca1	4.307	1.190	putative Myb family transcription factor
43	MSTRG.2283	Ca_25075	Ca1	5.619	1.144	1,4-dihydroxy-2-naphthoyl-CoA thioesterase 1
44	MSTRG.1758	Ca_07074	Ca1	4.033	1.128	F-box protein At2g27310
45	MSTRG.1337	Ca_02699	Ca1	2.384	1.114	transmembrane protein, putative
46	MSTRG.961	Ca_07956	Ca1	6.026	1.109	probable leucine-rich repeat receptor-like protein kinase At5g49770
47	MSTRG.427	Ca_00218	Ca1	4.532	1.094	receptor-like serine/threonine-protein kinase SD1-8
48	MSTRG.1433	Ca_02613	Ca1	3.744	1.091	protein TRM32
49	MSTRG.2172	Ca_22105	Ca1	5.531	1.090	plant intracellular Ras-group-related LRR protein 6
50	MSTRG.2440	-	Ca1	4.601	1.023	F-box/FBD/LRR-repeat protein At3g14710-like
51	MSTRG.2009	Ca_14776	Ca1	9.755	1.006	class-10 pathogenesis-related protein 1
52	MSTRG.1741	-	Ca1	3.161	-1.047	protein FAF-like, chloroplastic
53	MSTRG.1436	Ca_02610	Ca1	4.038	-1.054	actin
54	MSTRG.309	Ca_00113	Ca1	4.423	-1.062	soyasaponin III rhamnosyltransferase-like
55	MSTRG.909	Ca_07904	Ca1	6.331	-1.073	pollen-specific leucine-rich repeat extensin-like protein 1
56	MSTRG.1426	Ca_02620	Ca1	3.670	-1.077	expansin-A4
57	MSTRG.1670	Ca_14134	Ca1	6.633	-1.109	xyloglucan endotransglucosylase/hydrolase protein 9
58	MSTRG.335	Ca_00133	Ca1	6.476	-1.111	ICE-like protease (caspase) p20 domain protein
59	MSTRG.1006	Ca_07994	Ca1	4.406	-1.113	homeobox-leucine zipper protein ATHB-14
60	MSTRG.2321	Ca_18618	Ca1	0.714	-1.113	chloroplast envelope quinone oxidoreductase homolog
61	MSTRG.2484	Ca_19433	Ca1	3.789	-1.121	dof zinc finger protein DOF5.4-like
62	MSTRG.1678	Ca_14141	Ca1	2.066	-1.123	formin-like protein 3
63	MSTRG.346	Ca_00144	Ca1	2.336	-1.130	---NA---
64	MSTRG.1107	Ca_02938	Ca1	1.115	-1.135	fasciclin-like arabinogalactan protein 14
65	MSTRG.596	Ca_00391	Ca1	2.262	-1.151	olee1-like protein
66	MSTRG.960	Ca_07955	Ca1	2.753	-1.181	ferric reduction oxidase 7, chloroplastic
67	MSTRG.1506	Ca_02533	Ca1	10.636	-1.197	aquaporin PIP2-7
68	MSTRG.1129	Ca_02921	Ca1	5.582	-1.221	aquaporin NIP6-1
69	MSTRG.2726	Ca_23112	Ca1	8.159	-1.221	probable glutathione S-transferase
70	MSTRG.2893	Ca_25715	Ca1	7.440	-1.223	beta-amyrin synthase
71	MSTRG.1792	Ca_07045	Ca1	1.914	-1.287	fatty acyl-CoA reductase 3
72	MSTRG.2120	Ca_17338	Ca1	2.798	-1.299	nifU-like protein 3, chloroplastic
73	MSTRG.334	Ca_00133	Ca1	3.748	-1.306	---NA---
74	MSTRG.2495	Ca_19441	Ca1	1.593	-1.311	probable galacturonosyltransferase 11
75	MSTRG.1009	Ca_07997	Ca1	1.346	-1.322	transmembrane protein, putative
76	MSTRG.2228	Ca_19300	Ca1	0.856	-1.340	---NA---
77	MSTRG.1451	Ca_02593	Ca1	6.218	-1.364	myb transcription factor
78	MSTRG.2394	Ca_18504	Ca1	5.545	-1.389	probable inositol transporter 2
79	MSTRG.1727	Ca_07105	Ca1	-0.667	-1.401	uncharacterized protein LOC101515047
80	MSTRG.1401	Ca_02638	Ca1	2.561	-1.409	zinc finger protein ZAT3-like
81	MSTRG.1239	Ca_02809	Ca1	1.388	-1.413	---NA---
82	MSTRG.2952	Ca_12949	Ca1	3.674	-1.424	protein NEOXANTHIN-DEFICIENT 1 isoform X2
83	MSTRG.2847	Ca_13545	Ca1	1.616	-1.488	glutathione S-transferase F9-like
84	MSTRG.1395	Ca_02643	Ca1	3.683	-1.489	aluminum-activated citrate transporter

85	MSTRG.1573	Ca_02465	Ca1	6.983	-1.521	fasciclin-like arabinogalactan protein 13
86	MSTRG.1055	Ca_08045	Ca1	3.696	-1.525	ent-kaurenoic acid oxidase 2
87	MSTRG.1202	Ca_02845	Ca1	0.791	-1.561	gibberellin 3-beta-dioxygenase 1
88	MSTRG.1654	Ca_14119	Ca1	3.531	-1.561	transcription factor MYB41
89	MSTRG.1651	Ca_14118	Ca1	3.913	-1.601	coumaroyl-CoA:anthocyanidin 3-O-glucoside-6"-O-coumaroyltransferase 1-like
90	MSTRG.2182	Ca_20634	Ca1	5.205	-1.604	probable xyloglucan endotransglucosylase/hydrolase protein 23
91	MSTRG.324	Ca_00127	Ca1	6.008	-1.605	protein LNK1-like isoform X4
92	MSTRG.2422	Ca_22558	Ca1	1.972	-1.612	transcription termination factor MTEF1, chloroplastic
93	MSTRG.1872	Ca_06955	Ca1	3.664	-1.646	thioredoxin-like protein CXXS1
94	MSTRG.458	Ca_00252	Ca1	4.148	-1.691	endonuclease 1
95	MSTRG.1198	Ca_02846	Ca1	3.325	-1.964	gibberellin 3-beta-dioxygenase 1
96	MSTRG.438	Ca_00232	Ca1	1.167	-2.041	transcription factor MYB102
97	MSTRG.2246	Ca_19281	Ca1	3.007	-2.054	transmembrane protein, putative
98	MSTRG.1986	Ca_22784	Ca1	3.679	-2.086	outer envelope pore protein 16-2, chloroplastic
99	MSTRG.1085	Ca_08081	Ca1	0.059	-2.089	cell wall / vacuolar inhibitor of fructosidase 1-like
100	MSTRG.2677	Ca_18448	Ca1	-0.289	-2.166	uncharacterized protein LOC101496808
101	MSTRG.2739	Ca_25800	Ca1	0.965	-2.228	9-cis-epoxycarotenoid dioxygenase
102	MSTRG.453	Ca_00247	Ca1	-0.092	-2.318	DUF4408 domain protein
103	MSTRG.320	Ca_00123	Ca1	5.467	-2.587	chlorophyll a-b binding protein CP24 10A, chloroplastic
104	MSTRG.1665	Ca_14127	Ca1	3.465	-2.631	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130
105	MSTRG.1904	Ca_06917	Ca1	6.451	-2.773	chlorophyll a-b binding protein 13, chloroplastic
106	MSTRG.2592	Ca_21843	Ca1	0.784	-2.986	2-alkenal reductase (NADP(+)-dependent)-like
107	MSTRG.1345	Ca_02689	Ca1	6.327	-3.103	salt tolerance protein
108	MSTRG.2702	-	Ca1	0.599	-3.468	---NA---
109	MSTRG.1684	-	Ca1	-0.180	-4.804	B-box domain protein 30
110	MSTRG.200	Ca_00003	Ca1	0.328	-7.383	---NA---
111	MSTRG.4517	-	Ca2	-0.389	6.713	probable 2-oxoglutarate-dependent dioxygenase At5g05600
112	MSTRG.4808	Ca_15276	Ca2	-1.149	4.551	Small heat shock protein C2
113	MSTRG.4231	Ca_17243	Ca2	-0.954	3.390	Protein CHLOROPLAST IMPORT APPARATUS 2
114	MSTRG.4602	Ca_17822	Ca2	1.807	2.980	arogenate dehydratase/prephenate dehydratase 2, chloroplastic
115	MSTRG.4447	Ca_16099	Ca2	2.803	2.881	elicitor-responsive protein 1-like
116	MSTRG.3412	-	Ca2	-2.924	2.166	hypothetical protein L195_g054813, partial
117	MSTRG.4262	Ca_17280	Ca2	1.403	2.092	probable O-methyltransferase 3
118	MSTRG.3875	Ca_11637	Ca2	2.906	1.956	glycoside hydrolase family 1 protein
119	MSTRG.3097	Ca_20673	Ca2	5.179	1.915	PQQ-dependent membrane bound dehydrogenase, glucose/quinate/shikimate-related
120	MSTRG.4541	Ca_12448	Ca2	5.250	1.833	abscisic acid receptor PYL4
121	MSTRG.3371	Ca_10455	Ca2	3.864	1.698	phenolic glucoside malonyltransferase 1-like
122	MSTRG.4413	Ca_16139	Ca2	3.968	1.618	probable methyltransferase PMT19
123	MSTRG.3372	-	Ca2	3.858	1.536	transcription factor TCP13
124	MSTRG.4421	Ca_16136	Ca2	3.158	1.498	putative transcription factor bHLH086
125	MSTRG.4305	Ca_15676	Ca2	6.500	1.479	probable LRR receptor-like serine/threonine-protein kinase At1g06840
126	MSTRG.3651	Ca_22309	Ca2	0.703	1.459	transcription factor bHLH18-like
127	MSTRG.4991	Ca_09797	Ca2	5.129	1.453	NAD(P)H-dependent 6'-deoxychalcone synthase

128	MSTRG.4494	Ca_12499	Ca2	2.312	1.381	nematode resistance protein-like HSPRO2
129	MSTRG.3647	Ca_22312	Ca2	2.997	1.354	calcium-dependent protein kinase 26-like
130	MSTRG.4993	Ca_09797	Ca2	3.976	1.331	NAD(P)H-dependent 6'-deoxychalcone synthase
131	MSTRG.4446	Ca_16100	Ca2	1.058	1.316	transcription factor, putative
132	MSTRG.3306	Ca_10518	Ca2	2.829	1.302	myb-related protein 306-like
133	MSTRG.3278	Ca_10545	Ca2	5.858	1.226	AAA-ATPase ASD, mitochondrial-like
134	MSTRG.4425	Ca_16130	Ca2	3.683	1.222	plastid movement impaired protein
135	MSTRG.4724	Ca_10191	Ca2	2.198	1.203	calcium-dependent protein kinase 17-like
136	MSTRG.4825	Ca_15290	Ca2	2.864	1.170	taxadiene 5-alpha hydroxylase-like
137	MSTRG.4286	Ca_15660	Ca2	10.077	1.156	trans-cinnamate 4-monooxygenase
138	MSTRG.3733	Ca_17578	Ca2	0.867	1.150	TMV resistance protein N-like
139	MSTRG.4493	Ca_12500	Ca2	3.143	1.141	putative tetratricopeptide-like helical domain-containing protein
140	MSTRG.4566	Ca_12420	Ca2	2.419	1.051	LOB domain-containing protein 15
141	MSTRG.3099	Ca_20675	Ca2	3.758	1.031	probable WRKY transcription factor 72
142	MSTRG.4448	Ca_16098	Ca2	4.183	1.008	Elicitor-responsive protein 1
143	MSTRG.4705	Ca_10210	Ca2	6.434	1.006	cysteine proteinase inhibitor
144	MSTRG.3970	Ca_16005	Ca2	3.433	1.005	methyltransferase domain protein, putative
145	MSTRG.3732	-	Ca2	6.257	1.003	TMV resistance protein N-like
146	MSTRG.4255	Ca_17271	Ca2	2.718	-1.002	DUF4228 domain protein
147	MSTRG.3955	Ca_24770	Ca2	4.987	-1.009	serine/threonine-protein kinase STN7, chloroplastic
148	MSTRG.3613	Ca_21476	Ca2	3.556	-1.023	F-box/kelch-repeat protein At1g23390
149	MSTRG.4497	Ca_12495	Ca2	5.826	-1.034	auxin transporter-like protein 1
150	MSTRG.4790	Ca_15255	Ca2	3.202	-1.035	AT-hook motif nuclear-localized protein 16
151	MSTRG.3756	Ca_25885	Ca2	3.429	-1.073	protein NRT1/ PTR FAMILY 4.6
152	MSTRG.3713	-	Ca2	2.448	-1.075	Retrotransposable element Tf2
153	MSTRG.3240	Ca_10579	Ca2	5.252	-1.077	peroxidase 31
154	MSTRG.3725	Ca_17587	Ca2	3.430	-1.081	wall-associated receptor kinase-like 20
155	MSTRG.3243	Ca_10576	Ca2	2.128	-1.085	zinc finger AN1 domain-containing stress-associated protein 12
156	MSTRG.3393	Ca_21103	Ca2	2.130	-1.140	copper transport protein CCH-like
157	MSTRG.3715	Ca_17597	Ca2	4.849	-1.217	transcription factor MYB1R1
158	MSTRG.4605	Ca_17820	Ca2	6.298	-1.229	E3 ubiquitin-protein ligase COP1
159	MSTRG.3812	Ca_18074	Ca2	3.262	-1.236	E3 ubiquitin-protein ligase MPSR1
160	MSTRG.4361	-	Ca2	1.345	-1.243	R2R3 MYB protein
161	MSTRG.4280	Ca_15651	Ca2	4.742	-1.249	probable serine/threonine-protein kinase WNK4
162	MSTRG.4641	-	Ca2	1.666	-1.280	protein SPA, chloroplastic isoform X2
163	MSTRG.3570	Ca_18112	Ca2	5.567	-1.333	mitochondrial uncoupling protein 5
164	MSTRG.4677	Ca_10238	Ca2	5.002	-1.343	NDR1/HIN1-like protein 13
165	MSTRG.4770	Ca_15235	Ca2	6.814	-1.348	glutathione S-transferase F9-like
166	MSTRG.3580	Ca_18121	Ca2	5.920	-1.355	protein DETOXIFICATION 27-like
167	MSTRG.3067	Ca_16983	Ca2	3.024	-1.406	cytokinin hydroxylase
168	MSTRG.4710	Ca_10204	Ca2	5.655	-1.461	blue copper protein-like
169	MSTRG.4604	-	Ca2	-0.154	-1.485	---NA---
170	MSTRG.4779	Ca_15244	Ca2	1.678	-1.493	transmembrane protein, putative

171	MSTRG.4941	Ca_09747	Ca2	5.236	-1.502	LRR receptor-like serine/threonine-protein kinase
172	MSTRG.4119	Ca_21674	Ca2	1.531	-1.533	protein DETOXIFICATION 48-like
173	MSTRG.4455	Ca_16091	Ca2	5.590	-1.534	protein phosphatase 2C 37
174	MSTRG.4891	Ca_09698	Ca2	1.846	-1.537	transmembrane protein
175	MSTRG.4973	Ca_09781	Ca2	2.725	-1.542	uncharacterized protein LOC101505296
176	MSTRG.3402	Ca_21097	Ca2	4.299	-1.609	serine carboxypeptidase-like 25
177	MSTRG.3394	Ca_21102	Ca2	4.391	-1.634	copper transport protein CCH-like
178	MSTRG.3133	Ca_12622	Ca2	4.978	-1.654	---NA---
179	MSTRG.4553	Ca_12434	Ca2	-0.777	-1.736	heavy metal-associated isoprenylated plant protein 33
180	MSTRG.4228	-	Ca2	2.261	-1.737	receptor-like kinase
181	MSTRG.3346	Ca_10479	Ca2	2.793	-1.742	DUF4336 domain protein
182	MSTRG.4252	Ca_17269	Ca2	-0.172	-1.796	exocyst complex component EXO70B1-like
183	MSTRG.3542	Ca_19147	Ca2	1.899	-1.816	myb-related protein 2-like isoform X1
184	MSTRG.4042	Ca_24630	Ca2	2.472	-1.828	protein DMR6-LIKE OXYGENASE 2-like
185	MSTRG.5011	Ca_09819	Ca2	6.825	-1.836	chlorophyll a-b binding protein 8, chloroplastic
186	MSTRG.4400	Ca_14327	Ca2	3.222	-1.836	aspartic proteinase PCS1-like
187	MSTRG.3816	Ca_18079	Ca2	0.821	-1.924	dof zinc finger protein
188	MSTRG.4399	Ca_14327	Ca2	1.444	-1.929	---NA---
189	MSTRG.3045	-	Ca2	-0.275	-1.951	---NA---
190	MSTRG.4625	Ca_10290	Ca2	3.687	-2.068	protein DMP3-like
191	MSTRG.4475	-	Ca2	3.361	-2.089	haloacid dehalogenase superfamily protein isoform X1
192	MSTRG.3673	Ca_20024	Ca2	2.264	-2.115	putative disease resistance protein RGA3
193	MSTRG.3897	Ca_18564	Ca2	3.281	-2.420	ninja-family protein AFP3
194	MSTRG.4253	-	Ca2	0.636	-2.492	WRKY family transcription factor
195	MSTRG.4261	Ca_17277	Ca2	0.565	-2.675	probable O-methyltransferase 3
196	MSTRG.3305	Ca_10519	Ca2	0.269	-2.734	light-harvesting complex I chlorophyll A/B-binding protein
197	MSTRG.4971	Ca_09779	Ca2	7.354	-3.425	chlorophyll a-b binding protein 215, chloroplastic
198	MSTRG.4031	Ca_23768	Ca2	0.490	-3.889	protein MAIN-LIKE 1-like
199	MSTRG.4694	Ca_10219	Ca2	-0.149	-3.957	zinc finger protein ZAT2-like
200	MSTRG.7587	Ca_01309	Ca3	-1.633	4.628	cyclic nucleotide-gated ion channel 1
201	MSTRG.7586	Ca_01309	Ca3	-1.013	4.570	cyclic nucleotide-gated ion channel 1-like
202	MSTRG.6610	Ca_07345	Ca3	-0.744	3.487	sugar transporter ERD6-like 7
203	MSTRG.5705	-	Ca3	4.530	2.920	GDSL esterase/lipase CPRD49-like
204	MSTRG.7363	Ca_01113	Ca3	2.562	2.772	dnaJ homolog subfamily B member 6
205	MSTRG.5703	-	Ca3	3.973	2.388	GDSL esterase/lipase CPRD49
206	MSTRG.7591	Ca_01309	Ca3	0.872	2.338	---NA---
207	MSTRG.7590	Ca_01309	Ca3	1.288	2.121	cyclic nucleotide-gated ion channel 1 isoform X1
208	MSTRG.5819	Ca_09495	Ca3	2.203	2.083	probable WRKY transcription factor 70
209	MSTRG.7543	Ca_01273	Ca3	-2.029	1.696	carboxyl-terminal peptidase
210	MSTRG.7584	Ca_01308	Ca3	5.777	1.665	cyclic nucleotide-gated ion channel 1
211	MSTRG.5067	Ca_22642	Ca3	3.881	1.608	2OG-Fe(II) oxygenase family oxidoreductase
212	MSTRG.5602	Ca_21116	Ca3	4.700	1.598	putative respiratory burst oxidase homolog protein H
213	MSTRG.7447	Ca_01193	Ca3	3.401	1.594	histidine-containing phosphotransfer protein 1

214	MSTRG.6891	Ca_12046	Ca3	4.812	1.572	chromodomain-helicase-DNA-binding protein 3-like isoform X1
215	MSTRG.6800	Ca_11962	Ca3	5.410	1.570	cation/H(+) antiporter 20
216	MSTRG.6602	Ca_07339	Ca3	8.507	1.534	dirigent protein 22-like
217	MSTRG.7107	Ca_00861	Ca3	3.855	1.506	E3 ubiquitin-protein ligase PUB22
218	MSTRG.7551	Ca_01281	Ca3	1.275	1.470	probable receptor-like protein kinase At5g18500
219	MSTRG.7025	Ca_00776	Ca3	5.371	1.461	drug resistance transporter-like ABC domain protein
220	MSTRG.5859	Ca_20433	Ca3	2.173	1.456	methylsterol monooxygenase 1-1-like
221	MSTRG.6338	Ca_08155	Ca3	6.205	1.425	dihydrofolate reductase
222	MSTRG.7409	Ca_01153	Ca3	7.174	1.395	respiratory burst oxidase homolog protein B-like
223	MSTRG.7064	Ca_00814	Ca3	4.521	1.394	1-aminocyclopropane-1-carboxylate oxidase homolog 4-like
224	MSTRG.6977	Ca_00734	Ca3	4.843	1.392	purine-uracil permease NCS1
225	MSTRG.7449	Ca_01191	Ca3	7.757	1.321	sugar transporter ERD6-like 5 isoform X1
226	MSTRG.5792	-	Ca3	3.174	1.314	uncharacterized protein LOC101490888
227	MSTRG.5585	Ca_23345	Ca3	4.058	1.266	protein PHLOEM PROTEIN 2-LIKE A1
228	MSTRG.5393	-	Ca3	0.816	1.226	serine/threonine protein kinase SRPK1
229	MSTRG.5085	Ca_19403	Ca3	7.545	1.225	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform
230	MSTRG.5752	Ca_09431	Ca3	0.377	1.190	pentatricopeptide repeat-containing protein At3g18020
231	MSTRG.5474	Ca_23302	Ca3	5.648	1.176	L-type lectin-domain containing receptor kinase IV.1
232	MSTRG.7108	Ca_00859	Ca3	5.064	1.157	BEL1-like homeodomain protein 1
233	MSTRG.7309	Ca_01059	Ca3	5.019	1.114	putative expansin-A17
234	MSTRG.7418	Ca_01160	Ca3	4.316	1.103	DNA polymerase zeta catalytic subunit
235	MSTRG.5961	Ca_06190	Ca3	6.467	1.078	bifunctional L-3-cyanoalanine synthase/cysteine synthase 1, mitochondrial
236	MSTRG.7171	Ca_00927	Ca3	5.229	1.067	zinc finger protein CONSTANS-LIKE 13
237	MSTRG.7287	Ca_01032	Ca3	4.645	1.046	short-chain dehydrogenase reductase 3b
238	MSTRG.6120	Ca_06021	Ca3	6.506	1.027	putative glycerophosphodiester phosphodiesterase, protein kinase RLK-Pelle-LRK10L-2 family
239	MSTRG.7641	Ca_01360	Ca3	2.939	-1.002	NDR1/HIN1-like protein 12
240	MSTRG.7182	Ca_00938	Ca3	5.323	-1.010	spermatogenesis-associated protein 20
241	MSTRG.6458	Ca_07202	Ca3	4.200	-1.018	uncharacterized protein LOC101515199
242	MSTRG.5189	Ca_22097	Ca3	7.367	-1.031	cyclic nucleotide-gated ion channel 2
243	MSTRG.6586	Ca_07322	Ca3	2.079	-1.067	homeobox-leucine zipper protein HOX11
244	MSTRG.6961	Ca_00723	Ca3	11.598	-1.069	probable aquaporin TIP-type
245	MSTRG.7255	Ca_01004	Ca3	5.579	-1.070	bZIP transcription factor 53
246	MSTRG.6035	Ca_06114	Ca3	4.528	-1.119	thioredoxin F-type, chloroplastic
247	MSTRG.5570	Ca_18297	Ca3	5.103	-1.128	chloroplast envelope quinone oxidoreductase homolog
248	MSTRG.7391	Ca_01140	Ca3	9.507	-1.141	dormancy-associated protein homolog 3-like isoform X2
249	MSTRG.5695	Ca_19341	Ca3	3.140	-1.151	E3 ubiquitin-protein ligase AIRP2-like
250	MSTRG.6416	Ca_07159	Ca3	3.115	-1.157	transcription factor bHLH106
251	MSTRG.6874	Ca_12036	Ca3	6.507	-1.164	peptide upstream ORF protein, putative
252	MSTRG.6957	Ca_00719	Ca3	3.493	-1.175	probable pectate lyase 12
253	MSTRG.6935	Ca_20889	Ca3	5.075	-1.188	condensation domain protein
254	MSTRG.7488	Ca_01230	Ca3	6.081	-1.200	probable aldo-keto reductase 1
255	MSTRG.7626	Ca_01345	Ca3	2.147	-1.218	3-ketoacyl-CoA synthase 1
256	MSTRG.6568	Ca_07306	Ca3	1.860	-1.219	non-structural maintenance of chromosomes element 4 homolog A-like isoform X1

257	MSTRG.6661	-	Ca3	4.496	-1.228	protein MARD1
258	MSTRG.6124	Ca_06013	Ca3	3.424	-1.245	lipid phosphate phosphatase 2 isoform X1
259	MSTRG.7623	-	Ca3	2.400	-1.259	putative permease/transmembrane protein
260	MSTRG.6450	Ca_07195	Ca3	4.315	-1.262	haloacid dehalogenase-like hydrolase domain-containing protein 3
261	MSTRG.5386	Ca_19357	Ca3	4.804	-1.262	metal tolerance protein 11 isoform X2
262	MSTRG.7636	Ca_01352	Ca3	1.971	-1.276	DNA-directed RNA polymerase III subunit RPC10-like
263	MSTRG.6962	-	Ca3	0.016	-1.284	uncharacterized protein LOC101504872
264	MSTRG.6149	Ca_05989	Ca3	2.060	-1.287	NAC domain-containing protein 83
265	MSTRG.7045	Ca_00794	Ca3	2.900	-1.299	Protein BIC1
266	MSTRG.7350	Ca_01092	Ca3	4.442	-1.321	chloroplast stem-loop binding protein of 41 kDa b, chloroplastic
267	MSTRG.5916	Ca_06244	Ca3	2.556	-1.385	Zinc finger, CCHC-type
268	MSTRG.6693	Ca_12204	Ca3	3.752	-1.388	PRA1 family protein F2-like
269	MSTRG.6747	-	Ca3	1.534	-1.416	---NA---
270	MSTRG.6691	Ca_12198	Ca3	2.728	-1.438	phospholipase A1-Igamma2, chloroplastic-like
271	MSTRG.6913	Ca_20870	Ca3	3.061	-1.455	germin-like protein subfamily 3 member 2
272	MSTRG.5700	Ca_19346	Ca3	7.059	-1.458	vacuolar cation/proton exchanger 3
273	MSTRG.7330	Ca_01073	Ca3	6.279	-1.490	low temprature induced-like protein
274	MSTRG.6675	Ca_12183	Ca3	5.007	-1.518	heat stress transcription factor A-7a-like
275	MSTRG.6803	Ca_11967	Ca3	1.161	-1.539	transmembrane protein, putative
276	MSTRG.5924	Ca_06237	Ca3	3.443	-1.545	(+)-neomenthol dehydrogenase
277	MSTRG.5370	Ca_18807	Ca3	2.984	-1.564	probable aldo-keto reductase 2
278	MSTRG.6513	Ca_07254	Ca3	2.505	-1.663	polygalacturonase
279	MSTRG.5154	Ca_22383	Ca3	1.358	-1.680	cyclic dof factor 2
280	MSTRG.5340	-	Ca3	-0.803	-1.704	---NA---
281	MSTRG.5955	Ca_06198	Ca3	5.027	-1.729	ascorbate transporter, chloroplastic
282	MSTRG.6518	Ca_07258	Ca3	2.142	-1.736	myosin-11-like protein
283	MSTRG.6634	Ca_07368	Ca3	3.512	-1.770	---NA---
284	MSTRG.6569	Ca_07308	Ca3	2.517	-1.783	lactosylceramide 4-alpha-glycosyltransferase
285	MSTRG.5644	-	Ca3	3.567	-1.810	conserved Plasmodium protein, unknown function
286	MSTRG.7257	Ca_01005	Ca3	5.832	-1.847	calvin cycle protein CP12-2, chloroplastic
287	MSTRG.6848	Ca_12007	Ca3	4.272	-1.855	thioredoxin-like protein AAED1, chloroplastic
288	MSTRG.6104	Ca_06032	Ca3	5.391	-1.860	ethylene-responsive transcription factor 1-like
289	MSTRG.7128	Ca_00882	Ca3	3.017	-1.870	ABC transporter G family member 22 isoform X1
290	MSTRG.6847	-	Ca3	2.523	-1.882	thioredoxin-like protein AAED1, chloroplastic
291	MSTRG.7307	Ca_01056	Ca3	1.599	-1.976	uncharacterized protein LOC101492848
292	MSTRG.6782	Ca_12291	Ca3	2.218	-2.047	photosystem I reaction center subunit IV A, chloroplastic-like
293	MSTRG.6315	Ca_08178	Ca3	7.142	-2.107	protein MAIN-LIKE 1-like
294	MSTRG.6788	Ca_12296	Ca3	-0.554	-2.243	---NA---
295	MSTRG.7270	Ca_01017	Ca3	5.753	-2.280	stachyose synthase
296	MSTRG.6515	Ca_07257	Ca3	3.451	-2.319	remorin 4.1
297	MSTRG.7640	Ca_01359	Ca3	5.108	-2.442	two-component response regulator-like APRR9 isoform X1
298	MSTRG.5638	Ca_19627	Ca3	0.639	-2.558	universal stress protein PHOS32-like
299	MSTRG.6615	-	Ca3	0.754	-2.583	protein bunched, class 2/F/G isoform

300	MSTRG.5510	-	Ca3	-1.109	-2.914	---NA---
301	MSTRG.6570	Ca_07309	Ca3	4.154	-3.551	seed maturation protein LEA 4
302	MSTRG.5773	Ca_09449	Ca3	-1.503	-3.691	senescence associated gene 20-like
303	MSTRG.7647	Ca_01365	Ca3	1.241	-5.954	protein LHY isoform X1
304	MSTRG.7646	Ca_01365	Ca3	4.761	-6.589	protein LHY isoform X1
305	MSTRG.5151	-	Ca3	-3.521	-8.282	cell morphogenesis protein PAG1 isoform X2
306	MSTRG.10809	-	Ca4	0.538	3.598	cold regulated protein, putative
307	MSTRG.9691	Ca_20142	Ca4	-1.208	3.083	plant/T32M21-140 protein
308	MSTRG.9893	Ca_23165	Ca4	6.208	2.961	probable inorganic phosphate transporter 1-3
309	MSTRG.8437	Ca_03479	Ca4	5.353	2.509	proline-rich protein 1-like
310	MSTRG.9430	-	Ca4	0.531	2.208	GEM-like protein 4
311	MSTRG.9895	Ca_23163	Ca4	3.447	2.183	transcription factor MYB14-like
312	MSTRG.7782	Ca_07754	Ca4	2.908	2.036	ethylene-responsive transcription factor 1B
313	MSTRG.8705	Ca_04282	Ca4	0.911	2.030	hypothetical protein TSUD_41230
314	MSTRG.8102	Ca_03817	Ca4	1.633	1.998	subtilisin-like protease SBT1.9
315	MSTRG.9460	Ca_18629	Ca4	1.475	1.876	F-box protein At2g39490
316	MSTRG.10123	-	Ca4	0.191	1.867	---NA---
317	MSTRG.10852	-	Ca4	0.803	1.828	---NA---
318	MSTRG.10190	Ca_15136	Ca4	7.692	1.819	translocation protein TolB
319	MSTRG.8870	Ca_04426	Ca4	3.639	1.780	heavy metal-associated isoprenylated plant protein 39
320	MSTRG.9243	Ca_05546	Ca4	1.896	1.767	putative zinc finger protein At1g68190 isoform X1
321	MSTRG.8170	Ca_03750	Ca4	5.634	1.744	neurogenic locus notch-like protein
322	MSTRG.10085	Ca_20019	Ca4	7.332	1.668	peroxidase 5
323	MSTRG.10423	Ca_11017	Ca4	6.386	1.664	putative cadmium-transporting ATPase
324	MSTRG.7678	Ca_07655	Ca4	0.758	1.659	probable membrane-associated kinase regulator 4
325	MSTRG.9968	-	Ca4	0.534	1.637	---NA---
326	MSTRG.7923	Ca_12068	Ca4	6.002	1.615	cellulose synthase-like protein G2
327	MSTRG.10826	Ca_19247	Ca4	7.734	1.609	patatin-like protein 2
328	MSTRG.9852	Ca_20437	Ca4	0.166	1.599	Transcription factor MYB48
329	MSTRG.8742	Ca_04313	Ca4	2.893	1.547	transcription factor UPBEAT1
330	MSTRG.8347	Ca_03574	Ca4	3.498	1.527	putative expansin-A17
331	MSTRG.10330	Ca_13052	Ca4	4.697	1.492	stress-induced receptor-like kinase
332	MSTRG.10342	Ca_14930	Ca4	3.639	1.481	stress-induced receptor-like kinase
333	MSTRG.9199	Ca_05585	Ca4	1.088	1.475	heavy metal-associated isoprenylated plant protein 37
334	MSTRG.10326	-	Ca4	-0.340	1.451	---NA---
335	MSTRG.8178	-	Ca4	-1.033	1.430	ribonuclease H
336	MSTRG.9319	Ca_05464	Ca4	5.418	1.398	MFS transporter
337	MSTRG.9287	Ca_05499	Ca4	2.380	1.392	VQ motif-containing protein 8, chloroplastic-like
338	MSTRG.9481	Ca_18651	Ca4	8.516	1.385	chalcone isomerase
339	MSTRG.10229	-	Ca4	1.693	1.351	Transmembrane protein
340	MSTRG.10853	-	Ca4	4.369	1.334	DNA-directed primase/polymerase protein isoform X1
341	MSTRG.9564	Ca_14028	Ca4	1.016	1.333	transmembrane protein, putative
342	MSTRG.9621	Ca_17144	Ca4	10.024	1.309	phenylalanine ammonia-lyase class 2

343	MSTRG.10341	Ca_14935	Ca4	3.394	1.286	receptor-like protein kinase
344	MSTRG.10543	Ca_23685	Ca4	5.307	1.278	G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300
345	MSTRG.9967	Ca_14223	Ca4	3.858	1.252	transcription factor bHLH130
346	MSTRG.10783	Ca_18351	Ca4	6.958	1.231	probable isoaspartyl peptidase/L-asparaginase 2
347	MSTRG.9988	Ca_15448	Ca4	1.792	1.216	phosphatase 2C-like protein 44
348	MSTRG.9739	-	Ca4	2.492	1.215	RING-H2 finger protein ATL70
349	MSTRG.10324	Ca_13058	Ca4	4.575	1.215	putative wall-associated receptor kinase-like 16
350	MSTRG.8541	Ca_08351	Ca4	3.700	1.191	receptor-like protein kinase
351	MSTRG.10026	-	Ca4	1.242	1.171	transcription factor bHLH92
352	MSTRG.10859	Ca_10841	Ca4	1.307	1.171	lysM domain receptor-like kinase 4
353	MSTRG.9453	Ca_18625	Ca4	2.632	1.165	zinc finger protein ZAT11-like
354	MSTRG.9703	Ca_20135	Ca4	2.497	1.164	heat stress transcription factor A-3
355	MSTRG.9067	Ca_04620	Ca4	8.502	1.154	2-hydroxyisoflavanone dehydratase
356	MSTRG.8504	Ca_08316	Ca4	1.366	1.150	Auxin-binding protein T85
357	MSTRG.10743	-	Ca4	2.388	1.105	U-box domain-containing protein 30
358	MSTRG.9742	Ca_14453	Ca4	5.242	1.099	syntaxin-121-like
359	MSTRG.10346	Ca_14929	Ca4	9.595	1.073	glutamate synthase [NADH], amyloplastic isoform X1
360	MSTRG.10252	Ca_13131	Ca4	8.429	1.069	putative alpha-L-fucosidase
361	MSTRG.9562	-	Ca4	-0.125	1.034	protein NYNRIN-like
362	MSTRG.7695	-	Ca4	-2.415	1.029	protein DETOXIFICATION 16-like
363	MSTRG.10805	Ca_19266	Ca4	3.624	1.028	Feruloyl esterase A
364	MSTRG.8253	Ca_03670	Ca4	4.443	1.025	respiratory burst oxidase homolog protein B
365	MSTRG.10534	Ca_10892	Ca4	6.739	1.023	aspartyl protease AED3-like
366	MSTRG.9750	Ca_14438	Ca4	6.009	1.020	E3 ubiquitin-protein ligase PUB23-like
367	MSTRG.8372	Ca_03546	Ca4	5.990	1.019	peroxidase 5
368	MSTRG.8851	Ca_04406	Ca4	6.131	1.003	hevamine-A
369	MSTRG.9062	Ca_04614	Ca4	4.337	1.002	mental retardation GTPase activating protein homolog 4
370	MSTRG.10758	Ca_18371	Ca4	7.079	-1.001	strigolactone esterase RMS3
371	MSTRG.10468	Ca_10974	Ca4	5.114	-1.014	protein ACTIVITY OF BC1 COMPLEX KINASE 1, chloroplastic isoform X1
372	MSTRG.9676	Ca_19075	Ca4	3.789	-1.033	peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic
373	MSTRG.9642	Ca_17162	Ca4	1.872	-1.061	50S ribosomal protein l18-like
374	MSTRG.10383	Ca_14886	Ca4	2.372	-1.061	metal-nicotianamine transporter YSL3
375	MSTRG.9239	-	Ca4	2.935	-1.064	hypothetical protein PHAVU_007G033400g
376	MSTRG.7848	Ca_07812	Ca4	4.770	-1.073	non-specific lipid-transfer protein-like protein At2g13820
377	MSTRG.8682	Ca_08487	Ca4	5.914	-1.074	GATA transcription factor 8
378	MSTRG.9639	Ca_17161	Ca4	0.086	-1.081	PREDICTED: uncharacterized protein LOC109184126
379	MSTRG.9187	Ca_05596	Ca4	5.186	-1.092	stress enhanced protein 1, chloroplastic
380	MSTRG.10023	Ca_15488	Ca4	5.021	-1.118	serine/threonine receptor-like kinase NFP
381	MSTRG.9730	Ca_14465	Ca4	6.266	-1.135	protein WVD2-like 4
382	MSTRG.7816	Ca_07784	Ca4	5.958	-1.148	probable galacturonosyltransferase 6 isoform X2
383	MSTRG.9274	Ca_05511	Ca4	2.161	-1.151	zinc finger protein GIS3
384	MSTRG.10723	Ca_09205	Ca4	6.542	-1.156	CSC1-like protein RXW8 isoform X1
385	MSTRG.9502	Ca_21618	Ca4	4.855	-1.159	protein EMBRYO SAC DEVELOPMENT ARREST 3, chloroplastic

386	MSTRG.8686	Ca_08491	Ca4	7.852	-1.161	aquaporin PIP2-2
387	MSTRG.10270	Ca_13107	Ca4	4.640	-1.191	SUN domain-containing protein 2-like
388	MSTRG.8957	-	Ca4	-0.281	-1.195	ribonuclease H
389	MSTRG.8063	Ca_03852	Ca4	2.248	-1.223	NDR1/HIN1-like protein 6
390	MSTRG.8743	Ca_04315	Ca4	4.381	-1.225	ABC transporter G family member 25
391	MSTRG.10684	Ca_09166	Ca4	2.931	-1.241	zinc transporter 4, chloroplastic-like
392	MSTRG.10797	Ca_19272	Ca4	3.720	-1.262	WUSCHEL-related homeobox 4
393	MSTRG.10962	Ca_23012	Ca4	2.398	-1.274	putative transcription factor bZIP family
394	MSTRG.9020	-	Ca4	0.853	-1.277	hypothetical protein MTR_1g103410
395	MSTRG.10215	Ca_15105	Ca4	3.523	-1.285	MLP-like protein 328
396	MSTRG.9022	Ca_04574	Ca4	5.540	-1.294	non-specific lipid-transfer protein-like protein At2g13820
397	MSTRG.7839	Ca_07807	Ca4	4.523	-1.306	sulfate transporter 3.1
398	MSTRG.9526	Ca_13992	Ca4	7.289	-1.310	INO80 complex subunit D-like
399	MSTRG.10609	-	Ca4	4.229	-1.335	WAT1-related protein At4g15540-like
400	MSTRG.9726	Ca_14471	Ca4	5.626	-1.366	ABC transporter G family member 22-like isoform X1
401	MSTRG.10774	Ca_18358	Ca4	6.901	-1.380	subtilisin-like protease SBT1.7
402	MSTRG.10672	Ca_09156	Ca4	3.632	-1.389	glutaredoxin-C6
403	MSTRG.8929	Ca_04485	Ca4	1.647	-1.397	3-hexulose-6-phosphate isomerase
404	MSTRG.10629	Ca_09111	Ca4	-0.288	-1.406	protein GLUTAMINE DUMPER 5
405	MSTRG.8368	Ca_03552	Ca4	4.342	-1.409	protein RADIALIS-like 3
406	MSTRG.10627	Ca_09110	Ca4	4.692	-1.446	CONSTANS-like 5 protein
407	MSTRG.7955	Ca_12094	Ca4	4.528	-1.453	P-loop nucleoside triphosphate hydrolase superfamily protein
408	MSTRG.9581	Ca_14048	Ca4	2.828	-1.497	protein REVEILLE 8-like isoform X1
409	MSTRG.10007	Ca_15469	Ca4	4.864	-1.507	RNA polymerase II transcription elongation factor DSIF/SUPT5H/SPT5
410	MSTRG.10710	Ca_09192	Ca4	6.746	-1.531	---NA---
411	MSTRG.8357	Ca_03564	Ca4	2.910	-1.545	transcription factor MYB61
412	MSTRG.9529	Ca_13994	Ca4	2.413	-1.551	inositol transporter 1-like
413	MSTRG.9511	Ca_21607	Ca4	3.053	-1.625	probable plastid-lipid-associated protein 12, chloroplastic isoform X2
414	MSTRG.8997	Ca_04552	Ca4	9.764	-1.627	early light-induced protein, chloroplastic
415	MSTRG.8036	Ca_12171	Ca4	6.714	-1.643	peroxidase 47
416	MSTRG.9128	Ca_05651	Ca4	3.489	-1.645	LIM domain-containing protein WLIM1-like
417	MSTRG.9874	Ca_21318	Ca4	4.386	-1.693	protein PROTON GRADIENT REGULATION 5, chloroplastic
418	MSTRG.7851	Ca_07816	Ca4	2.922	-1.698	heat shock 22 kDa protein, putative
419	MSTRG.8487	Ca_03421	Ca4	3.058	-1.712	Peroxidase 3
420	MSTRG.9719	-	Ca4	-0.351	-1.720	Copia protein
421	MSTRG.8948	Ca_04504	Ca4	-0.427	-1.741	dehydration-responsive element-binding protein 1A-like
422	MSTRG.10952	Ca_10743	Ca4	3.619	-1.748	protein SPA, chloroplastic
423	MSTRG.9021	Ca_04573	Ca4	0.670	-1.782	hypothetical protein MTR_1g103410
424	MSTRG.8246	Ca_03677	Ca4	0.429	-1.872	psbP domain-containing protein 7, chloroplastic
425	MSTRG.7841	Ca_07800	Ca4	3.844	-1.875	heat stress transcription factor A-6b
426	MSTRG.8642	Ca_08447	Ca4	3.304	-1.947	ABC transporter G family member 21
427	MSTRG.10239	Ca_13140	Ca4	-0.911	-1.961	heavy metal-associated isoprenylated plant protein 22-like
428	MSTRG.10313	Ca_13069	Ca4	0.688	-1.993	probable protein phosphatase 2C 51

429	MSTRG.10284	-	Ca4	3.264	-2.014	bidirectional sugar transporter SWEET1
430	MSTRG.7832	Ca_07799	Ca4	2.662	-2.053	protein indeterminate-domain 12
431	MSTRG.10351	Ca_14921	Ca4	4.652	-2.149	photosystem I reaction center subunit psaK, chloroplastic
432	MSTRG.10654	Ca_09139	Ca4	5.302	-2.291	ultraviolet-B-repressible protein
433	MSTRG.8903	Ca_04466	Ca4	2.753	-2.324	PAR1 protein
434	MSTRG.10253	Ca_13125	Ca4	4.032	-2.363	chlorophyllide a oxygenase, chloroplastic
435	MSTRG.7852	Ca_07817	Ca4	-1.092	-2.397	late embryogenesis abundant protein D-34
436	MSTRG.10363	Ca_14909	Ca4	2.426	-2.422	ultraviolet-B receptor UVR8
437	MSTRG.8930	Ca_04486	Ca4	1.244	-2.475	uncharacterized protein LOC101504477
438	MSTRG.8571	Ca_08377	Ca4	1.627	-2.487	---NA---
439	MSTRG.8979	Ca_04534	Ca4	3.500	-2.676	cytochrome P450 704C1-like
440	MSTRG.7773	Ca_07743	Ca4	1.179	-2.729	protein CUP-SHAPED COTYLEDON 3-like
441	MSTRG.10685	Ca_09167	Ca4	0.377	-2.863	putative GATA transcription factor 22
442	MSTRG.9480	-	Ca4	-1.004	-3.033	allantoinase
443	MSTRG.7904	Ca_07872	Ca4	-1.608	-4.046	myb-related protein 305-like
444	MSTRG.8293	Ca_03626	Ca4	1.998	-4.930	nicotianamine synthase
445	MSTRG.10214	Ca_15106	Ca4	-0.120	-4.974	protein C2-DOMAIN ABA-RELATED 7-like
446	MSTRG.8914	Ca_04473	Ca4	2.570	-5.097	low-temperature-induced 65 kDa protein
447	MSTRG.12003	Ca_13416	Ca5	2.270	5.198	protein EARLY FLOWERING 4
448	MSTRG.13274	Ca_07641	Ca5	4.435	4.306	zinc finger protein CONSTANS-LIKE 9
449	MSTRG.11768	Ca_15586	Ca5	3.520	3.063	maternal effect embryo arrest protein, putative
450	MSTRG.11250	Ca_20342	Ca5	3.339	3.049	eugenol synthase 1
451	MSTRG.13753	Ca_04059	Ca5	2.294	2.731	protein DOWNY MILDEW RESISTANCE 6
452	MSTRG.12039	Ca_13380	Ca5	4.454	2.647	abscisic acid receptor PYL4
453	MSTRG.12011	Ca_13408	Ca5	1.886	2.418	probable 2-oxoglutarate-dependent dioxygenase At5g05600
454	MSTRG.11534	-	Ca5	-1.043	2.387	retrovirus-related Pol polyprotein from transposon TNT 1-94
455	MSTRG.12893	Ca_01531	Ca5	7.299	2.090	patatin-like protein 2
456	MSTRG.12869	Ca_01556	Ca5	1.274	1.927	ethylene-responsive transcription factor RAP2-1-like
457	MSTRG.13266	Ca_07635	Ca5	5.830	1.904	subtilisin-like protease SBT5.3
458	MSTRG.11788	Ca_15607	Ca5	3.997	1.829	phosphomethylpyrimidine synthase, chloroplastic isoform X2
459	MSTRG.11993	Ca_13426	Ca5	4.059	1.790	cytochrome P450 90A1
460	MSTRG.13337	Ca_19207	Ca5	4.651	1.759	NAD(P)H-dependent 6'-deoxychalcone synthase-like
461	MSTRG.11988	Ca_13431	Ca5	5.163	1.754	cysteine-rich receptor-like protein kinase 2
462	MSTRG.13302	Ca_11408	Ca5	5.880	1.749	chalcone synthase 4-like
463	MSTRG.13323	Ca_19222	Ca5	6.602	1.734	NAD(P)H-dependent 6'-deoxychalcone synthase-like
464	MSTRG.11545	Ca_24761	Ca5	4.772	1.733	F-box protein PP2-A13
465	MSTRG.11776	-	Ca5	0.413	1.707	putative P-loop containing nucleoside triphosphate hydrolase, leucine-rich repeat domain, L
466	MSTRG.11399	Ca_17091	Ca5	3.467	1.691	cysteine-rich receptor-like protein kinase 10
467	MSTRG.13565	Ca_03876	Ca5	6.166	1.684	amino acid permease 3
468	MSTRG.13852	Ca_04158	Ca5	2.293	1.682	WAT1-related protein At5g64700-like
469	MSTRG.12660	Ca_01767	Ca5	0.022	1.668	protein SPA, chloroplastic
470	MSTRG.12250	Ca_04771	Ca5	5.419	1.643	3,7-dimethylxanthine N-methyltransferase-like
471	MSTRG.13182	Ca_07542	Ca5	2.522	1.538	alcohol dehydrogenase-like 7

472	MSTRG.11293	Ca_20495	Ca5	5.522	1.480	probable glucan 1,3-beta-glucosidase A
473	MSTRG.12516	-	Ca5	3.382	1.453	lachrymatory-factor synthase
474	MSTRG.13645	Ca_03952	Ca5	0.912	1.422	probable WRKY transcription factor 53
475	MSTRG.12020	Ca_13401	Ca5	1.342	1.411	RING-H2 finger protein ATL66-like
476	MSTRG.11283	Ca_23782	Ca5	3.247	1.408	pectinesterase/pectinesterase inhibitor
477	MSTRG.12594	Ca_01845	Ca5	4.732	1.406	probable sarcosine oxidase
478	MSTRG.12073	Ca_13345	Ca5	6.252	1.395	WAT1-related protein At4g08300
479	MSTRG.13504	Ca_12688	Ca5	2.986	1.377	inactive TPR repeat-containing thioredoxin TTL3
480	MSTRG.12872	Ca_01553	Ca5	4.502	1.368	HXXXD-type acyl-transferase family protein
481	MSTRG.12802	Ca_01620	Ca5	4.522	1.309	early flowering 3/high response
482	MSTRG.13385	Ca_11360	Ca5	1.577	1.291	uncharacterized protein LOC101503749 isoform X2
483	MSTRG.11118	Ca_24950	Ca5	2.407	1.272	protein LONGIFOLIA 1
484	MSTRG.11821	Ca_09044	Ca5	1.837	1.258	putative serine/threonine-protein kinase-like protein CCR3
485	MSTRG.11852	-	Ca5	3.265	1.254	amino acid transporter AVT1I
486	MSTRG.11344	Ca_23749	Ca5	1.236	1.247	F-box/kelch-repeat protein At3g23880-like
487	MSTRG.11092	Ca_18684	Ca5	5.492	1.246	ABC transporter A family member 7
488	MSTRG.12113	Ca_16640	Ca5	7.172	1.241	sugar transport protein 5
489	MSTRG.13462	Ca_12733	Ca5	5.949	1.231	protein-tyrosine-phosphatase MKP1-like isoform X1
490	MSTRG.11655	Ca_21153	Ca5	3.510	1.229	DUF4228 domain protein
491	MSTRG.11812	Ca_15625	Ca5	3.364	1.219	3-oxo-Delta(4,5)-steroid 5-beta-reductase
492	MSTRG.13549	Ca_03870	Ca5	2.870	1.158	nuclear receptor subfamily 4 group A member 3-like
493	MSTRG.12082	Ca_23834	Ca5	3.862	1.115	fluoride export protein 2-like
494	MSTRG.12861	Ca_01564	Ca5	3.716	1.111	putative receptor protein kinase ZmPK1
495	MSTRG.11948	Ca_08906	Ca5	4.778	1.091	probable LRR receptor-like serine/threonine-protein kinase At1g06840
496	MSTRG.12974	-	Ca5	4.313	1.068	isoamylase 3, chloroplastic isoform X1
497	MSTRG.13538	Ca_12650	Ca5	9.440	1.039	protein disulfide-isomerase
498	MSTRG.13600	Ca_03902	Ca5	2.025	1.026	1-aminocyclopropane-1-carboxylate synthase 7
499	MSTRG.13869	Ca_04171	Ca5	4.895	1.011	U-box domain-containing protein 27
500	MSTRG.13707	Ca_04016	Ca5	4.161	1.009	AAA-ATPase At2g46620-like
501	MSTRG.12686	Ca_01733	Ca5	4.574	1.008	homeobox protein knotted-1-like 3 isoform X2
502	MSTRG.13719	Ca_04027	Ca5	3.376	-1.011	homeobox-leucine zipper protein ATHB-12-like
503	MSTRG.11748	Ca_17658	Ca5	2.986	-1.013	probable amino acid permease 7
504	MSTRG.12059	Ca_13361	Ca5	4.512	-1.041	BTB/POZ domain-containing protein At3g56230
505	MSTRG.12289	Ca_04806	Ca5	4.328	-1.042	protein MULTIPLE CHLOROPLAST DIVISION SITE 1
506	MSTRG.11460	Ca_26864	Ca5	2.901	-1.056	thylakoid lumenal 19 kDa protein, chloroplastic
507	MSTRG.11587	Ca_22812	Ca5	0.136	-1.058	hypothetical protein MtrunA17_Chr3g0096231
508	MSTRG.12361	Ca_04866	Ca5	2.365	-1.059	RNA pseudouridine synthase 2, chloroplastic
509	MSTRG.12720	Ca_01700	Ca5	5.149	-1.074	protein TIC 55, chloroplastic
510	MSTRG.12865	Ca_01561	Ca5	3.544	-1.094	cyclin-D3-1-like
511	MSTRG.12801	Ca_01619	Ca5	5.314	-1.098	zinc finger CCCH domain-containing protein 20-like
512	MSTRG.12238	Ca_04759	Ca5	9.521	-1.099	dehydrin ERD14-like
513	MSTRG.12451	Ca_04962	Ca5	3.321	-1.109	Putative GMP synthase [glutamine-hydrolyzing]
514	MSTRG.13162	Ca_07522	Ca5	7.651	-1.119	betaine aldehyde dehydrogenase 1, chloroplastic

515	MSTRG.12976	Ca_01445	Ca5	4.133	-1.127	alcohol dehydrogenase-like 2
516	MSTRG.13146	Ca_07509	Ca5	3.121	-1.175	NHL domain protein
517	MSTRG.12095	Ca_16620	Ca5	1.045	-1.175	sulfate transporter 1.3
518	MSTRG.11186	Ca_21574	Ca5	3.448	-1.180	uncharacterized oxidoreductase At1g06690, chloroplastic
519	MSTRG.12304	Ca_04823	Ca5	2.525	-1.211	WUSCHEL-related homeobox 8
520	MSTRG.12761	Ca_01661	Ca5	5.156	-1.221	ultraviolet-B-repressible protein
521	MSTRG.13365	Ca_11381	Ca5	6.513	-1.227	xyloglucan endotransglucosylase/hydrolase 2
522	MSTRG.13101	Ca_07459	Ca5	4.810	-1.235	copper amine oxidase, enzyme domain protein
523	MSTRG.11936	Ca_08918	Ca5	5.590	-1.243	DEAD-box ATP-dependent RNA helicase 20-like isoform X1
524	MSTRG.13614	Ca_03916	Ca5	6.504	-1.285	F-box protein SKP2A-like
525	MSTRG.12610	Ca_01829	Ca5	5.962	-1.314	cryptochrome DASH, chloroplastic/mitochondrial
526	MSTRG.12808	Ca_01613	Ca5	6.513	-1.350	Squalene monooxygenase
527	MSTRG.12273	Ca_04789	Ca5	6.738	-1.360	BURP domain-containing protein BNM2A-like
528	MSTRG.13892	Ca_04193	Ca5	4.159	-1.396	NAD(P)H-quinone oxidoreductase subunit O, chloroplastic
529	MSTRG.11584	-	Ca5	3.122	-1.408	cytochrome b561 domain-containing protein At2g30890-like
530	MSTRG.12269	Ca_04787	Ca5	3.744	-1.410	proline-rich receptor-like protein kinase PERK7
531	MSTRG.11976	Ca_08881	Ca5	2.922	-1.449	WAT1-related protein At3g02690, chloroplastic
532	MSTRG.11414	Ca_17073	Ca5	4.605	-1.468	protein MAINTENANCE OF PSII UNDER HIGH LIGHT 1
533	MSTRG.13147	Ca_07510	Ca5	1.987	-1.470	probable inactive receptor kinase At2g26730
534	MSTRG.11130	Ca_25894	Ca5	4.579	-1.506	protein CHROMATIN REMODELING 5
535	MSTRG.13153	Ca_07514	Ca5	0.304	-1.628	LIM domain-containing protein WLIM1-like
536	MSTRG.11455	Ca_21651	Ca5	5.627	-1.674	plant/F13G24-250 protein
537	MSTRG.12132	Ca_16662	Ca5	1.951	-1.728	calcium-binding protein CML38
538	MSTRG.11949	Ca_08904	Ca5	1.749	-1.746	60S ribosomal protein L10
539	MSTRG.12454	-	Ca5	1.773	-1.805	hypothetical protein MTR_3g111650
540	MSTRG.12367	Ca_04873	Ca5	6.022	-1.833	CO(2)-response secreted protease
541	MSTRG.13018	Ca_01402	Ca5	4.003	-1.887	transcription factor bHLH137
542	MSTRG.12999	Ca_01423	Ca5	5.465	-1.914	HVA22-like protein e
543	MSTRG.11714	-	Ca5	3.430	-1.928	BURP domain-containing protein BNM2A-like
544	MSTRG.11793	Ca_15611	Ca5	2.634	-1.934	sodium-dependent phosphate transport protein 1, chloroplastic
545	MSTRG.12450	Ca_04961	Ca5	1.079	-1.955	J domain-containing protein required for chloroplast accumulation response 1 isoform X1
546	MSTRG.12428	Ca_04936	Ca5	2.348	-1.965	mannan endo-1,4-beta-mannosidase 7-like
547	MSTRG.12140	Ca_16669	Ca5	1.462	-1.994	uncharacterized protein LOC101501288
548	MSTRG.13468	Ca_12727	Ca5	-0.625	-2.085	probable E3 ubiquitin-protein ligase XERICO
549	MSTRG.11127	Ca_25893	Ca5	8.324	-2.134	serine--glyoxylate aminotransferase
550	MSTRG.12274	-	Ca5	2.098	-2.166	organ-specific protein P4
551	MSTRG.11562	-	Ca5	0.100	-2.167	F-box protein interaction domain protein
552	MSTRG.13447	Ca_11301	Ca5	5.430	-2.179	photosystem II core complex proteins psbY, chloroplastic
553	MSTRG.11563	-	Ca5	0.301	-2.189	cysteine-rich receptor-like protein kinase
554	MSTRG.12016	-	Ca5	1.046	-2.302	Retrovirus-related Pol polyprotein from transposon TNT 1-94
555	MSTRG.12885	-	Ca5	0.929	-2.321	BRI1 kinase inhibitor 1
556	MSTRG.12022	-	Ca5	0.639	-2.330	LOB domain-containing protein 21
557	MSTRG.11318	Ca_20522	Ca5	5.289	-2.343	photosystem I reaction center subunit V, chloroplastic

558	MSTRG.12271	Ca_04788	Ca5	5.779	-2.353	specific tissue protein
559	MSTRG.12270	-	Ca5	1.809	-2.462	---NA---
560	MSTRG.11866	Ca_08997	Ca5	6.650	-2.581	cinnamoyl-CoA reductase 1-like
561	MSTRG.12272	Ca_04788	Ca5	9.065	-2.612	specific tissue protein
562	MSTRG.12874	Ca_01550	Ca5	-1.406	-2.640	transcription factor HEC2-like
563	MSTRG.12827	Ca_01600	Ca5	1.350	-2.935	uncharacterized protein LOC101498288 isoform X2
564	MSTRG.11844	Ca_09022	Ca5	-0.402	-3.069	probable N-acetyltransferase HLS1-like
565	MSTRG.13809	Ca_04111	Ca5	1.164	-4.325	putative GATA-type transcription activator
566	MSTRG.13381	-	Ca5	1.357	-4.530	transmembrane protein, putative
567	MSTRG.17263	Ca_16282	Ca6	3.934	2.744	sterile nodes
568	MSTRG.17228	Ca_18903	Ca6	2.267	2.675	lysine-specific demethylase JMJ30
569	MSTRG.14544	Ca_05720	Ca6	5.844	2.597	thaumatin-like pathogenesis-related protein 4-like precursor
570	MSTRG.16323	Ca_17483	Ca6	1.900	2.557	alpha carbonic anhydrase 7-like
571	MSTRG.16552	-	Ca6	0.021	2.505	PP890_SOYBNRecName: Full=Protein PROPEP890; Short=GmPROPEP890; Contains: RecName: Full=Peptide GmPep890; Flags: Precursor
572	MSTRG.14557	-	Ca6	-0.181	2.480	auxin-responsive protein SAUR32-like
573	MSTRG.16966	Ca_23440	Ca6	-0.218	2.461	UPF0481 protein At3g47200-like
574	MSTRG.15447	Ca_22015	Ca6	2.959	2.383	G-type lectin S-receptor-like serine/threonine-protein kinase B120
575	MSTRG.15215	Ca_05112	Ca6	1.454	2.364	isoflavone 2'-hydroxylase
576	MSTRG.15516	-	Ca6	-0.586	2.355	heat stress transcription factor B-2a
577	MSTRG.15573	Ca_06357	Ca6	3.251	2.252	isoflavone synthase
578	MSTRG.16181	Ca_16684	Ca6	5.661	2.183	receptor-like cytoplasmic kinase 176 isoform X1
579	MSTRG.15277	Ca_05166	Ca6	4.315	2.130	LRR receptor-like serine/threonine-protein kinase FLS2
580	MSTRG.15611	-	Ca6	-0.016	2.104	Transposon Tf2-6 polyprotein
581	MSTRG.17239	Ca_18916	Ca6	3.960	1.986	cyanogenic beta-glucosidase
582	MSTRG.15704	Ca_06488	Ca6	5.353	1.919	plastid movement impaired protein
583	MSTRG.15341	Ca_05233	Ca6	5.680	1.888	beta-xylosidase/alpha-L-arabinofuranosidase 2
584	MSTRG.15669	Ca_06456	Ca6	1.692	1.852	uncharacterized protein LOC101503228 isoform X1
585	MSTRG.15565	Ca_06354	Ca6	1.517	1.833	putative methyltransferase
586	MSTRG.15695	Ca_06482	Ca6	2.895	1.819	scopoletin glucosyltransferase
587	MSTRG.14193	Ca_10384	Ca6	3.075	1.810	uncharacterized protein LOC101509529
588	MSTRG.15572	Ca_06357	Ca6	5.801	1.781	isoflavone synthase
589	MSTRG.16955	-	Ca6	-0.135	1.747	ALC-interacting protein
590	MSTRG.15216	Ca_05112	Ca6	3.532	1.741	isoflavone 2'-hydroxylase
591	MSTRG.15213	Ca_05110	Ca6	9.202	1.728	isoflavone 2'-hydroxylase
592	MSTRG.17465	Ca_13651	Ca6	8.821	1.604	non-symbiotic hemoglobin 1
593	MSTRG.14747	Ca_09598	Ca6	4.458	1.601	uncharacterized protein LOC11437166
594	MSTRG.15571	Ca_06357	Ca6	11.418	1.600	isoflavone synthase
595	MSTRG.15962	Ca_11225	Ca6	7.578	1.566	geraniol 8-hydroxylase-like
596	MSTRG.15567	Ca_06355	Ca6	6.460	1.563	putative methyltransferase
597	MSTRG.16478	Ca_15198	Ca6	2.383	1.542	E3 ubiquitin-protein ligase PUB23-like
598	MSTRG.15098	Ca_23427	Ca6	2.939	1.533	---NA---
599	MSTRG.15568	Ca_06356	Ca6	10.045	1.506	isoflavone 4'-O-methyltransferase
600	MSTRG.15590	Ca_06380	Ca6	5.240	1.463	phospholipase A1-IIgamma

601	MSTRG.16840	Ca_24238	Ca6	5.467	1.450	disease resistance protein RPS6 isoform X1
602	MSTRG.16555	Ca_22055	Ca6	3.133	1.440	MDIS1-interacting receptor like kinase 2-like
603	MSTRG.17233	Ca_18911	Ca6	6.437	1.431	glycoside hydrolase family 1 protein
604	MSTRG.17278	Ca_21197	Ca6	7.164	1.404	probable glutathione S-transferase
605	MSTRG.15620	Ca_06411	Ca6	5.842	1.402	CCG-binding protein 1
606	MSTRG.17319	-	Ca6	0.082	1.376	transmembrane protein, putative
607	MSTRG.15403	Ca_05303	Ca6	2.285	1.346	L-type lectin-domain containing receptor kinase IX.1-like
608	MSTRG.15029	Ca_08529	Ca6	4.060	1.339	subtilisin-like protease SBT3.9 isoform X1
609	MSTRG.15423	Ca_05325	Ca6	3.556	1.339	putative branched-chain-amino-acid aminotransferase 7
610	MSTRG.17240	Ca_18917	Ca6	12.049	1.296	non-cyanogenic beta-glucosidase-like
611	MSTRG.16985	Ca_20707	Ca6	6.715	1.295	abscisic acid receptor PYL4-like
612	MSTRG.16596	Ca_15792	Ca6	3.444	1.288	protein BEARSKIN2-like
613	MSTRG.15093	Ca_23425	Ca6	2.506	1.282	metalloendoproteinase 2-MMP
614	MSTRG.16558	Ca_22054	Ca6	4.852	1.278	RALF-like protein
615	MSTRG.14593	Ca_05666	Ca6	2.844	1.245	transaldolase family protein
616	MSTRG.16807	Ca_23255	Ca6	4.498	1.241	putative E3 ubiquitin-protein ligase XBAT31
617	MSTRG.17520	Ca_15386	Ca6	1.624	1.216	DUF241 domain protein
618	MSTRG.14985	Ca_08570	Ca6	6.678	1.215	probable acyl-activating enzyme 18, peroxisomal isoform X1
619	MSTRG.15993	Ca_11190	Ca6	6.261	1.203	cinnamoyl-CoA reductase 1-like
620	MSTRG.17192	Ca_22917	Ca6	4.526	1.196	probable WRKY transcription factor 40 isoform X1
621	MSTRG.16219	Ca_16727	Ca6	4.266	1.186	exocyst complex component EXO70H1
622	MSTRG.17509	-	Ca6	6.185	1.185	isoflavone reductase homolog PCBER
623	MSTRG.15799	Ca_06582	Ca6	5.823	1.182	UDP-glycosyltransferase 13-like
624	MSTRG.16769	Ca_23155	Ca6	1.945	1.150	plant/F9H3-4 protein
625	MSTRG.15454	Ca_22023	Ca6	7.041	1.143	sugar carrier protein C-like
626	MSTRG.16856	Ca_13825	Ca6	3.239	1.139	PAR1 protein
627	MSTRG.17068	Ca_13466	Ca6	6.950	1.133	probable 2-oxoglutarate-dependent dioxygenase AOP1
628	MSTRG.16516	Ca_22222	Ca6	5.797	1.132	embryo-specific protein ATS3B
629	MSTRG.14793	Ca_09555	Ca6	5.409	1.105	putative calcium-transporting ATPase 11, plasma membrane-type
630	MSTRG.16793	Ca_23239	Ca6	3.162	1.105	putative vesicle-associated membrane protein 726
631	MSTRG.15989	Ca_11196	Ca6	6.762	1.095	isoflavone 2'-hydroxylase-like
632	MSTRG.14485	Ca_05782	Ca6	3.471	1.095	probable WRKY transcription factor 29
633	MSTRG.17235	Ca_18916	Ca6	2.479	1.077	cyanogenic beta-glucosidase
634	MSTRG.16869	Ca_13839	Ca6	3.440	1.072	disease resistance protein RPM1-like
635	MSTRG.15593	Ca_06384	Ca6	3.699	1.071	protein trichome birefringence-like 38
636	MSTRG.14852	Ca_16751	Ca6	3.371	1.070	cationic amino acid transporter 1
637	MSTRG.16120	Ca_11041	Ca6	1.630	1.068	disease resistance protein RPP13-like
638	MSTRG.14785	Ca_09562	Ca6	2.204	1.068	calmodulin-binding transcription activator
639	MSTRG.16703	Ca_15910	Ca6	2.428	1.048	putative cysteine-rich receptor-like protein kinase 35
640	MSTRG.16893	Ca_13864	Ca6	3.265	1.040	cytochrome P450 71D9-like
641	MSTRG.14075	Ca_13335	Ca6	6.426	1.025	wall-associated receptor kinase-like 20
642	MSTRG.17524	Ca_15390	Ca6	1.860	1.018	DUF241 domain protein
643	MSTRG.16854	Ca_13824	Ca6	6.315	1.017	putative PAR1 protein precursor

644	MSTRG.17580	Ca_18870	Ca6	7.461	1.015	D-3-phosphoglycerate dehydrogenase 2, chloroplastic
645	MSTRG.14220	Ca_10410	Ca6	5.516	1.014	adagio protein 3
646	MSTRG.16280	Ca_14576	Ca6	8.081	1.014	root cap/late embryogenesis-like protein
647	MSTRG.16871	Ca_13840	Ca6	4.907	1.012	disease resistance protein RPM1
648	MSTRG.16174	Ca_16682	Ca6	4.622	-1.003	expansin-A6 isoform X1
649	MSTRG.16231	Ca_14624	Ca6	4.485	-1.007	BTB/POZ domain-containing protein At5g60050
650	MSTRG.16156	Ca_26069	Ca6	3.983	-1.010	CTL-like protein DDB_G0274487
651	MSTRG.14008	Ca_13269	Ca6	2.761	-1.026	uncharacterized oxidoreductase At4g09670-like
652	MSTRG.15925	Ca_11261	Ca6	4.449	-1.026	ethylene-responsive transcription factor 9
653	MSTRG.16441	Ca_16497	Ca6	1.177	-1.036	late embryogenesis abundant hydroxyproline-rich glycoprotein
654	MSTRG.14547	Ca_05718	Ca6	2.478	-1.044	core-2/I-branching enzyme
655	MSTRG.14858	Ca_16748	Ca6	1.659	-1.070	lysine-specific demethylase JMJ18 isoform X2
656	MSTRG.15492	Ca_06285	Ca6	3.946	-1.076	transmembrane protein, putative
657	MSTRG.15031	Ca_08525	Ca6	7.408	-1.080	xyloglucan endotransglucosylase/hydrolase 2
658	MSTRG.14644	Ca_16944	Ca6	3.762	-1.082	aldehyde dehydrogenase family 3 member H1 isoform X1
659	MSTRG.17451	Ca_13659	Ca6	7.402	-1.096	allene oxide synthase 3-like
660	MSTRG.17492	Ca_13630	Ca6	7.719	-1.098	BURP domain-containing protein BNM2A-like
661	MSTRG.14253	Ca_10442	Ca6	4.120	-1.101	21 kDa protein-like
662	MSTRG.16101	Ca_11062	Ca6	3.998	-1.102	DUF3067 family protein
663	MSTRG.17452	Ca_13657	Ca6	7.643	-1.104	Cold-regulated 413 plasma membrane protein 2
664	MSTRG.17418	-	Ca6	1.485	-1.138	transmembrane protein, putative
665	MSTRG.14815	Ca_09537	Ca6	2.755	-1.156	putative magnesium-importing ATPase
666	MSTRG.15228	Ca_05124	Ca6	-0.161	-1.159	RING-H2 finger protein ATL74-like
667	MSTRG.17292	Ca_21219	Ca6	1.721	-1.161	BEL1-like homeodomain protein 9
668	MSTRG.15386	Ca_05279	Ca6	4.808	-1.180	protein PELPK1
669	MSTRG.14699	Ca_09646	Ca6	2.431	-1.181	probable plastid-lipid-associated protein 7, chloroplastic isoform X1
670	MSTRG.15810	Ca_16368	Ca6	0.849	-1.192	---NA---
671	MSTRG.14242	Ca_10434	Ca6	0.749	-1.198	dynein light chain LC6, flagellar outer arm-like
672	MSTRG.15097	-	Ca6	0.511	-1.201	LINE-1 reverse transcriptase isogeny
673	MSTRG.16038	Ca_11120	Ca6	5.359	-1.214	calcium-binding EF-hand protein
674	MSTRG.16803	Ca_23252	Ca6	3.349	-1.238	BTB/POZ domain-containing protein At5g48800
675	MSTRG.15417	Ca_05322	Ca6	7.360	-1.256	Squalene monooxygenase
676	MSTRG.15892	Ca_19862	Ca6	4.503	-1.267	putative erythromycin 3"-O-methyltransferase
677	MSTRG.14063	Ca_13322	Ca6	3.721	-1.273	probable transcriptional regulator RABBIT EARS
678	MSTRG.15849	Ca_16332	Ca6	1.176	-1.283	E3 ubiquitin-protein ligase DZIP3-like isoform X1
679	MSTRG.16568	Ca_15817	Ca6	4.165	-1.299	putative glycerol-3-phosphate transporter 1
680	MSTRG.16186	Ca_16693	Ca6	3.396	-1.299	heat shock cognate 70 kDa protein 2
681	MSTRG.14145	Ca_10329	Ca6	5.865	-1.304	UV-B-induced protein At3g17800, chloroplastic
682	MSTRG.14592	Ca_05667	Ca6	3.245	-1.307	transferring glycosyl group transferase
683	MSTRG.14365	Ca_05895	Ca6	0.888	-1.317	1-aminocyclopropane-1-carboxylate synthase 7
684	MSTRG.14660	Ca_09683	Ca6	2.759	-1.325	NAC domain-containing protein 104-like
685	MSTRG.15412	Ca_05316	Ca6	5.409	-1.326	K(+) efflux antiporter 3, chloroplastic isoform X1
686	MSTRG.17608	-	Ca6	-0.287	-1.348	auxin-induced protein 6B

687	MSTRG.16819	-	Ca6	3.175	-1.372	CASP-like protein 1C1
688	MSTRG.14270	-	Ca6	0.027	-1.414	arabinogalactan peptide 16-like
689	MSTRG.14977	Ca_08576	Ca6	4.354	-1.428	protochlorophyllide-dependent translocon component 52, chloroplastic
690	MSTRG.17123	Ca_19173	Ca6	2.659	-1.443	Haloalkane dehalogenase 2
691	MSTRG.14404	Ca_05860	Ca6	3.095	-1.521	short-chain dehydrogenase TIC 32, chloroplastic
692	MSTRG.16459	Ca_15174	Ca6	-0.669	-1.530	Gb:AAF02129.1, putative
693	MSTRG.15370	Ca_05262	Ca6	6.021	-1.539	protein EXORDIUM-like 2
694	MSTRG.14246	Ca_10433	Ca6	3.197	-1.553	F-box protein SKIP28
695	MSTRG.14151	Ca_10337	Ca6	2.954	-1.563	ABC transporter-like protein
696	MSTRG.14418	Ca_05844	Ca6	3.127	-1.576	glutaredoxin domain-containing cysteine-rich protein CG12206
697	MSTRG.14700	Ca_09644	Ca6	0.628	-1.578	WAT1-related protein At5g64700
698	MSTRG.17564	Ca_15425	Ca6	6.726	-1.600	fructose-bisphosphate aldolase 1, chloroplastic
699	MSTRG.16133	Ca_11028	Ca6	0.161	-1.606	protein EARLY-RESPONSIVE TO DEHYDRATION 7, chloroplastic-like
700	MSTRG.14891	Ca_08671	Ca6	3.679	-1.646	protein MET1, chloroplastic
701	MSTRG.14250	Ca_10440	Ca6	4.787	-1.663	Putative pectinesterase/pectinesterase inhibitor 6
702	MSTRG.14742	Ca_09604	Ca6	5.474	-1.691	protein ACTIVITY OF BC1 COMPLEX KINASE 8, chloroplastic
703	MSTRG.16458	Ca_15171	Ca6	-3.339	-1.694	secoisolariciresinol dehydrogenase-like
704	MSTRG.17379	Ca_17430	Ca6	6.274	-1.748	proline-rich protein 4
705	MSTRG.16621	Ca_26435	Ca6	2.030	-1.844	NAD(P)H-quinone oxidoreductase subunit T, chloroplastic
706	MSTRG.14761	Ca_09586	Ca6	0.904	-1.872	inositol-3-phosphate synthase
707	MSTRG.14289	Ca_05967	Ca6	4.008	-1.933	pentatricopeptide repeat-containing protein At5g21222-like
708	MSTRG.14636	Ca_16936	Ca6	3.479	-1.946	polyketide cyclase/dehydrase and lipid transporter
709	MSTRG.17420	Ca_13690	Ca6	6.267	-1.963	B-box zinc finger protein 24
710	MSTRG.16502	Ca_15222	Ca6	4.060	-1.998	cellulose synthase-like protein H1 isoform X1
711	MSTRG.16400	Ca_16452	Ca6	3.064	-2.006	probable 2-carboxy-D-arabinitol-1-phosphatase
712	MSTRG.16397	Ca_16454	Ca6	-1.388	-2.014	spermidine coumaroyl-CoA acyltransferase-like
713	MSTRG.14372	Ca_05889	Ca6	0.776	-2.062	transcription factor MYBS3
714	MSTRG.15932	Ca_11257	Ca6	1.839	-2.148	uncharacterized protein LOC101503424
715	MSTRG.17286	Ca_21212	Ca6	3.963	-2.247	protein NRT1/ PTR FAMILY 5.6-like
716	MSTRG.16533	Ca_24447	Ca6	2.601	-2.368	aquaporin SIP1-2
717	MSTRG.14873	Ca_16734	Ca6	0.657	-2.481	ferredoxin-like
718	MSTRG.17153	Ca_17524	Ca6	1.397	-2.510	B-box zinc finger protein 32
719	MSTRG.14330	Ca_05930	Ca6	1.372	-2.645	probable protein phosphatase 2C 6
720	MSTRG.15852	Ca_16327	Ca6	2.214	-2.741	chaperone protein dnaJ C76, chloroplastic isoform X1
721	MSTRG.14866	Ca_16738	Ca6	6.726	-2.748	Glutelin type-A 2
722	MSTRG.14071	Ca_13329	Ca6	2.757	-2.775	protein phosphatase 2C 37
723	MSTRG.16597	Ca_15786	Ca6	-0.552	-3.105	ethylene-responsive transcription factor ERF039-like
724	MSTRG.15920	Ca_11268	Ca6	2.419	-3.202	transcription activator GLK1-like isoform X1
725	MSTRG.16911	Ca_17751	Ca6	-1.442	-3.431	UPF0098 protein MTH-273
726	MSTRG.15353	Ca_05243	Ca6	4.728	-3.564	protein LNK1
727	MSTRG.16616	Ca_15766	Ca6	-0.363	-4.079	acyl-CoA N-acyltransferase (NAT) superfamily protein
728	MSTRG.14076	Ca_13334	Ca6	5.354	-5.350	ultraviolet-B receptor UVR8-like isoform X1
729	MSTRG.17085	Ca_13451	Ca6	-0.272	-7.301	late embryogenesis abundant protein 2

730	MSTRG.17086	Ca_13450	Ca6	-1.496	-9.355	late embryogenesis abundant protein 2-like
731	MSTRG.16749	-	Ca6	-5.005	-9.832	ABC transporter A family member 7-like protein
732	MSTRG.20225	Ca_16414	Ca7	2.600	3.714	UDP-glycosyltransferase 1
733	MSTRG.19862	Ca_10044	Ca7	7.109	2.762	ankyrin repeat protein
734	MSTRG.18758	Ca_12821	Ca7	-0.060	2.425	expansin-like B1
735	MSTRG.20005	-	Ca7	-0.515	2.334	B3 domain-containing transcription factor NGA1-like isoform X1
736	MSTRG.17870	Ca_03224	Ca7	3.695	2.305	DUF4228 domain protein
737	MSTRG.20252	-	Ca7	1.672	2.260	cytochrome P450 704C1-like
738	MSTRG.19903	Ca_10011	Ca7	3.835	2.170	germin-like protein subfamily 3 member 1
739	MSTRG.19236	Ca_15845	Ca7	6.483	2.138	CTP synthase-like
740	MSTRG.19109	-	Ca7	1.356	2.129	dirigent protein 19-like
741	MSTRG.19511	Ca_19906	Ca7	1.589	1.635	disease resistance protein (CC-NBS-LRR class) family protein
742	MSTRG.18540	Ca_13165	Ca7	6.093	1.617	two-component response regulator-like APRR1
743	MSTRG.17978	Ca_03124	Ca7	2.267	1.502	pectinesterase inhibitor 3
744	MSTRG.20200	Ca_16386	Ca7	3.244	1.476	homeobox-leucine zipper protein ANTHOCYANINLESS 2-like isoform X1
745	MSTRG.18452	Ca_06594	Ca7	1.885	1.460	putative phospholipid-transporting ATPase 9
746	MSTRG.19738	Ca_11697	Ca7	3.460	1.441	beta-amyrin 11-oxidase-like
747	MSTRG.19888	Ca_10020	Ca7	6.147	1.422	disease resistance protein RML1A
748	MSTRG.19480	Ca_19509	Ca7	3.840	1.373	kinase RLK-Pelle-LRR-XII-1 family
749	MSTRG.19984	Ca_16197	Ca7	4.291	1.366	glutamate receptor 2.7
750	MSTRG.19125	Ca_09882	Ca7	1.971	1.331	RING-H2 finger protein ATL8-like
751	MSTRG.17983	Ca_03121	Ca7	2.208	1.321	Indole-3-acetic acid-induced protein ARG7
752	MSTRG.19185	Ca_20578	Ca7	7.296	1.320	isoflavone reductase homolog
753	MSTRG.20044	Ca_17627	Ca7	4.377	1.300	myb-related protein 308-like
754	MSTRG.18229	Ca_06784	Ca7	3.872	1.299	binding protein
755	MSTRG.19022	Ca_23046	Ca7	3.279	1.264	3-epi-6-deoxocathasterone 23-monooxygenase
756	MSTRG.18210	-	Ca7	3.954	1.255	ribonuclease H
757	MSTRG.19194	Ca_15884	Ca7	2.922	1.250	high affinity nitrate transporter 2.5
758	MSTRG.19481	-	Ca7	4.913	1.238	TMV resistance protein N-like
759	MSTRG.19845	Ca_10065	Ca7	3.327	1.201	disease resistance-like protein DSC1
760	MSTRG.20014	-	Ca7	3.360	1.183	putative ATP-synthase-associated protein
761	MSTRG.19155	-	Ca7	0.814	1.125	transmembrane protein, putative
762	MSTRG.18612	Ca_15299	Ca7	2.907	1.101	UVI1, putative
763	MSTRG.18211	Ca_06803	Ca7	7.956	1.073	protein DMP2-like
764	MSTRG.18038	Ca_03068	Ca7	8.739	1.068	S-adenosylmethionine synthase
765	MSTRG.17910	Ca_03188	Ca7	4.452	1.040	pathogen-associated molecular patterns-induced protein A70
766	MSTRG.18592	Ca_15320	Ca7	8.547	1.012	HIPL1 protein
767	MSTRG.19768	Ca_10142	Ca7	9.172	1.010	ABC transporter G family member 36
768	MSTRG.19510	-	Ca7	0.667	1.004	disease resistance protein At4g27190
769	MSTRG.18910	Ca_09256	Ca7	4.269	-1.001	3-ketodihydrosphingosine reductase
770	MSTRG.18784	Ca_12847	Ca7	-0.094	-1.004	ferredoxin C 2, chloroplastic
771	MSTRG.20135	Ca_13740	Ca7	5.065	-1.013	cytochrome P450 86A8
772	MSTRG.18846	Ca_09321	Ca7	4.034	-1.016	Zinc finger protein 7

773	MSTRG.17792	Ca_03293	Ca7	1.841	-1.030	uncharacterized protein LOC101503656
774	MSTRG.19913	Ca_10002	Ca7	1.312	-1.047	serine rich protein
775	MSTRG.19856	Ca_10057	Ca7	10.443	-1.078	linoleate 9S-lipoxygenase
776	MSTRG.19380	Ca_12414	Ca7	7.764	-1.093	O-fucosyltransferase 39 isoform X2
777	MSTRG.18417	Ca_06624	Ca7	6.668	-1.101	sodium/pyruvate cotransporter BASS2, chloroplastic
778	MSTRG.19854	Ca_10054	Ca7	9.317	-1.105	seed linoleate 9S-lipoxygenase
779	MSTRG.19545	Ca_23639	Ca7	-0.030	-1.117	dynein light chain 2, cytoplasmic
780	MSTRG.19786	Ca_10124	Ca7	1.722	-1.123	pentatricopeptide repeat-containing protein At4g26680, mitochondrial
781	MSTRG.17865	Ca_03233	Ca7	4.627	-1.133	LOW QUALITY PROTEIN: uncharacterized protein LOC101502059
782	MSTRG.18548	Ca_13157	Ca7	2.485	-1.143	cyclic dof factor 3
783	MSTRG.19189	Ca_15887	Ca7	3.347	-1.155	heme-binding protein 2-like
784	MSTRG.18531	Ca_13173	Ca7	3.967	-1.188	protein IMPAIRED IN BABA-INDUCED STERILITY 1
785	MSTRG.18156	Ca_02953	Ca7	4.991	-1.188	protein RALF-like 33
786	MSTRG.20450	Ca_15741	Ca7	8.494	-1.190	putative START-like domain-containing protein
787	MSTRG.18650	Ca_17309	Ca7	2.818	-1.199	U-box domain-containing protein 19-like
788	MSTRG.19748	Ca_23327	Ca7	1.358	-1.206	Dehydration-responsive element-binding protein 3
789	MSTRG.18748	Ca_12811	Ca7	4.967	-1.225	BOI-related E3 ubiquitin-protein ligase 1 isoform X1
790	MSTRG.19431	Ca_14532	Ca7	1.403	-1.249	DUF4228 domain protein
791	MSTRG.19906	Ca_10009	Ca7	8.245	-1.250	auxin-binding protein ABP19a
792	MSTRG.18838	Ca_09327	Ca7	0.988	-1.269	probable membrane-associated kinase regulator 1
793	MSTRG.20049	Ca_17633	Ca7	1.646	-1.281	transmembrane protein, putative
794	MSTRG.18962	Ca_16036	Ca7	4.925	-1.286	calcium uniporter protein 2, mitochondrial
795	MSTRG.17833	Ca_03256	Ca7	6.045	-1.287	4-coumarate--CoA ligase 1-like
796	MSTRG.17858	Ca_03237	Ca7	4.519	-1.293	probable receptor-like serine/threonine-protein kinase At5g57670
797	MSTRG.18141	Ca_02961	Ca7	0.958	-1.302	late embryogenesis abundant protein Lea5
798	MSTRG.17939	-	Ca7	2.841	-1.303	uncharacterized membrane protein C776.05-like
799	MSTRG.17722	Ca_03348	Ca7	7.203	-1.306	temperature-induced lipocalin
800	MSTRG.17900	Ca_03201	Ca7	2.526	-1.325	transmembrane protein, putative
801	MSTRG.19244	Ca_15838	Ca7	4.085	-1.328	plastidal glycolate/glycerate translocator 1, chloroplastic
802	MSTRG.20452	Ca_15742	Ca7	8.086	-1.335	putative START-like domain-containing protein
803	MSTRG.19316	Ca_12342	Ca7	4.079	-1.341	hydroxyproline-rich glycoprotein family protein, putative
804	MSTRG.19329	-	Ca7	1.255	-1.342	---NA---
805	MSTRG.17811	Ca_03275	Ca7	1.235	-1.353	---NA---
806	MSTRG.17721	Ca_03348	Ca7	4.685	-1.367	temperature-induced lipocalin
807	MSTRG.18992	Ca_16061	Ca7	0.891	-1.368	late embryogenesis abundant protein D-29-like
808	MSTRG.20447	Ca_15740	Ca7	7.472	-1.376	putative START-like domain-containing protein
809	MSTRG.20502	-	Ca7	3.580	-1.387	protein piccolo-like
810	MSTRG.18021	Ca_03083	Ca7	4.498	-1.392	protein CHUP1, chloroplastic isoform X1
811	MSTRG.20119	Ca_13721	Ca7	4.396	-1.411	transferring glycosyl group transferase
812	MSTRG.19039	Ca_09979	Ca7	1.833	-1.445	auxin-responsive protein SAUR50
813	MSTRG.17927	Ca_03173	Ca7	3.099	-1.446	putative lactoylglutathione lyase
814	MSTRG.18750	-	Ca7	-0.647	-1.493	BOI-related E3 ubiquitin-protein ligase 1 isoform X1
815	MSTRG.19274	Ca_12303	Ca7	4.074	-1.533	inorganic phosphate transporter 2-1, chloroplastic

816	MSTRG.18889	Ca_09279	Ca7	5.680	-1.552	zeaxanthin epoxidase, chloroplastic-like
817	MSTRG.19962	-	Ca7	-4.072	-1.562	---NA---
818	MSTRG.19063	-	Ca7	1.259	-1.584	putative RNA-directed DNA polymerase
819	MSTRG.17963	Ca_03140	Ca7	1.371	-1.589	DUF1677 family protein
820	MSTRG.17716	-	Ca7	3.382	-1.657	uncharacterized protein LOC101505708
821	MSTRG.18199	Ca_06812	Ca7	4.866	-1.692	probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic
822	MSTRG.18011	Ca_03094	Ca7	5.328	-1.697	pectin acetylesterase 10-like
823	MSTRG.18713	Ca_12773	Ca7	2.974	-1.782	nudix hydrolase 8
824	MSTRG.17623	Ca_20238	Ca7	4.183	-1.822	nuclear transcription factor Y subunit B-3
825	MSTRG.17869	-	Ca7	-0.509	-1.834	protein ALP1-like
826	MSTRG.18546	Ca_13159	Ca7	1.204	-1.860	agamous-like MADS-box protein AGL65 isoform X1
827	MSTRG.19586	Ca_26609	Ca7	1.699	-1.870	cyclic nucleotide-gated ion channel 4-like isoform X1
828	MSTRG.19215	Ca_15866	Ca7	-0.816	-1.887	proline-rich extensin-like protein EPR1
829	MSTRG.20216	-	Ca7	-0.071	-1.900	ubiquitin-related modifier 1 homolog 2
830	MSTRG.19951	Ca_16173	Ca7	2.084	-1.914	auxin-responsive protein SAUR50
831	MSTRG.19218	Ca_15861	Ca7	4.348	-1.934	non-specific lipid-transfer protein 4
832	MSTRG.18240	Ca_06777	Ca7	1.531	-1.946	adenylate isopentenyltransferase 5, chloroplastic
833	MSTRG.20501	-	Ca7	0.073	-1.997	uncharacterized protein LOC105851360 isoform X2
834	MSTRG.17789	Ca_03294	Ca7	6.291	-2.020	WAT1-related protein At4g28040
835	MSTRG.20400	-	Ca7	-1.139	-2.078	---NA---
836	MSTRG.18458	Ca_06589	Ca7	4.349	-2.150	calcium sensing receptor, chloroplastic
837	MSTRG.19377	Ca_12415	Ca7	0.327	-2.447	uncharacterized protein LOC25497972
838	MSTRG.20103	Ca_17794	Ca7	-0.361	-2.458	DUF2996 family protein
839	MSTRG.20010	Ca_20981	Ca7	-0.284	-2.472	protein DMR6-LIKE OXYGENASE 2-like
840	MSTRG.18249	Ca_06767	Ca7	0.451	-2.587	cysteine-rich RLK (receptor-like kinase) protein
841	MSTRG.17704	Ca_03370	Ca7	0.765	-2.768	senescence regulator
842	MSTRG.18387	Ca_06650	Ca7	0.002	-2.833	aspartate racemase
843	MSTRG.20275	Ca_25097	Ca7	0.062	-2.944	uncharacterized protein LOC101513856
844	MSTRG.20025	Ca_17608	Ca7	3.330	-3.062	homeobox-leucine zipper protein ATHB-12
845	MSTRG.17729	Ca_03341	Ca7	5.028	-3.109	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
846	MSTRG.19243	Ca_15837	Ca7	0.660	-3.332	protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1
847	MSTRG.17788	Ca_03294	Ca7	1.078	-3.488	hypothetical protein CUMW_228080
848	MSTRG.18067	Ca_03040	Ca7	-0.230	-4.381	cell wall / vacuolar inhibitor of fructosidase 1-like
849	MSTRG.18796	Ca_09372	Ca7	0.827	-4.599	probable xyloglucan endotransglucosylase/hydrolase protein 6
850	MSTRG.20363	Ca_20210	Ca7	3.169	-4.605	protein LNK3
851	MSTRG.18066	Ca_03041	Ca7	2.987	-5.134	cell wall / vacuolar inhibitor of fructosidase 1-like
852	MSTRG.20982	Ca_02190	Ca8	-0.068	2.874	probable indole-3-acetic acid-amido synthetase GH3.1
853	MSTRG.20599	-	Ca8	-0.461	2.751	2-hydroxyisoflavanone dehydratase-like
854	MSTRG.20598	Ca_11885	Ca8	3.513	2.749	2-hydroxyisoflavanone dehydratase
855	MSTRG.20990	Ca_02185	Ca8	1.047	2.501	cytochrome P450 81E8-like
856	MSTRG.21768	Ca_13048	Ca8	3.117	2.432	WAT1-related protein At3g18200
857	MSTRG.21092	Ca_02090	Ca8	5.737	2.415	cytochrome P450 71D8-like
858	MSTRG.21282	Ca_23585	Ca8	5.211	2.351	lysine histidine transporter-like 8

859	MSTRG.20708	Ca_15039	Ca8	1.322	2.067	GDSL esterase/lipase At4g10955-like
860	MSTRG.21381	Ca_10657	Ca8	-0.422	2.061	probable LRR receptor-like serine/threonine-protein kinase At3g47570
861	MSTRG.20774	Ca_02410	Ca8	1.628	1.800	protein DETOXIFICATION 49
862	MSTRG.20939	Ca_02239	Ca8	1.728	1.674	VQ motif-containing protein 29-like
863	MSTRG.20716	Ca_15029	Ca8	2.031	1.661	MYB-like transcription factor ETC3
864	MSTRG.21566	-	Ca8	-0.202	1.648	7-deoxyloganetic acid glucosyltransferase-like
865	MSTRG.21129	Ca_02055	Ca8	5.988	1.638	cytochrome P450 71D8-like
866	MSTRG.21286	Ca_23588	Ca8	3.047	1.631	probable acyl-activating enzyme 1, peroxisomal
867	MSTRG.20855	Ca_02325	Ca8	2.830	1.548	ethylene-responsive transcription factor 2
868	MSTRG.21837	Ca_12995	Ca8	1.472	1.541	cytochrome P450 CYP736A12-like
869	MSTRG.21711	Ca_23843	Ca8	1.796	1.506	TMV resistance protein N
870	MSTRG.21395	Ca_10643	Ca8	1.823	1.413	glycosyltransferase family protein
871	MSTRG.21928	Ca_17872	Ca8	3.814	1.382	2-oxoglutarate-Fe(II) type oxidoreductase hxnY-like isoform X1
872	MSTRG.21446	Ca_11443	Ca8	5.155	1.351	disease resistance protein rpm1-like
873	MSTRG.21859	Ca_12980	Ca8	2.679	1.349	probable sulfate transporter 3.5
874	MSTRG.21078	Ca_02106	Ca8	4.061	1.347	wall-associated receptor kinase-like 14
875	MSTRG.21505	Ca_11501	Ca8	6.563	1.317	cinnamoyl-CoA reductase-like SNL6
876	MSTRG.20586	Ca_11897	Ca8	4.931	1.279	putative receptor-like protein kinase At4g00960
877	MSTRG.21225	Ca_01961	Ca8	3.456	1.255	protein NUCLEAR FUSION DEFECTIVE 4-like
878	MSTRG.21290	Ca_23592	Ca8	5.419	1.243	phosphoserine aminotransferase 2, chloroplastic-like
879	MSTRG.21043	Ca_02137	Ca8	6.402	1.220	patatin-like protein 1
880	MSTRG.20664	Ca_11822	Ca8	10.550	1.142	chalcone synthase
881	MSTRG.20665	Ca_11822	Ca8	5.869	1.077	chalcone synthase
882	MSTRG.21838	Ca_12995	Ca8	5.586	1.042	cytochrome P450 CYP736A12-like
883	MSTRG.21038	Ca_02141	Ca8	2.808	1.010	BEST plant protein match is: (TAIR:plant.1) protein, putative
884	MSTRG.20976	Ca_02201	Ca8	3.981	-1.007	protein CONSERVED IN THE GREEN LINEAGE AND DIATOMS 27, chloroplastic isoform X1
885	MSTRG.20585	Ca_11898	Ca8	5.496	-1.021	DUF1005 family protein
886	MSTRG.21519	Ca_11511	Ca8	5.256	-1.030	---NA---
887	MSTRG.21322	Ca_10708	Ca8	5.800	-1.031	monosaccharide-sensing protein 2-like
888	MSTRG.21956	-	Ca8	-0.235	-1.034	---NA---
889	MSTRG.20807	Ca_02377	Ca8	5.172	-1.040	deoxyribodipyrimidine photo-lyase
890	MSTRG.20971	Ca_02206	Ca8	3.480	-1.041	BTB/POZ domain-containing protein SR1IP1
891	MSTRG.21853	Ca_12987	Ca8	4.597	-1.084	fe-S cluster assembly factor HCF101, chloroplastic
892	MSTRG.21334	Ca_10694	Ca8	4.370	-1.087	subtilisin-like protease SBT3.9 isoform X2
893	MSTRG.21045	-	Ca8	1.846	-1.088	putative encoded peptide
894	MSTRG.21845	Ca_12991	Ca8	4.611	-1.089	protein ASPARTIC PROTEASE IN GUARD CELL 1
895	MSTRG.21086	Ca_02098	Ca8	3.626	-1.113	STS14 protein
896	MSTRG.20819	Ca_02364	Ca8	4.512	-1.127	thylakoid lumenal protein TL20.3, chloroplastic isoform X1
897	MSTRG.20993	Ca_02182	Ca8	5.687	-1.134	transcription factor MYB44
898	MSTRG.21791	Ca_13033	Ca8	6.003	-1.137	non-specific lipid-transfer protein 2
899	MSTRG.21426	Ca_10604	Ca8	4.067	-1.150	histone-lysine N-methyltransferase ASHR2
900	MSTRG.21788	-	Ca8	-3.361	-1.157	---NA---
901	MSTRG.20639	Ca_11846	Ca8	6.119	-1.159	non-specific lipid-transfer protein-like protein At5g64080

902	MSTRG.20713	Ca_15031	Ca8	1.292	-1.163	ethylene-responsive transcription factor ERF061
903	MSTRG.21270	Ca_23578	Ca8	4.818	-1.163	thiosulfate sulfurtransferase 16, chloroplastic-like isoform X2
904	MSTRG.20948	Ca_02229	Ca8	6.888	-1.167	ADP-ribosylation factor-like protein 8a
905	MSTRG.20923	-	Ca8	2.742	-1.183	CLE16 protein
906	MSTRG.21982	Ca_15543	Ca8	5.843	-1.192	cytidine deaminase 1
907	MSTRG.21027	Ca_02151	Ca8	5.625	-1.212	carboxy-terminal region remorin
908	MSTRG.21067	Ca_02115	Ca8	1.629	-1.219	salicylic acid-binding protein 2-like
909	MSTRG.21643	Ca_19746	Ca8	4.605	-1.229	alpha-galactosidase-like isoform X2
910	MSTRG.21498	-	Ca8	1.080	-1.243	---NA---
911	MSTRG.21582	Ca_18412	Ca8	7.757	-1.262	BTB/POZ domain-containing protein At2g30600 isoform X2
912	MSTRG.21125	Ca_02060	Ca8	1.848	-1.282	plant/T3A5-60 protein
913	MSTRG.21379	Ca_10658	Ca8	2.508	-1.306	transmembrane protein, putative
914	MSTRG.20785	Ca_02401	Ca8	5.835	-1.318	phospholipase D beta 1
915	MSTRG.21390	Ca_10648	Ca8	5.397	-1.319	pectin acetylesterase 8-like isoform X1
916	MSTRG.21127	Ca_02059	Ca8	0.017	-1.341	proline-rich receptor-like protein kinase PERK4
917	MSTRG.21343	Ca_10684	Ca8	1.825	-1.360	probable carotenoid cleavage dioxygenase 4, chloroplastic
918	MSTRG.21271	Ca_23579	Ca8	0.006	-1.421	seryl-tRNA synthetase gb
919	MSTRG.21330	Ca_10697	Ca8	4.222	-1.463	protein PIN-LIKES 3-like
920	MSTRG.21200	Ca_01985	Ca8	5.241	-1.490	B-box zinc finger protein 18-like
921	MSTRG.20844	Ca_02337	Ca8	4.224	-1.502	formyltetrahydrofolate deformylase
922	MSTRG.20640	Ca_11845	Ca8	6.415	-1.510	non-specific lipid-transfer protein-like protein At2g13820
923	MSTRG.21864	Ca_12975	Ca8	2.896	-1.751	multiprotein-bridging factor 1c
924	MSTRG.21029	Ca_02150	Ca8	3.907	-1.817	zeaxanthin epoxidase
925	MSTRG.20566	Ca_11914	Ca8	-0.386	-1.822	putative Late embryogenesis abundant protein, LEA5-type
926	MSTRG.21921	-	Ca8	-0.542	-1.827	cysteine-rich receptor-like protein kinase
927	MSTRG.20638	Ca_11847	Ca8	1.881	-1.889	non-specific lipid transfer protein GPI-anchored 2
928	MSTRG.20622	Ca_11865	Ca8	1.627	-1.961	heat shock 22 kDa protein
929	MSTRG.21570	Ca_18399	Ca8	6.696	-2.506	chlorophyll a-b binding protein CP26, chloroplastic
930	MSTRG.20901	Ca_02279	Ca8	3.812	-2.514	protein NRT1/ PTR FAMILY 7.3
931	MSTRG.21987	Ca_15550	Ca8	-1.666	-5.174	sodium transporter HKT1-like
932	MSTRG.21832	Ca_12999	Ca8	0.180	-6.441	dehydrin
933	MSTRG.22025	-	scaffold1006	0.752	3.011	probable cyclic nucleotide-gated ion channel 20, chloroplastic isoform X2
934	MSTRG.22037	-	scaffold1006	4.774	1.257	nucleotide-diphospho-sugar transferase family protein
935	MSTRG.22026	-	scaffold1006	5.048	-1.721	beta-amylase 1, chloroplastic
936	MSTRG.22028	-	scaffold1006	2.576	-3.155	protein REVEILLE 7-like
937	MSTRG.22067	Ca_28086	scaffold10227	4.025	1.356	Transcription factor bHLH96
938	MSTRG.22113	Ca_17199	scaffold1047	4.670	4.966	putative phospholipase A(2)
939	MSTRG.22109	Ca_17198	scaffold1047	2.384	-5.773	putative phospholipase A(2)
940	MSTRG.22220	-	scaffold109_1	4.328	1.108	IQ domain-containing protein IQM1
941	MSTRG.22274	Ca_24644	scaffold1115	4.583	-1.889	uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic-like
942	MSTRG.22295	Ca_26846	scaffold1135	3.503	-1.579	ABC transporter C family member 12
943	MSTRG.22297	Ca_26366	scaffold1145	4.894	1.019	glycosyltransferase family 2 protein
944	MSTRG.22321	-	scaffold1176_2	3.628	-1.428	transcription factor bHLH18

945	MSTRG.22383	-	scaffold1197	0.015	-1.729	annexin-like protein RJ4
946	MSTRG.22393	Ca_22983	scaffold12	-0.135	1.670	uncharacterized protein LOC113848277
947	MSTRG.22399	Ca_24664	scaffold1202	6.573	-1.636	inositol transporter 1-like
948	MSTRG.22425	Ca_27804	scaffold1231	-2.993	-3.582	leucine-rich repeat receptor-like serine/threonine-protein kinase At1g17230 isoform X1
949	MSTRG.22493	-	scaffold1301_1	4.306	-5.373	heavy metal-associated isoprenylated plant protein 24
950	MSTRG.22556	-	scaffold1324	1.659	2.329	Protein Rev like
951	MSTRG.22550	Ca_19763	scaffold1324	4.009	-1.057	E3 ubiquitin-protein ligase ATL6-like
952	MSTRG.22560	Ca_19775	scaffold1324	0.884	-2.438	CEN-like protein 1
953	MSTRG.22590	Ca_22590	scaffold134	3.541	1.356	G-type lectin S-receptor-like serine/threonine-protein kinase
954	MSTRG.22578	-	scaffold134	1.256	-1.079	transmembrane protein, putative
955	MSTRG.22583	Ca_22584	scaffold134	0.376	-1.620	beta-amylase isoform X1
956	MSTRG.22684	-	scaffold1348_1	0.781	2.380	GDSL esterase/lipase At3g48460
957	MSTRG.22724	-	scaffold1348_1	3.170	1.084	armadillo repeat only 1 protein
958	MSTRG.22706	-	scaffold1348_1	0.431	-1.154	manganese-dependent ADP-ribose/CDP-alcohol diphosphatase-like
959	MSTRG.22691	-	scaffold1348_1	4.451	-1.278	probable pectate lyase 18
960	MSTRG.22744	Ca_21997	scaffold1351	5.940	1.167	alpha carbonic anhydrase 7-like
961	MSTRG.22815	Ca_26982	scaffold1419	2.959	-1.304	granule-bound starch synthase 1, chloroplastic/amyloplastic-like
962	MSTRG.22822	Ca_23649	scaffold1439	5.564	1.203	MLO1
963	MSTRG.22824	Ca_23650	scaffold1439	5.984	-2.206	Chlorophyll a-b binding protein 6A, chloroplastic
964	MSTRG.22845	Ca_26807	scaffold1467	3.095	-2.160	putative cytochrome P450
965	MSTRG.22893	-	scaffold1543	0.934	-1.286	Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrB
966	MSTRG.22904	Ca_23862	scaffold1545	3.254	-1.343	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 7-like
967	MSTRG.22932	Ca_21083	scaffold157	-0.075	1.305	glucan endo-1,3-beta-glucosidase 8
968	MSTRG.22925	Ca_21071	scaffold157	2.777	1.080	peroxisomal nicotinamide adenine dinucleotide carrier-like
969	MSTRG.22943	-	scaffold1580	0.808	-1.961	---NA---
970	MSTRG.22997	Ca_24188	scaffold1659	1.981	-1.494	protein PELPK1
971	MSTRG.23057	-	scaffold171	3.881	1.414	---NA---
972	MSTRG.23098	Ca_21709	scaffold174	2.099	-1.697	carboxyl-terminal-processing peptidase 3, chloroplastic
973	MSTRG.23146	Ca_27324	scaffold1771	4.657	-1.453	flavin-containing monooxygenase FMO GS-OX-like 9
974	MSTRG.23208	Ca_24792	scaffold186	3.443	1.302	TMV resistance protein N
975	MSTRG.23209	Ca_24791	scaffold186	0.569	1.226	PKS-NRPS hybrid synthetase CHGG_01239-like
976	MSTRG.23246	Ca_24715	scaffold1918	5.054	1.061	trehalose-phosphate phosphatase A
977	MSTRG.23254	Ca_25164	scaffold193	3.231	1.205	receptor-like protein EIX2
978	MSTRG.23262	-	scaffold193	-2.188	-1.061	ubiquitin carboxyl-terminal hydrolase 31-like
979	MSTRG.23292	Ca_25214	scaffold1964	2.810	1.611	mitochondrial phosphate carrier protein 3, mitochondrial-like
980	MSTRG.23346	Ca_26673	scaffold1991	5.428	-2.795	chromosome condensation regulator RCC1 repeat protein
981	MSTRG.23359	Ca_26286	scaffold2027	3.169	-1.242	GDSL esterase/lipase At2g03980-like
982	MSTRG.23374	Ca_26067	scaffold2036	5.905	-1.039	omega-hydroxypalmitate O-feruloyl transferase
983	MSTRG.23428	Ca_24892	scaffold212	2.709	-1.194	Zinc finger protein GIS3
984	MSTRG.23474	Ca_27612	scaffold221	6.518	-1.194	oxalate--CoA ligase-like
985	MSTRG.23515	Ca_25197	scaffold227	3.125	-1.544	glutaredoxin domain-containing cysteine-rich protein CG12206
986	MSTRG.23527	-	scaffold2330	4.486	1.147	transmembrane protein, putative
987	MSTRG.23538	Ca_24344	scaffold2356	6.922	1.447	alcohol dehydrogenase-like 1

988	MSTRG.23571	Ca_27073	scaffold2373	0.030	1.124	putative pentatricopeptide repeat-containing protein At1g12700, mitochondrial
989	MSTRG.23575	-	scaffold2373	5.581	-1.187	BURP domain-containing protein BNM2A-like
990	MSTRG.23609	Ca_22267	scaffold242	5.104	1.096	calcium-dependent protein kinase 32
991	MSTRG.23624	Ca_27038	scaffold250	4.446	-1.131	peptide methionine sulfoxide reductase B1, chloroplastic
992	MSTRG.23653	Ca_22988	scaffold2575	0.374	1.461	uncharacterized protein LOC101503941 isoform X2
993	MSTRG.23669	Ca_23005	scaffold2575	2.736	-1.317	RHOMBOID-like protein 9, chloroplastic
994	MSTRG.23656	Ca_22991	scaffold2575	3.497	-1.831	protein ABA DEFICIENT 4, chloroplastic-like isoform X2
995	MSTRG.23713	-	scaffold2711	-1.220	-1.332	---NA---
996	MSTRG.23756	Ca_24403	scaffold2763	8.845	1.284	isoliquiritigenin 2'-O-methyltransferase-like
997	MSTRG.23754	-	scaffold2763	0.877	1.231	---NA---
998	MSTRG.23835	-	scaffold290	-1.481	-1.046	U3 small nucleolar RNA-associated protein
999	MSTRG.23821	Ca_19826	scaffold290	7.346	-2.254	magnesium-chelatase subunit ChlH, chloroplastic
1000	MSTRG.23873	Ca_20547	scaffold296	8.517	-1.873	aspartyl protease family protein At5g10770-like
1001	MSTRG.23876	Ca_20553	scaffold296	3.497	-3.181	extracellular ligand-gated ion channel protein
1002	MSTRG.23901	Ca_26659	scaffold303	5.033	-2.718	chlorophyll a-b binding protein P4, chloroplastic
1003	MSTRG.23963	-	scaffold314	0.131	3.285	---NA---
1004	MSTRG.23987	Ca_24182	scaffold3170	4.602	1.369	Nuclear-pore anchor
1005	MSTRG.24098	-	scaffold340	-2.511	-1.276	Ulp1 protease family, carboxy-terminal domain protein
1006	MSTRG.24105	Ca_24719	scaffold342	3.530	1.511	glutamate receptor 2.7
1007	MSTRG.24189	-	scaffold362	-1.115	-1.319	MFS transporter
1008	MSTRG.24275	Ca_24520	scaffold395	6.156	-1.383	suppressor of disruption of TFIIS
1009	MSTRG.24282	Ca_23555	scaffold396	2.151	-1.332	Heptahelical transmembrane protein 2
1010	MSTRG.24299	-	scaffold398	-0.907	-1.260	---NA---
1011	MSTRG.24399	-	scaffold420	1.498	1.192	glycine-rich RNA-binding protein GRP1A
1012	MSTRG.24418	Ca_22210	scaffold420	4.449	1.139	beta-glucosidase 11
1013	MSTRG.24435	-	scaffold421_2	2.246	1.596	zinc ion-binding protein
1014	MSTRG.24465	Ca_25412	scaffold44	4.018	1.123	probable LRR receptor-like serine/threonine-protein kinase At1g53430 isoform X1
1015	MSTRG.24499	Ca_22618	scaffold451	2.018	-1.482	transcription factor HY5-like isoform X1
1016	MSTRG.24562	Ca_23568	scaffold48	1.733	1.194	putative calcium-transporting ATPase 11, plasma membrane-type
1017	MSTRG.24586	Ca_21184	scaffold484	0.277	-1.185	uncharacterized protein LOC101494448 isoform X3
1018	MSTRG.24622	-	scaffold4978	-1.076	-1.117	ABC transporter A family member 7-like protein
1019	MSTRG.24678	Ca_24531	scaffold528	2.904	-1.260	Peptidyl-prolyl cis-trans isomerase FKBP53
1020	MSTRG.24697	Ca_22397	scaffold531	6.659	1.571	probable endo-1,3(4)-beta-glucanase ARB_01444
1021	MSTRG.24696	-	scaffold531	1.200	-1.124	histone acetyltransferase HAC12-like
1022	MSTRG.24689	Ca_22388	scaffold531	5.739	-1.176	protein trichome birefringence-like 19
1023	MSTRG.24758	Ca_23922	scaffold545	2.801	1.423	mitochondrial uncoupling protein 1
1024	MSTRG.24918	Ca_27770	scaffold627	4.680	-2.996	protein LNK2 isoform X1
1025	MSTRG.24987	-	scaffold661	-0.923	-1.545	---NA---
1026	MSTRG.25044	Ca_23199	scaffold682	6.301	-1.100	oxalate--CoA ligase-like
1027	MSTRG.25054	-	scaffold702	-0.095	-1.427	---NA---
1028	MSTRG.25076	Ca_24738	scaffold720	3.022	1.826	probable WRKY transcription factor 75
1029	MSTRG.25099	Ca_23807	scaffold731	5.592	1.506	lysine histidine transporter 1
1030	MSTRG.25131	Ca_25929	scaffold753	1.650	-2.460	cyclic dof factor 3

1031	MSTRG.25151	Ca_23410	scaffold775	8.882	1.234	Pectinesterase 2
1032	MSTRG.25171	-	scaffold787	-0.245	-2.261	putative copia-type protein
1033	MSTRG.25179	Ca_27918	scaffold7887	3.908	-1.407	protein trichome birefringence-like 19
1034	MSTRG.25205	-	scaffold809	2.083	-1.171	hypothetical protein L195_g052424
1035	MSTRG.25209	-	scaffold811	-0.500	-1.483	---NA---
1036	MSTRG.25219	Ca_23368	scaffold812	0.125	1.832	hypothetical protein L195_g039441, partial
1037	MSTRG.25307	-	scaffold87	4.383	1.643	peroxidase 55
1038	MSTRG.25315	-	scaffold873	2.991	1.604	transmembrane protein, putative
1039	MSTRG.25345	Ca_22178	scaffold88	4.758	-1.506	methylecgonone reductase-like
1040	MSTRG.25405	-	scaffold895	2.733	1.482	TMV resistance protein N-like
1041	MSTRG.25410	-	scaffold895	4.352	-1.107	glycoside hydrolase family 1 protein
1042	MSTRG.25431	-	scaffold913	4.778	1.480	protein DETOXIFICATION 40
1043	MSTRG.25442	-	scaffold913	2.949	1.340	MYB-like transcription factor ETC1
1044	MSTRG.25432	-	scaffold913	5.626	1.171	protein DETOXIFICATION 40-like
1045	MSTRG.25496	Ca_25673	scaffold924	1.227	-1.348	UDP-glycosyltransferase 1
1046	MSTRG.25507	-	scaffold93	6.456	-1.357	linoleate 9S-lipoxygenase
1047	MSTRG.25579	Ca_21394	scaffold98	5.866	1.632	putative pectinesterase
1048	MSTRG.25602	Ca_25582	scaffold996	2.991	-1.289	uncharacterized protein LOC101496302

Supplementary Table 5: Genes differntly expressed in PRR resistant breeding line 04067-81-2-1-1 (Bc-I) differently expressed under the Interaction-1 (Bc-I vs Bc-C) vs (Rup-I vs Rup-C)

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)	Description of the gene
1	MSTRG.157	Ca_28203	C11166868	2.638	-2.084	probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
2	MSTRG.200	Ca_00003	Ca1	0.328	7.340	---NA---
3	MSTRG.2122	Ca_08869	Ca1	1.001	2.989	Peroxidase 16
4	MSTRG.2966	Ca_12936	Ca1	4.006	2.022	protein trichome birefringence-like 41
5	MSTRG.346	Ca_00144	Ca1	2.336	1.885	---NA---
6	MSTRG.2961	Ca_12939	Ca1	3.652	1.679	B-box zinc finger protein 22
7	MSTRG.909	Ca_07904	Ca1	6.331	1.593	pollen-specific leucine-rich repeat extensin-like protein 1
8	MSTRG.1075	Ca_08071	Ca1	2.526	1.569	hypothetical protein MtrunA17_Chr2g0293951
9	MSTRG.1872	Ca_06955	Ca1	3.664	1.395	thioredoxin-like protein CXXS1
10	MSTRG.1986	Ca_22784	Ca1	3.679	1.290	outer envelope pore protein 16-2, chloroplastic
11	MSTRG.2689	Ca_18463	Ca1	5.070	1.278	11-oxo-beta-amyrin 30-oxidase
12	MSTRG.753	Ca_00565	Ca1	3.997	1.236	peptide methionine sulfoxide reductase B5-like
13	MSTRG.2753	Ca_22519	Ca1	7.432	1.198	proline-rich extensin-like protein EPR1
14	MSTRG.1240	Ca_02809	Ca1	5.177	1.184	protein NRT1/ PTR FAMILY 1.2-like
15	MSTRG.596	Ca_00391	Ca1	2.262	1.161	olee1-like protein
16	MSTRG.1189	Ca_02857	Ca1	4.532	1.053	acyl-protein thioesterase 2-like
17	MSTRG.2038	Ca_14744	Ca1	5.940	1.051	bidirectional sugar transporter SWEET17
18	MSTRG.962	Ca_07957	Ca1	2.023	-1.171	ATRAD3, putative
19	MSTRG.1742	Ca_07092	Ca1	4.225	-1.331	E3 ubiquitin-protein ligase PUB23-like
20	MSTRG.1682	Ca_14146	Ca1	3.034	-1.383	transferring glycosyl group transferase
21	MSTRG.2745	Ca_22515	Ca1	3.553	-1.530	protein GRIM REAPER
22	MSTRG.690	Ca_00497	Ca1	1.943	-2.414	gibberellin 2-beta-dioxygenase
23	MSTRG.4941	Ca_09747	Ca2	5.236	1.651	LRR receptor-like serine/threonine-protein kinase
24	MSTRG.4557	Ca_12430	Ca2	5.336	1.524	putative sodium-coupled neutral amino acid transporter 10
25	MSTRG.3402	Ca_21097	Ca2	4.299	1.440	serine carboxypeptidase-like 25
26	MSTRG.4558	Ca_12428	Ca2	4.128	1.325	amino acid transporter AVT6C-like
27	MSTRG.3394	Ca_21102	Ca2	4.391	1.282	copper transport protein CCH-like
28	MSTRG.5001	Ca_09809	Ca2	7.734	1.091	fasciclin-like arabinogalactan protein 2
29	MSTRG.4710	Ca_10204	Ca2	5.655	1.088	blue copper protein-like
30	MSTRG.3970	Ca_16005	Ca2	3.433	-1.118	methyltransferase domain protein, putative
31	MSTRG.4413	Ca_16139	Ca2	3.968	-1.137	probable methyltransferase PMT19
32	MSTRG.3924	Ca_18535	Ca2	3.123	-1.478	salicylate carboxymethyltransferase
33	MSTRG.4566	Ca_12420	Ca2	2.419	-1.557	LOB domain-containing protein 15
34	MSTRG.3249	Ca_10572	Ca2	4.300	-1.648	Cytochrome P450 82A3
35	MSTRG.3306	Ca_10518	Ca2	2.829	-2.076	myb-related protein 306-like
36	MSTRG.4602	Ca_17822	Ca2	1.807	-3.884	arogenate dehydratase/prephenate dehydratase 2, chloroplastic
37	MSTRG.6570	Ca_07309	Ca3	4.154	2.390	seed maturation protein LEA 4
38	MSTRG.7257	Ca_01005	Ca3	5.832	1.546	calvin cycle protein CP12-2, chloroplastic
39	MSTRG.6196	Ca_08294	Ca3	3.996	1.488	chalcone synthase
40	MSTRG.5700	Ca_19346	Ca3	7.059	1.285	vacuolar cation/proton exchanger 3
41	MSTRG.6935	Ca_20889	Ca3	5.075	1.194	condensation domain protein
42	MSTRG.5553	Ca_18271	Ca3	6.659	1.128	DUF538 family protein
43	MSTRG.6035	Ca_06114	Ca3	4.528	1.068	thioredoxin F-type, chloroplastic
44	MSTRG.7121	Ca_00877	Ca3	7.389	1.008	fasciclin-like arabinogalactan protein 16

45	MSTRG.5474	Ca_23302	Ca3	5.648	-1.202	L-type lectin-domain containing receptor kinase IV.1
46	MSTRG.5859	Ca_20433	Ca3	2.173	-1.438	methylsterol monooxygenase 1-1-like
47	MSTRG.5792	-	Ca3	3.174	-1.493	uncharacterized protein LOC101490888
48	MSTRG.7309	Ca_01059	Ca3	5.019	-1.694	putative expansin-A17
49	MSTRG.5705	-	Ca3	4.530	-2.993	GDSL esterase/lipase CPRD49-like
50	MSTRG.8914	Ca_04473	Ca4	2.570	5.158	low-temperature-induced 65 kDa protein
51	MSTRG.8930	Ca_04486	Ca4	1.244	4.264	uncharacterized protein LOC101504477
52	MSTRG.10685	Ca_09167	Ca4	0.377	2.659	putative GATA transcription factor 22
53	MSTRG.8979	Ca_04534	Ca4	3.500	2.567	cytochrome P450 704C1-like
54	MSTRG.9764	Ca_14421	Ca4	6.153	1.427	NDR1/HIN1-like protein 1
55	MSTRG.9384	Ca_05398	Ca4	4.111	1.272	hippocampus abundant transcript-like protein 1
56	MSTRG.10710	Ca_09192	Ca4	6.746	1.268	---NA---
57	MSTRG.8981	Ca_04537	Ca4	4.002	1.253	xyloglucan galactosyltransferase XLT2
58	MSTRG.10797	Ca_19272	Ca4	3.720	1.167	WUSCHEL-related homeobox 4
59	MSTRG.9176	Ca_05606	Ca4	7.215	1.008	probable cinnamyl alcohol dehydrogenase
60	MSTRG.9062	Ca_04614	Ca4	4.337	-1.084	mental retardation GTPase activating protein homolog 4
61	MSTRG.9739	-	Ca4	2.492	-1.266	RING-H2 finger protein ATL70
62	MSTRG.9751	-	Ca4	4.172	-1.649	E3 ubiquitin-protein ligase PUB24-like
63	MSTRG.9319	Ca_05464	Ca4	5.418	-1.682	MFS transporter
64	MSTRG.10346	Ca_14929	Ca4	9.595	-1.690	glutamate synthase [NADH], amyloplastic isoform X1
65	MSTRG.8347	Ca_03574	Ca4	3.498	-2.038	putative expansin-A17
66	MSTRG.8870	Ca_04426	Ca4	3.639	-2.160	heavy metal-associated isoprenylated plant protein 39
67	MSTRG.8102	Ca_03817	Ca4	1.633	-2.538	subtilisin-like protease SBT1.9
68	MSTRG.12016	-	Ca5	1.046	3.507	Retrovirus-related Pol polyprotein from transposon TNT 1-94
69	MSTRG.11563	-	Ca5	0.301	3.418	cysteine-rich receptor-like protein kinase
70	MSTRG.12454	-	Ca5	1.773	1.933	hypothetical protein MTR_3g111650
71	MSTRG.13239	Ca_07604	Ca5	3.583	1.865	oligopeptide transporter 7-like
72	MSTRG.12579	Ca_01862	Ca5	2.369	1.739	plant/F12B17-70 protein
73	MSTRG.12976	Ca_01445	Ca5	4.133	1.716	alcohol dehydrogenase-like 2
74	MSTRG.11714	-	Ca5	3.430	1.670	BURP domain-containing protein BNM2A-like
75	MSTRG.11866	Ca_08997	Ca5	6.650	1.656	cinnamoyl-CoA reductase 1-like
76	MSTRG.13101	Ca_07459	Ca5	4.810	1.440	copper amine oxidase, enzyme domain protein
77	MSTRG.11130	Ca_25894	Ca5	4.579	1.365	protein CHROMATIN REMODELING 5
78	MSTRG.12288	Ca_04805	Ca5	6.438	1.346	Monosaccharide-sensing protein 2
79	MSTRG.11989	Ca_13430	Ca5	5.509	1.086	protein DJ-1 homolog D
80	MSTRG.13735	Ca_04041	Ca5	3.282	1.064	RNA-binding protein 38-like
81	MSTRG.12289	Ca_04806	Ca5	4.328	1.003	protein MULTIPLE CHLOROPLAST DIVISION SITE 1
82	MSTRG.11858	Ca_09004	Ca5	3.917	1.001	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6-like
83	MSTRG.13266	Ca_07635	Ca5	5.830	-1.098	subtilisin-like protease SBT5.3
84	MSTRG.11995	Ca_13424	Ca5	5.529	-1.128	alpha/beta hydrolase-like protein
85	MSTRG.13145	Ca_07508	Ca5	3.284	-1.145	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9
86	MSTRG.13507	Ca_12684	Ca5	4.633	-1.457	protein DOWNSTREAM OF FLC
87	MSTRG.12011	Ca_13408	Ca5	1.886	-3.628	probable 2-oxoglutarate-dependent dioxygenase At5g05600
88	MSTRG.16749	-	Ca6	-5.005	10.093	ABC transporter A family member 7-like protein
89	MSTRG.16459	Ca_15174	Ca6	-0.669	2.910	Gb:AAF02129.1, putative
90	MSTRG.15920	Ca_11268	Ca6	2.419	2.470	transcription activator GLK1-like isoform X1
91	MSTRG.14071	Ca_13329	Ca6	2.757	2.151	protein phosphatase 2C 37

92	MSTRG.16803	Ca_23252	Ca6	3.349	1.912	BTB/POZ domain-containing protein At5g48800
93	MSTRG.14717	Ca_09628	Ca6	1.352	1.640	probable WRKY transcription factor 13
94	MSTRG.16533	Ca_24447	Ca6	2.601	1.612	aquaporin SIP1-2
95	MSTRG.16817	Ca_24868	Ca6	5.535	1.537	protein EXORDIUM-like 3
96	MSTRG.16400	Ca_16452	Ca6	3.064	1.398	probable 2-carboxy-D-arabinitol-1-phosphatase
97	MSTRG.14752	Ca_09594	Ca6	6.295	1.340	heavy metal-associated isoprenylated plant protein 23
98	MSTRG.16162	Ca_24014	Ca6	3.676	1.230	---NA---
99	MSTRG.14371	Ca_05890	Ca6	4.412	1.196	cytidine deaminase 1-like
100	MSTRG.16389	Ca_16443	Ca6	8.838	1.110	glucomannan 4-beta-mannosyltransferase 2
101	MSTRG.16773	Ca_23154	Ca6	4.263	1.093	ELMO domain-containing protein A isoform X3
102	MSTRG.17289	Ca_21216	Ca6	4.678	1.015	aldehyde oxidase GLOX
103	MSTRG.15593	Ca_06384	Ca6	3.699	-1.040	protein trichome birefringence-like 38
104	MSTRG.16280	Ca_14576	Ca6	8.081	-1.061	root cap/late embryogenesis-like protein
105	MSTRG.17278	Ca_21197	Ca6	7.164	-1.266	probable glutathione S-transferase
106	MSTRG.15287	Ca_05177	Ca6	5.908	-1.276	stress up-regulated Nod 19 protein
107	MSTRG.16596	Ca_15792	Ca6	3.444	-1.552	protein BEARSKIN2-like
108	MSTRG.14023	Ca_13284	Ca6	5.084	-1.575	nudix hydrolase 18, mitochondrial-like
109	MSTRG.17068	Ca_13466	Ca6	6.950	-1.619	probable 2-oxoglutarate-dependent dioxygenase AOP1
110	MSTRG.17520	Ca_15386	Ca6	1.624	-1.752	DUF241 domain protein
111	MSTRG.16893	Ca_13864	Ca6	3.265	-1.812	cytochrome P450 71D9-like
112	MSTRG.17465	Ca_13651	Ca6	8.821	-2.140	non-symbiotic hemoglobin 1
113	MSTRG.19377	Ca_12415	Ca7	0.327	2.164	uncharacterized protein LOC25497972
114	MSTRG.17789	Ca_03294	Ca7	6.291	1.524	WAT1-related protein At4g28040
115	MSTRG.20407	Ca_21371	Ca7	3.737	1.484	protein YLS3-like
116	MSTRG.20534	Ca_26358	Ca7	5.138	1.443	dirigent protein 21
117	MSTRG.18247	Ca_06769	Ca7	7.110	-1.034	basic 7S globulin-like
118	MSTRG.18950	Ca_16022	Ca7	2.906	-1.494	STS14 protein
119	MSTRG.17870	Ca_03224	Ca7	3.695	-2.029	DUF4228 domain protein
120	MSTRG.19738	Ca_11697	Ca7	3.460	-2.085	beta-amyrin 11-oxidase-like
121	MSTRG.19903	Ca_10011	Ca7	3.835	-2.106	germin-like protein subfamily 3 member 1
122	MSTRG.17978	Ca_03124	Ca7	2.267	-2.111	pectinesterase inhibitor 3
123	MSTRG.19236	Ca_15845	Ca7	6.483	-2.312	CTP synthase-like
124	MSTRG.20252	-	Ca7	1.672	-2.503	cytochrome P450 704C1-like
125	MSTRG.20639	Ca_11846	Ca8	6.119	1.483	non-specific lipid-transfer protein-like protein At5g64080
126	MSTRG.20622	Ca_11865	Ca8	1.627	1.450	heat shock 22 kDa protein
127	MSTRG.21322	Ca_10708	Ca8	5.800	1.435	monosaccharide-sensing protein 2-like
128	MSTRG.21643	Ca_19746	Ca8	4.605	1.389	alpha-galactosidase-like isoform X2
129	MSTRG.20640	Ca_11845	Ca8	6.415	1.131	non-specific lipid-transfer protein-like protein At2g13820
130	MSTRG.21982	Ca_15543	Ca8	5.843	1.091	cytidine deaminase 1
131	MSTRG.21426	Ca_10604	Ca8	4.067	1.030	histone-lysine N-methyltransferase ASHR2
132	MSTRG.20774	Ca_02410	Ca8	1.628	-2.217	protein DETOXIFICATION 49
133	MSTRG.20598	Ca_11885	Ca8	3.513	-2.768	2-hydroxyisoflavanone dehydratase
134	MSTRG.21859	Ca_12980	Ca8	2.679	-2.788	probable sulfate transporter 3.5
135	MSTRG.21381	Ca_10657	Ca8	-0.422	-3.133	probable LRR receptor-like serine/threonine-protein kinase At3g47570
136	MSTRG.22474	Ca_21523	scaffold1281	2.738	1.022	RING-H2 finger protein ATL33-like
137	MSTRG.22472	Ca_21517	scaffold1281	3.846	-1.115	LRR receptor-like serine/threonine-protein kinase RCH1
138	MSTRG.22493	-	scaffold1301_1	4.306	2.804	heavy metal-associated isoprenylated plant protein 24

139	MSTRG.22574	Ca_27715	scaffold1330	4.069	-1.073	putative disease resistance RPP13-like protein 1
140	MSTRG.22695	-	scaffold1348_1	5.603	-1.184	BTB/POZ and TAZ domain-containing protein 1
141	MSTRG.22904	Ca_23862	scaffold1545	3.254	1.644	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 7-like
142	MSTRG.23359	Ca_26286	scaffold2027	3.169	1.653	GDSL esterase/lipase At2g03980-like
143	MSTRG.23474	Ca_27612	scaffold221	6.518	1.193	oxalate--CoA ligase-like
144	MSTRG.23615	Ca_22270	scaffold242	4.287	1.355	remorin 4.1
145	MSTRG.23792	Ca_20600	scaffold284	7.728	-2.737	nitrate reductase [NADH] 2
146	MSTRG.24469	Ca_26058	scaffold4452	2.926	-1.562	protein DMR6-LIKE OXYGENASE 1-like
147	MSTRG.24562	Ca_23568	scaffold48	1.733	-1.485	putative calcium-transporting ATPase 11, plasma membrane-type
148	MSTRG.24836	-	scaffold5792	3.394	1.040	DExH-box ATP-dependent RNA helicase DExH15 chloroplastic
149	MSTRG.24971	-	scaffold653	5.141	-1.094	putative P-loop containing nucleoside triphosphate hydrolase, leucine-rich repeat domain, L
150	MSTRG.25044	Ca_23199	scaffold682	6.301	1.162	oxalate--CoA ligase-like
151	MSTRG.25410	-	scaffold895	4.352	1.107	glycoside hydrolase family 1 protein
152	MSTRG.25431	-	scaffold913	4.778	-1.167	protein DETOXIFICATION 40

Supplementary Table 6: PRR resistance genes in PRR resistant breeding line 04067-81-2-1-1 (Bc-I) differently expressed under the Interaction-2 (Bc-I vs Bc-C) vs (Yor-I vs Yor-C)

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)	Description of the gene
1	MSTRG.1994	Ca_14786	Ca1	4.141	-1.888	keratin, type I cytoskeletal 9
2	MSTRG.2961	Ca_12939	Ca1	3.652	2.321	B-box zinc finger protein 22
3	MSTRG.4380	Ca_14343	Ca2	4.173	-2.532	GDSL esterase/lipase At5g37690
4	MSTRG.4399	Ca_14327	Ca2	1.444	-1.763	---NA---
5	MSTRG.4235	Ca_17248	Ca2	7.959	-1.747	cytochrome P450 83B1
6	MSTRG.3077	Ca_16998	Ca2	4.844	-1.201	heparan-alpha-glucosaminide N-acetyltransferase
7	MSTRG.5281	Ca_16514	Ca3	3.081	-3.641	basic leucine zipper 43
8	MSTRG.12177	-	Ca5	-3.398	5.802	---NA---
9	MSTRG.16533	Ca_24447	Ca6	2.601	-2.652	aquaporin SIP1-2
10	MSTRG.15580	Ca_06369	Ca6	3.445	-1.864	GDSL esterase/lipase At5g45960
11	MSTRG.16567	Ca_15818	Ca6	4.678	-1.069	maltose excess protein 1-like, chloroplastic isoform X1
12	MSTRG.18550	Ca_13155	Ca7	5.855	-1.796	GDSL esterase/lipase At1g74460-like
13	MSTRG.24968	-	scaffold6458	1.827	3.380	digestive organ expansion factor-like protein

Supplementary Table 7: PRR resistance genes in PRR mderately resistant genotype YorI differently expressed under the Interaction-3 (Yor-I vs Yor-C) vs (Rup-I vs Rup-C)

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)	Description of the gene
1	MSTRG.78	Ca_27990	C11107558	-4.665	10.184	protein CURVATURE THYLAKOID 1B, chloroplastic-like
2	MSTRG.146	Ca_28056	C11164954	2.670	1.114	protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB4, chloroplastic
3	MSTRG.171	Ca_27440	C11176802	4.725	1.291	magnesium-chelatase subunit ChlD, chloroplastic isoform X2
4	MSTRG.200	Ca_00003	Ca1	0.328	7.647	---NA---
5	MSTRG.2122	Ca_08869	Ca1	1.001	3.323	Peroxidase 16
6	MSTRG.2702	-	Ca1	0.599	3.076	---NA---
7	MSTRG.566	Ca_00361	Ca1	2.459	2.627	GDSL esterase/lipase At5g45960
8	MSTRG.1792	Ca_07045	Ca1	1.914	2.512	fatty acyl-CoA reductase 3
9	MSTRG.406	Ca_00201	Ca1	5.665	2.398	sulfite exporter TauE/SafE family protein 2
10	MSTRG.2394	Ca_18504	Ca1	5.545	2.193	probable inositol transporter 2
11	MSTRG.1994	Ca_14786	Ca1	4.141	2.160	keratin, type I cytoskeletal 9
12	MSTRG.535	Ca_00331	Ca1	3.244	2.045	protein E6
13	MSTRG.3005	Ca_12890	Ca1	2.438	2.012	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10
14	MSTRG.2966	Ca_12936	Ca1	4.006	1.996	protein trichome birefringence-like 41
15	MSTRG.2639	Ca_13942	Ca1	6.523	1.969	non-specific lipid-transfer protein 8
16	MSTRG.909	Ca_07904	Ca1	6.331	1.966	pollen-specific leucine-rich repeat extensin-like protein 1
17	MSTRG.1231	Ca_02818	Ca1	3.436	1.961	dynein light chain 1, cytoplasmic-like
18	MSTRG.1239	Ca_02809	Ca1	1.388	1.944	---NA---
19	MSTRG.1075	Ca_08071	Ca1	2.526	1.874	hypothetical protein MtrunA17_Chr2g0293951
20	MSTRG.1426	Ca_02620	Ca1	3.670	1.811	expansin-A4
21	MSTRG.1006	Ca_07994	Ca1	4.406	1.751	homeobox-leucine zipper protein ATHB-14
22	MSTRG.1401	Ca_02638	Ca1	2.561	1.722	zinc finger protein ZAT3-like
23	MSTRG.2847	Ca_13545	Ca1	1.616	1.647	glutathione S-transferase F9-like
24	MSTRG.2182	Ca_20634	Ca1	5.205	1.583	probable xyloglucan endotransglucosylase/hydrolase protein 23
25	MSTRG.423	Ca_00215	Ca1	6.077	1.560	NAD(P)H dehydrogenase (quinone) FQR1
26	MSTRG.2809	-	Ca1	0.715	1.463	Transcription factor MYB63
27	MSTRG.1992	Ca_14787	Ca1	2.115	1.462	cAMP-regulated phosphoprotein-like protein
28	MSTRG.356	-	Ca1	6.973	1.440	protein PELPK1-like
29	MSTRG.2311	Ca_18606	Ca1	5.996	1.439	CASP-like protein 1B1
30	MSTRG.2038	Ca_14744	Ca1	5.940	1.425	bidirectional sugar transporter SWEET17
31	MSTRG.1240	Ca_02809	Ca1	5.177	1.425	protein NRT1/ PTR FAMILY 1.2-like
32	MSTRG.2300	Ca_18588	Ca1	3.907	1.381	DUF538 family protein
33	MSTRG.1848	Ca_06980	Ca1	3.355	1.380	UDP-glycosyltransferase 79B30-like
34	MSTRG.1670	Ca_14134	Ca1	6.633	1.356	xyloglucan endotransglucosylase/hydrolase protein 9
35	MSTRG.2689	Ca_18463	Ca1	5.070	1.345	11-oxo-beta-amyrin 30-oxidase
36	MSTRG.1986	Ca_22784	Ca1	3.679	1.319	outer envelope pore protein 16-2, chloroplastic
37	MSTRG.1230	Ca_02819	Ca1	6.338	1.309	late embryogenesis abundant protein
38	MSTRG.1917	-	Ca1	3.102	1.276	transmembrane protein, putative
39	MSTRG.1189	Ca_02857	Ca1	4.532	1.202	acyl-protein thioesterase 2-like
40	MSTRG.1517	Ca_02524	Ca1	5.930	1.180	beta-galactosidase 8
41	MSTRG.587	Ca_00376	Ca1	4.815	1.130	GDSL esterase/lipase

42	MSTRG.2987	Ca_12914	Ca1	6.806	1.127	gamma-glutamyl hydrolase 2-like
43	MSTRG.1413	Ca_02628	Ca1	3.547	1.029	haloacid dehalogenase-like hydrolase
44	MSTRG.1933	Ca_06895	Ca1	5.650	1.003	COP1-interacting protein 7
45	MSTRG.2647	Ca_13924	Ca1	6.844	-1.042	CTP synthase-like
46	MSTRG.427	Ca_00218	Ca1	4.532	-1.087	receptor-like serine/threonine-protein kinase SD1-8
47	MSTRG.1755	Ca_07077	Ca1	5.201	-1.150	hypothetical protein L195_g035980, partial
48	MSTRG.2811	Ca_13592	Ca1	3.931	-1.220	YUP8H12R.23 protein, putative
49	MSTRG.2984	-	Ca1	3.363	-1.264	hypothetical protein MTR_2g075490
50	MSTRG.1144	Ca_02901	Ca1	3.657	-1.337	sterile alpha motif domain-containing protein
51	MSTRG.2620	Ca_13970	Ca1	2.124	-1.339	transmembrane protein, putative
52	MSTRG.728	Ca_00535	Ca1	7.671	-1.343	inactive beta-amylase 9
53	MSTRG.1776	Ca_07059	Ca1	0.368	-1.384	protein BIC2
54	MSTRG.2771	Ca_22680	Ca1	3.606	-1.398	cytochrome P450 CYP736A12-like
55	MSTRG.1837	Ca_06993	Ca1	4.307	-1.404	putative Myb family transcription factor
56	MSTRG.2745	Ca_22515	Ca1	3.553	-1.405	protein GRIM REAPER
57	MSTRG.1724	Ca_07110	Ca1	5.671	-1.460	cellulose synthase-like protein H1
58	MSTRG.497	Ca_00295	Ca1	1.689	-1.548	dof zinc finger protein DOF1.4
59	MSTRG.1391	Ca_02649	Ca1	3.755	-1.807	ADP,ATP carrier protein, mitochondrial
60	MSTRG.1120	Ca_02925	Ca1	2.011	-2.034	probable WRKY transcription factor 40
61	MSTRG.1168	Ca_02879	Ca1	4.970	-2.043	probable polygalacturonase At3g15720
62	MSTRG.1281	Ca_02766	Ca1	3.525	-2.133	probable LRR receptor-like serine/threonine-protein kinase At1g05700
63	MSTRG.690	Ca_00497	Ca1	1.943	-2.182	gibberellin 2-beta-dioxygenase
64	MSTRG.569	Ca_00363	Ca1	4.734	-2.254	glutamate receptor 2.7-like
65	MSTRG.655	Ca_00464	Ca1	-0.222	-4.135	serine carboxypeptidase-like 11
66	MSTRG.2555	-	Ca1	0.600	-5.316	nucleosome assembly protein 1-like 3
67	MSTRG.3737	Ca_17575	Ca2	2.637	3.007	thioredoxin H2
68	MSTRG.4042	Ca_24630	Ca2	2.472	2.973	protein DMR6-LIKE OXYGENASE 2-like
69	MSTRG.4380	Ca_14343	Ca2	4.173	2.605	GDSL esterase/lipase At5g37690
70	MSTRG.3067	Ca_16983	Ca2	3.024	2.531	cytokinin hydroxylase
71	MSTRG.4557	Ca_12430	Ca2	5.336	2.527	putative sodium-coupled neutral amino acid transporter 10
72	MSTRG.3402	Ca_21097	Ca2	4.299	2.476	serine carboxypeptidase-like 25
73	MSTRG.4235	Ca_17248	Ca2	7.959	2.327	cytochrome P450 83B1
74	MSTRG.3403	-	Ca2	2.411	2.194	serine carboxypeptidase-like 25
75	MSTRG.4399	Ca_14327	Ca2	1.444	2.126	---NA---
76	MSTRG.4941	Ca_09747	Ca2	5.236	2.112	LRR receptor-like serine/threonine-protein kinase
77	MSTRG.3394	Ca_21102	Ca2	4.391	2.109	copper transport protein CCH-like
78	MSTRG.3390	-	Ca2	3.679	1.987	copper transport protein CCH-like
79	MSTRG.4400	Ca_14327	Ca2	3.222	1.934	aspartic proteinase PCS1-like
80	MSTRG.4781	-	Ca2	1.791	1.878	transmembrane protein, putative
81	MSTRG.3093	Ca_20670	Ca2	4.836	1.856	O-acyltransferase WSD1
82	MSTRG.4176	Ca_14257	Ca2	4.833	1.849	cytochrome P450 86A1
83	MSTRG.3990	Ca_15978	Ca2	4.678	1.805	peroxidase 11
84	MSTRG.4797	Ca_15263	Ca2	2.447	1.718	neurofilament medium polypeptide-like isoform X1
85	MSTRG.3613	Ca_21476	Ca2	3.556	1.648	F-box/kelch-repeat protein At1g23390

86	MSTRG.4952	Ca_09761	Ca2	1.041	1.540	probable amino acid permease 7
87	MSTRG.4556	Ca_12431	Ca2	1.617	1.506	Alpha-soluble NSF attachment protein 2
88	MSTRG.4436	Ca_16115	Ca2	4.316	1.428	glycerol-3-phosphate acyltransferase 5
89	MSTRG.3512	Ca_20936	Ca2	6.644	1.393	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
90	MSTRG.4223	Ca_14311	Ca2	4.285	1.345	Serine/threonine-protein kinase HT1
91	MSTRG.4710	Ca_10204	Ca2	5.655	1.335	blue copper protein-like
92	MSTRG.3238	Ca_10584	Ca2	4.483	1.300	putative heavy metal-associated domain, HMA
93	MSTRG.3841	Ca_11684	Ca2	4.686	1.299	CSC1-like protein At1g69450 isoform X1
94	MSTRG.3094	Ca_20671	Ca2	4.630	1.257	O-acyltransferase WSD1
95	MSTRG.4770	Ca_15235	Ca2	6.814	1.244	glutathione S-transferase F9-like
96	MSTRG.4132	Ca_21659	Ca2	2.500	1.221	probable inactive receptor kinase At5g58300
97	MSTRG.3837	-	Ca2	1.547	1.169	putative reverse transcriptase zinc-binding domain-containing protein
98	MSTRG.3570	Ca_18112	Ca2	5.567	1.152	mitochondrial uncoupling protein 5
99	MSTRG.4540	Ca_12449	Ca2	6.296	1.094	protein trichome birefringence-like 33
100	MSTRG.3929	Ca_24652	Ca2	3.767	1.087	protein BIG GRAIN 1-like E
101	MSTRG.4229	Ca_14315	Ca2	4.837	1.030	cinnamoyl-CoA reductase 1
102	MSTRG.4194	Ca_14278	Ca2	2.505	1.029	phosphoinositide phospholipase C 2-like
103	MSTRG.4967	Ca_09772	Ca2	4.931	-1.011	disease resistance protein SUMM2-like
104	MSTRG.3499	Ca_19707	Ca2	4.183	-1.057	transcription factor IIIB 90 kDa subunit isoform X1
105	MSTRG.4900	Ca_09705	Ca2	4.525	-1.149	ABC transporter C family member 3
106	MSTRG.3970	Ca_16005	Ca2	3.433	-1.182	methyltransferase domain protein, putative
107	MSTRG.4591	Ca_12421	Ca2	7.861	-1.185	probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840
108	MSTRG.4248	Ca_17259	Ca2	3.922	-1.222	exocyst complex component
109	MSTRG.3830	Ca_18090	Ca2	4.836	-1.295	NAC transcription factor 29
110	MSTRG.4896	Ca_09702	Ca2	2.400	-1.357	heavy metal-associated isoprenylated plant protein 47-like
111	MSTRG.4627	-	Ca2	0.231	-1.387	receptor-like protein EIX2
112	MSTRG.3249	Ca_10572	Ca2	4.300	-1.463	Cytochrome P450 82A3
113	MSTRG.4566	Ca_12420	Ca2	2.419	-1.485	LOB domain-containing protein 15
114	MSTRG.4413	Ca_16139	Ca2	3.968	-1.555	probable methyltransferase PMT19
115	MSTRG.4247	Ca_17263	Ca2	1.433	-1.854	exocyst complex component EXO70B1-like
116	MSTRG.3372	-	Ca2	3.858	-1.923	transcription factor TCP13
117	MSTRG.4602	Ca_17822	Ca2	1.807	-3.057	arogenate dehydratase/prephenate dehydratase 2, chloroplastic
118	MSTRG.5151	-	Ca3	-3.521	13.500	cell morphogenesis protein PAG1 isoform X2
119	MSTRG.5638	Ca_19627	Ca3	0.639	3.948	universal stress protein PHOS32-like
120	MSTRG.5376	-	Ca3	0.506	3.103	protein LAZY 1 isoform X1
121	MSTRG.5913	Ca_06245	Ca3	3.914	2.848	SPX domain-containing membrane protein At4g22990 isoform X1
122	MSTRG.6570	Ca_07309	Ca3	4.154	2.662	seed maturation protein LEA 4
123	MSTRG.6782	Ca_12291	Ca3	2.218	2.432	photosystem I reaction center subunit IV A, chloroplastic-like
124	MSTRG.6280	Ca_08212	Ca3	8.325	2.308	protein SRC1
125	MSTRG.6589	Ca_07325	Ca3	3.058	2.299	thioredoxin-like 3-1, chloroplastic
126	MSTRG.6518	Ca_07258	Ca3	2.142	2.146	myosin-11-like protein
127	MSTRG.6957	Ca_00719	Ca3	3.493	2.140	probable pectate lyase 12
128	MSTRG.6515	Ca_07257	Ca3	3.451	2.038	remorin 4.1
129	MSTRG.7563	Ca_01292	Ca3	3.693	1.998	GDSL esterase/lipase At4g01130 isoform X1

130	MSTRG.5231	-	Ca3	1.135	1.993	hypothetical protein
131	MSTRG.6803	Ca_11967	Ca3	1.161	1.936	transmembrane protein, putative
132	MSTRG.6667	-	Ca3	4.498	1.907	Lipid transfer protein
133	MSTRG.6874	Ca_12036	Ca3	6.507	1.858	peptide upstream ORF protein, putative
134	MSTRG.5991	Ca_06163	Ca3	2.943	1.834	probable WRKY transcription factor 43
135	MSTRG.6655	Ca_07390	Ca3	1.756	1.787	plant/T24G3-80 protein
136	MSTRG.6176	Ca_23888	Ca3	5.067	1.762	light-regulated protein
137	MSTRG.7257	Ca_01005	Ca3	5.832	1.700	calvin cycle protein CP12-2, chloroplastic
138	MSTRG.7636	Ca_01352	Ca3	1.971	1.656	DNA-directed RNA polymerase III subunit RPC10-like
139	MSTRG.7217	Ca_00966	Ca3	3.815	1.550	caffeoylshikimate esterase isoform X1
140	MSTRG.6232	Ca_08259	Ca3	5.447	1.446	apyrase
141	MSTRG.5879	Ca_20407	Ca3	3.801	1.365	Extended synaptotagmin-2
142	MSTRG.6901	Ca_23676	Ca3	4.385	1.296	CASP-like protein 2D1
143	MSTRG.6935	Ca_20889	Ca3	5.075	1.232	condensation domain protein
144	MSTRG.7200	Ca_00952	Ca3	3.723	1.187	protein LOW PSII ACCUMULATION 1, chloroplastic
145	MSTRG.5553	Ca_18271	Ca3	6.659	1.181	DUF538 family protein
146	MSTRG.5609	Ca_21122	Ca3	7.854	1.143	metallothionein-like protein 2
147	MSTRG.5238	Ca_25770	Ca3	5.598	1.138	protein SIEVE ELEMENT OCCLUSION B-like
148	MSTRG.5189	Ca_22097	Ca3	7.367	1.136	cyclic nucleotide-gated ion channel 2
149	MSTRG.6035	Ca_06114	Ca3	4.528	1.070	thioredoxin F-type, chloroplastic
150	MSTRG.7494	Ca_01235	Ca3	3.386	1.065	sec-independent protein translocase protein TATA, chloroplastic
151	MSTRG.6986	Ca_00743	Ca3	2.878	1.052	probable carboxylesterase 18
152	MSTRG.6092	Ca_06046	Ca3	7.442	1.018	subtilisin-like protease Glyma18g48580
153	MSTRG.6431	Ca_07176	Ca3	4.291	1.014	regulatory protein NPR5-like
154	MSTRG.6454	Ca_07198	Ca3	5.285	-1.032	triacylglycerol lipase SDP1
155	MSTRG.6338	Ca_08155	Ca3	6.205	-1.062	dihydrofolate reductase
156	MSTRG.7287	Ca_01032	Ca3	4.645	-1.062	short-chain dehydrogenase reductase 3b
157	MSTRG.5494	Ca_22500	Ca3	2.844	-1.135	---NA---
158	MSTRG.5498	Ca_22496	Ca3	4.892	-1.177	hydroquinone glucosyltransferase
159	MSTRG.5474	Ca_23302	Ca3	5.648	-1.203	L-type lectin-domain containing receptor kinase IV.1
160	MSTRG.7108	Ca_00859	Ca3	5.064	-1.208	BEL1-like homeodomain protein 1
161	MSTRG.6921	Ca_20876	Ca3	4.821	-1.267	protein BIC1
162	MSTRG.7085	Ca_00833	Ca3	1.540	-1.319	uncharacterized protein LOC101497048
163	MSTRG.5585	Ca_23345	Ca3	4.058	-1.364	protein PHLOEM PROTEIN 2-LIKE A1
164	MSTRG.7449	Ca_01191	Ca3	7.757	-1.433	sugar transporter ERD6-like 5 isoform X1
165	MSTRG.5724	Ca_09400	Ca3	2.358	-1.449	Putative Myb family transcription factor
166	MSTRG.7584	Ca_01308	Ca3	5.777	-1.488	cyclic nucleotide-gated ion channel 1
167	MSTRG.6495	Ca_07234	Ca3	5.627	-1.506	heat stress transcription factor B-3
168	MSTRG.5401	-	Ca3	4.083	-1.679	zinc finger protein ZAT11-like
169	MSTRG.7309	Ca_01059	Ca3	5.019	-1.783	putative expansin-A17
170	MSTRG.5859	Ca_20433	Ca3	2.173	-1.913	methylsterol monooxygenase 1-1-like
171	MSTRG.7551	Ca_01281	Ca3	1.275	-2.038	probable receptor-like protein kinase At5g18500
172	MSTRG.7590	Ca_01309	Ca3	1.288	-2.111	cyclic nucleotide-gated ion channel 1 isoform X1
173	MSTRG.6602	Ca_07339	Ca3	8.507	-2.407	dirigent protein 22-like

174	MSTRG.7543	Ca_01273	Ca3	-2.029	-2.432	carboxyl-terminal peptidase
175	MSTRG.5705	-	Ca3	4.530	-3.147	GDSL esterase/lipase CPRD49-like
176	MSTRG.5819	Ca_09495	Ca3	2.203	-4.540	probable WRKY transcription factor 70
177	MSTRG.8903	Ca_04466	Ca4	2.753	3.826	PAR1 protein
178	MSTRG.8914	Ca_04473	Ca4	2.570	3.622	low-temperature-induced 65 kDa protein
179	MSTRG.9480	-	Ca4	-1.004	3.510	allantoinase
180	MSTRG.8979	Ca_04534	Ca4	3.500	3.318	cytochrome P450 704C1-like
181	MSTRG.9878	Ca_21313	Ca4	1.109	3.179	cyclopropane-fatty-acyl-phospholipid synthase
182	MSTRG.10760	Ca_18369	Ca4	4.745	2.852	beta-galactosidase-like isoform X1
183	MSTRG.10685	Ca_09167	Ca4	0.377	2.590	putative GATA transcription factor 22
184	MSTRG.8948	Ca_04504	Ca4	-0.427	2.563	dehydration-responsive element-binding protein 1A-like
185	MSTRG.10383	Ca_14886	Ca4	2.372	2.378	metal-nicotianamine transporter YSL3
186	MSTRG.10225	Ca_15089	Ca4	1.961	2.242	auxin efflux carrier component 3
187	MSTRG.10420	Ca_11021	Ca4	2.865	2.109	protein CUP-SHAPED COTYLEDON 1-like
188	MSTRG.10313	Ca_13069	Ca4	0.688	2.059	probable protein phosphatase 2C 51
189	MSTRG.9529	Ca_13994	Ca4	2.413	1.965	inositol transporter 1-like
190	MSTRG.9127	Ca_05652	Ca4	4.313	1.891	nucleobase-ascorbate transporter 4
191	MSTRG.7848	Ca_07812	Ca4	4.770	1.776	non-specific lipid-transfer protein-like protein At2g13820
192	MSTRG.7839	Ca_07807	Ca4	4.523	1.710	sulfate transporter 3.1
193	MSTRG.10147	Ca_14818	Ca4	6.117	1.640	long chain acyl-CoA synthetase 2-like
194	MSTRG.10797	Ca_19272	Ca4	3.720	1.624	WUSCHEL-related homeobox 4
195	MSTRG.8761	Ca_04334	Ca4	3.363	1.571	geraniol 8-hydroxylase-like
196	MSTRG.9836	Ca_25308	Ca4	2.668	1.527	golgin subfamily A member 6-like protein 6
197	MSTRG.10738	Ca_09218	Ca4	1.640	1.466	uncharacterized protein LOC101497748 isoform X2
198	MSTRG.9022	Ca_04574	Ca4	5.540	1.442	non-specific lipid-transfer protein-like protein At2g13820
199	MSTRG.9384	Ca_05398	Ca4	4.111	1.421	hippocampus abundant transcript-like protein 1
200	MSTRG.9855	Ca_20441	Ca4	3.876	1.391	transmembrane protein, putative
201	MSTRG.7877	Ca_07845	Ca4	2.052	1.283	adenylate isopentenyltransferase 3, chloroplastic
202	MSTRG.9927	Ca_14170	Ca4	2.423	1.259	homeobox-leucine zipper protein HOX11-like
203	MSTRG.8519	Ca_08332	Ca4	4.109	1.245	blue copper protein
204	MSTRG.8878	Ca_04438	Ca4	2.910	1.226	probable receptor-like protein kinase At5g24010
205	MSTRG.7949	Ca_12090	Ca4	6.210	1.219	protein SIEVE ELEMENT OCCLUSION B-like
206	MSTRG.9049	Ca_04604	Ca4	6.057	1.197	primary amine oxidase
207	MSTRG.8762	Ca_04335	Ca4	3.222	1.195	protein COFACTOR ASSEMBLY OF COMPLEX C SUBUNIT B CCB3, chloroplastic
208	MSTRG.8356	Ca_03565	Ca4	6.144	1.188	pectin acetylesterase 6
209	MSTRG.9764	Ca_14421	Ca4	6.153	1.144	NDR1/HIN1-like protein 1
210	MSTRG.8036	Ca_12171	Ca4	6.714	1.131	peroxidase 47
211	MSTRG.9466	Ca_18637	Ca4	7.569	1.124	glutathione S-transferase DHAR2-like
212	MSTRG.10774	Ca_18358	Ca4	6.901	1.113	subtilisin-like protease SBT1.7
213	MSTRG.9526	Ca_13992	Ca4	7.289	1.111	INO80 complex subunit D-like
214	MSTRG.9748	Ca_14444	Ca4	5.822	1.107	glucan endo-1,3-beta-glucosidase 12
215	MSTRG.9059	Ca_04611	Ca4	3.427	1.078	mavicyanin-like
216	MSTRG.7871	Ca_07835	Ca4	2.720	1.075	uncharacterized protein LOC101507063
217	MSTRG.10669	Ca_09152	Ca4	2.522	1.073	DUF3511 domain protein

218	MSTRG.8981	Ca_04537	Ca4	4.002	1.070	xyloglucan galactosyltransferase XLT2
219	MSTRG.9033	Ca_04588	Ca4	2.499	1.034	cysteine synthase
220	MSTRG.9176	Ca_05606	Ca4	7.215	1.025	probable cinnamyl alcohol dehydrogenase
221	MSTRG.10710	Ca_09192	Ca4	6.746	1.023	---NA---
222	MSTRG.8368	Ca_03552	Ca4	4.342	1.013	protein RADIALIS-like 3
223	MSTRG.8682	Ca_08487	Ca4	5.914	1.010	GATA transcription factor 8
224	MSTRG.10543	Ca_23685	Ca4	5.307	-1.008	G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300
225	MSTRG.8868	Ca_04424	Ca4	2.303	-1.043	protein SAR DEFICIENT 4
226	MSTRG.9481	Ca_18651	Ca4	8.516	-1.059	chalcone isomerase
227	MSTRG.9621	Ca_17144	Ca4	10.024	-1.153	phenylalanine ammonia-lyase class 2
228	MSTRG.9141	Ca_05640	Ca4	5.269	-1.169	BTB/POZ domain-containing protein NPY2
229	MSTRG.10834	Ca_10861	Ca4	4.099	-1.207	probable disease resistance protein At4g33300
230	MSTRG.9703	Ca_20135	Ca4	2.497	-1.210	heat stress transcription factor A-3
231	MSTRG.8626	Ca_08436	Ca4	5.355	-1.251	AP2/ERF and B3 domain-containing transcription factor RAV1-like
232	MSTRG.9739	-	Ca4	2.492	-1.272	RING-H2 finger protein ATL70
233	MSTRG.10754	Ca_18376	Ca4	3.587	-1.311	ZCF37, putative
234	MSTRG.10099	Ca_22448	Ca4	3.295	-1.413	transmembrane protein, putative
235	MSTRG.9988	Ca_15448	Ca4	1.792	-1.434	phosphatase 2C-like protein 44
236	MSTRG.7815	Ca_07780	Ca4	0.635	-1.441	GABA transporter 1-like isoform X1
237	MSTRG.10321	Ca_13061	Ca4	3.404	-1.452	rust resistance kinase Lr10-like
238	MSTRG.9751	-	Ca4	4.172	-1.475	E3 ubiquitin-protein ligase PUB24-like
239	MSTRG.9132	Ca_05646	Ca4	3.784	-1.513	putative beta-D-xylosidase 5-like protein
240	MSTRG.9429	Ca_05361	Ca4	5.223	-1.550	GEM-like protein 4
241	MSTRG.8102	Ca_03817	Ca4	1.633	-1.574	subtilisin-like protease SBT1.9
242	MSTRG.10219	Ca_15097	Ca4	4.070	-1.621	putative glycerophosphodiester phosphodiesterase, protein kinase RLK-Pelle-LRK10L-2 family
243	MSTRG.10735	-	Ca4	2.986	-1.696	uncharacterized protein LOC101497077
244	MSTRG.10346	Ca_14929	Ca4	9.595	-1.703	glutamate synthase [NADH], amyloplastic isoform X1
245	MSTRG.9174	Ca_05608	Ca4	5.636	-1.768	putative UDP-glucose glucosyltransferase
246	MSTRG.10718	Ca_09200	Ca4	2.624	-1.772	transcription factor RAX2-like
247	MSTRG.9166	Ca_05616	Ca4	4.239	-1.899	uncharacterized protein LOC101504693
248	MSTRG.8692	-	Ca4	2.342	-1.949	hypothetical protein POPTR_010G221266
249	MSTRG.7923	Ca_12068	Ca4	6.002	-2.209	cellulose synthase-like protein G2
250	MSTRG.10525	Ca_10900	Ca4	0.342	-2.436	Sigma factor binding protein 1, chloroplastic
251	MSTRG.9430	-	Ca4	0.531	-2.571	GEM-like protein 4
252	MSTRG.8870	Ca_04426	Ca4	3.639	-2.573	heavy metal-associated isoprenylated plant protein 39
253	MSTRG.8588	Ca_08397	Ca4	3.438	-2.837	geraniol 8-hydroxylase-like
254	MSTRG.8589	Ca_08398	Ca4	3.295	-2.870	geraniol 8-hydroxylase-like
255	MSTRG.12874	Ca_01550	Ca5	-1.406	6.554	transcription factor HEC2-like
256	MSTRG.12271	Ca_04788	Ca5	5.779	4.921	specific tissue protein
257	MSTRG.12272	Ca_04788	Ca5	9.065	4.622	specific tissue protein
258	MSTRG.12270	-	Ca5	1.809	4.219	---NA---
259	MSTRG.12976	Ca_01445	Ca5	4.133	3.149	alcohol dehydrogenase-like 2
260	MSTRG.11831	Ca_09038	Ca5	3.697	2.779	internal alternative NAD(P)H-ubiquinone oxidoreductase A1, mitochondrial
261	MSTRG.11714	-	Ca5	3.430	2.608	BURP domain-containing protein BNM2A-like

262	MSTRG.11866	Ca_08997	Ca5	6.650	2.486	cinnamoyl-CoA reductase 1-like
263	MSTRG.13892	Ca_04193	Ca5	4.159	2.453	NAD(P)H-quinone oxidoreductase subunit O, chloroplastic
264	MSTRG.13357	Ca_11390	Ca5	0.051	2.333	probable xyloglucan galactosyltransferase GT14
265	MSTRG.11584	-	Ca5	3.122	2.331	cytochrome b561 domain-containing protein At2g30890-like
266	MSTRG.12022	-	Ca5	0.639	2.317	LOB domain-containing protein 21
267	MSTRG.12140	Ca_16669	Ca5	1.462	2.167	uncharacterized protein LOC101501288
268	MSTRG.12730	Ca_01693	Ca5	2.606	2.100	protein GLUTAMINE DUMPER 5
269	MSTRG.12273	Ca_04789	Ca5	6.738	1.887	BURP domain-containing protein BNM2A-like
270	MSTRG.11130	Ca_25894	Ca5	4.579	1.793	protein CHROMATIN REMODELING 5
271	MSTRG.12761	Ca_01661	Ca5	5.156	1.740	ultraviolet-B-repressible protein
272	MSTRG.13377	Ca_11365	Ca5	3.526	1.726	15-cis-zeta-carotene isomerase, chloroplastic
273	MSTRG.12096	Ca_16624	Ca5	6.040	1.674	FCS-Like Zinc finger 5-like
274	MSTRG.11790	Ca_15610	Ca5	5.528	1.673	cytochrome P450 86A1
275	MSTRG.13239	Ca_07604	Ca5	3.583	1.601	oligopeptide transporter 7-like
276	MSTRG.13061	Ca_07421	Ca5	5.795	1.590	probable pectate lyase 5
277	MSTRG.13220	Ca_07584	Ca5	1.636	1.583	endoglucanase 11
278	MSTRG.12269	Ca_04787	Ca5	3.744	1.525	proline-rich receptor-like protein kinase PERK7
279	MSTRG.13669	Ca_03975	Ca5	3.343	1.518	flavonol synthase/flavanone 3-hydroxylase
280	MSTRG.12454	-	Ca5	1.773	1.513	hypothetical protein MTR_3g111650
281	MSTRG.13944	Ca_04246	Ca5	5.037	1.481	aspartic proteinase nepenthesin-1
282	MSTRG.13194	Ca_07556	Ca5	3.998	1.469	linoleate 13S-lipoxygenase 2-1, chloroplastic-like
283	MSTRG.13162	Ca_07522	Ca5	7.651	1.427	betaine aldehyde dehydrogenase 1, chloroplastic
284	MSTRG.11989	Ca_13430	Ca5	5.509	1.407	protein DJ-1 homolog D
285	MSTRG.12304	Ca_04823	Ca5	2.525	1.401	WUSCHEL-related homeobox 8
286	MSTRG.13284	Ca_11424	Ca5	3.761	1.382	glucan endo-1,3-beta-glucosidase 4
287	MSTRG.11239	Ca_20333	Ca5	2.590	1.326	bifunctional protein FolD 1, mitochondrial-like
288	MSTRG.12579	Ca_01862	Ca5	2.369	1.320	plant/F12B17-70 protein
289	MSTRG.11936	Ca_08918	Ca5	5.590	1.261	DEAD-box ATP-dependent RNA helicase 20-like isoform X1
290	MSTRG.13125	Ca_07483	Ca5	6.546	1.246	probable boron transporter 2 isoform X1
291	MSTRG.13735	Ca_04041	Ca5	3.282	1.243	RNA-binding protein 38-like
292	MSTRG.11578	Ca_22825	Ca5	6.906	1.236	glutathione S-transferase F9
293	MSTRG.13365	Ca_11381	Ca5	6.513	1.222	xyloglucan endotransglucosylase/hydrolase 2
294	MSTRG.12865	Ca_01561	Ca5	3.544	1.208	cyclin-D3-1-like
295	MSTRG.12166	Ca_04695	Ca5	5.368	1.189	50S ribosomal protein L3, chloroplastic
296	MSTRG.12265	Ca_04782	Ca5	3.461	1.117	probable receptor-like serine/threonine-protein kinase At4g34500
297	MSTRG.12877	Ca_01546	Ca5	3.601	1.100	protein DCL, chloroplastic
298	MSTRG.13750	Ca_04055	Ca5	4.288	1.076	ribosome-binding factor PSRP1, chloroplastic
299	MSTRG.12091	Ca_23824	Ca5	5.137	1.072	30S ribosomal protein S13, chloroplastic
300	MSTRG.12583	Ca_01857	Ca5	3.257	1.071	AIG2-like protein D
301	MSTRG.13278	Ca_07645	Ca5	3.862	1.068	transmembrane protein, putative
302	MSTRG.13782	Ca_04085	Ca5	4.948	1.022	cytochrome P450 714A1-like
303	MSTRG.12451	Ca_04962	Ca5	3.321	1.006	Putative GMP synthase [glutamine-hydrolyzing]
304	MSTRG.13824	Ca_04126	Ca5	1.649	-1.011	LOB domain-containing protein 15
305	MSTRG.11384	Ca_17101	Ca5	5.516	-1.036	disease resistance protein RPM1

306	MSTRG.12073	Ca_13345	Ca5	6.252	-1.071	WAT1-related protein At4g08300
307	MSTRG.13634	Ca_03943	Ca5	3.331	-1.078	protein MKS1
308	MSTRG.12904	Ca_01518	Ca5	5.945	-1.125	mitogen-activated protein kinase kinase kinase 5-like
309	MSTRG.13497	Ca_12695	Ca5	4.883	-1.206	putative C2 domain-containing protein
310	MSTRG.11971	Ca_08880	Ca5	4.710	-1.246	NDR1/HIN1-like protein 6
311	MSTRG.13495	Ca_12697	Ca5	3.012	-1.278	putative C2 domain-containing protein
312	MSTRG.13751	Ca_04056	Ca5	5.094	-1.282	two-component response regulator-like APRR5 isoform X1
313	MSTRG.11821	Ca_09044	Ca5	1.837	-1.298	putative serine/threonine-protein kinase-like protein CCR3
314	MSTRG.13302	Ca_11408	Ca5	5.880	-1.324	chalcone synthase 4-like
315	MSTRG.13145	Ca_07508	Ca5	3.284	-1.326	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9
316	MSTRG.11995	Ca_13424	Ca5	5.529	-1.334	alpha/beta hydrolase-like protein
317	MSTRG.13196	Ca_07559	Ca5	4.929	-1.384	NADH--cytochrome b5 reductase 1-like
318	MSTRG.11118	Ca_24950	Ca5	2.407	-1.404	protein LONGIFOLIA 1
319	MSTRG.13857	Ca_04163	Ca5	1.108	-1.436	---NA---
320	MSTRG.11403	Ca_17085	Ca5	3.460	-1.482	TMV resistance protein N
321	MSTRG.13189	Ca_07550	Ca5	0.776	-1.550	UPF0481 protein At3g47200-like
322	MSTRG.12455	-	Ca5	3.003	-1.740	elongation of fatty acids protein 3-like
323	MSTRG.11655	Ca_21153	Ca5	3.510	-1.799	DUF4228 domain protein
324	MSTRG.13507	Ca_12684	Ca5	4.633	-1.887	protein DOWNSTREAM OF FLC
325	MSTRG.12094	Ca_16620	Ca5	4.848	-1.917	sulfate transporter 1.3
326	MSTRG.13764	Ca_04067	Ca5	3.466	-2.068	heavy metal-associated isoprenylated plant protein 9
327	MSTRG.13059	-	Ca5	0.918	-2.693	sucrase-like protein
328	MSTRG.12869	Ca_01556	Ca5	1.274	-2.725	ethylene-responsive transcription factor RAP2-1-like
329	MSTRG.11283	Ca_23782	Ca5	3.247	-2.876	pectinesterase/pectinesterase inhibitor
330	MSTRG.11988	Ca_13431	Ca5	5.163	-3.184	cysteine-rich receptor-like protein kinase 2
331	MSTRG.13753	Ca_04059	Ca5	2.294	-3.266	protein DOWNY MILDEW RESISTANCE 6
332	MSTRG.12177	-	Ca5	-3.398	-4.670	---NA---
333	MSTRG.16749	-	Ca6	-5.005	9.858	ABC transporter A family member 7-like protein
334	MSTRG.14866	Ca_16738	Ca6	6.726	4.334	Glutelin type-A 2
335	MSTRG.16533	Ca_24447	Ca6	2.601	4.264	aquaporin SIP1-2
336	MSTRG.16459	Ca_15174	Ca6	-0.669	2.153	Gb:AAF02129.1, putative
337	MSTRG.15097	-	Ca6	0.511	2.151	LINE-1 reverse transcriptase isogeny
338	MSTRG.15907	Ca_11281	Ca6	0.320	2.041	UDP-glycosyltransferase 79B30
339	MSTRG.16803	Ca_23252	Ca6	3.349	1.973	BTB/POZ domain-containing protein At5g48800
340	MSTRG.14242	Ca_10434	Ca6	0.749	1.878	dynein light chain LC6, flagellar outer arm-like
341	MSTRG.16348	Ca_17463	Ca6	8.536	1.871	xyloglucan endotransglucosylase/hydrolase protein 31
342	MSTRG.16174	Ca_16682	Ca6	4.622	1.853	expansin-A6 isoform X1
343	MSTRG.15580	Ca_06369	Ca6	3.445	1.851	GDSL esterase/lipase At5g45960
344	MSTRG.15386	Ca_05279	Ca6	4.808	1.839	protein PELPK1
345	MSTRG.14071	Ca_13329	Ca6	2.757	1.796	protein phosphatase 2C 37
346	MSTRG.14448	Ca_05820	Ca6	7.722	1.753	endoglucanase 6
347	MSTRG.15344	Ca_05236	Ca6	6.252	1.705	non-specific lipid-transfer protein-like protein At5g64080
348	MSTRG.16354	Ca_17460	Ca6	1.959	1.624	shugoshin-1
349	MSTRG.14898	Ca_08667	Ca6	3.286	1.598	homeobox-leucine zipper protein ATHB-14

350	MSTRG.16817	Ca_24868	Ca6	5.535	1.592	protein EXORDIUM-like 3
351	MSTRG.17492	Ca_13630	Ca6	7.719	1.585	BURP domain-containing protein BNM2A-like
352	MSTRG.15385	Ca_05277	Ca6	7.496	1.565	protein PELPK1
353	MSTRG.15475	Ca_19667	Ca6	3.291	1.468	PAP-specific phosphatase HAL2-like
354	MSTRG.17382	Ca_17429	Ca6	4.226	1.436	O-fucosyltransferase 34
355	MSTRG.14824	Ca_16780	Ca6	3.839	1.428	chloroplast sensor kinase, chloroplastic
356	MSTRG.17091	Ca_13443	Ca6	2.758	1.411	lipid transfer-like protein VAS
357	MSTRG.14859	Ca_16747	Ca6	2.013	1.390	gamma-soluble NSF attachment protein
358	MSTRG.16902	Ca_13878	Ca6	4.692	1.376	30S ribosomal protein S10, chloroplastic
359	MSTRG.15182	Ca_05079	Ca6	2.851	1.351	Protein SRG1
360	MSTRG.14517	Ca_05752	Ca6	2.990	1.336	DUF3741 family protein
361	MSTRG.16605	Ca_15778	Ca6	2.830	1.298	receptor protein-tyrosine kinase CEPR2
362	MSTRG.16156	Ca_26069	Ca6	3.983	1.284	CTL-like protein DDB_G0274487
363	MSTRG.15718	Ca_06502	Ca6	2.744	1.254	transcription termination factor MTERF6, chloroplastic/mitochondrial
364	MSTRG.15322	Ca_05206	Ca6	4.172	1.195	uncharacterized protein LOC101507621 isoform X1
365	MSTRG.15750	Ca_06532	Ca6	5.107	1.193	protein PHLOEM PROTEIN 2-LIKE A1
366	MSTRG.14032	Ca_13294	Ca6	4.265	1.192	glutathione S-transferase DHAR3, chloroplastic
367	MSTRG.16480	Ca_15199	Ca6	4.592	1.145	protein FAF-like, chloroplastic
368	MSTRG.14275	Ca_25241	Ca6	8.530	1.141	aldehyde dehydrogenase family 2 member C4-like
369	MSTRG.14302	Ca_05956	Ca6	5.517	1.137	auxin-responsive protein IAA27
370	MSTRG.17018	Ca_13515	Ca6	4.637	1.113	protein CURVATURE THYLAKOID 1C, chloroplastic
371	MSTRG.17565	Ca_15428	Ca6	7.877	1.084	arginine decarboxylase
372	MSTRG.16117	Ca_11044	Ca6	3.487	1.078	dirigent protein 23
373	MSTRG.14819	Ca_16782	Ca6	4.292	1.075	uncharacterized protein LOC101498300
374	MSTRG.15689	Ca_06474	Ca6	3.870	1.074	filament-like plant protein 7
375	MSTRG.17452	Ca_13657	Ca6	7.643	1.070	Cold-regulated 413 plasma membrane protein 2
376	MSTRG.15793	Ca_06579	Ca6	6.090	1.069	nodulin-related protein 1-like
377	MSTRG.17289	Ca_21216	Ca6	4.678	1.064	aldehyde oxidase GLOX
378	MSTRG.14815	Ca_09537	Ca6	2.755	1.056	putative magnesium-importing ATPase
379	MSTRG.17257	Ca_16278	Ca6	4.749	1.046	D-xylose-proton symporter-like 3, chloroplastic
380	MSTRG.14852	Ca_16751	Ca6	3.371	-1.000	cationic amino acid transporter 1
381	MSTRG.15799	Ca_06582	Ca6	5.823	-1.028	UDP-glycosyltransferase 13-like
382	MSTRG.17068	Ca_13466	Ca6	6.950	-1.033	probable 2-oxoglutarate-dependent dioxygenase AOP1
383	MSTRG.16280	Ca_14576	Ca6	8.081	-1.041	root cap/late embryogenesis-like protein
384	MSTRG.16456	Ca_15168	Ca6	3.989	-1.087	plant/F24K9-26 protein
385	MSTRG.15568	Ca_06356	Ca6	10.045	-1.141	isoflavone 4'-O-methyltransferase
386	MSTRG.14339	Ca_05922	Ca6	5.256	-1.146	probable pectinesterase 53
387	MSTRG.14023	Ca_13284	Ca6	5.084	-1.162	nudix hydrolase 18, mitochondrial-like
388	MSTRG.14075	Ca_13335	Ca6	6.426	-1.184	wall-associated receptor kinase-like 20
389	MSTRG.15028	Ca_08527	Ca6	3.069	-1.204	crocetin glucosyltransferase, chloroplastic
390	MSTRG.17240	Ca_18917	Ca6	12.049	-1.210	non-cyanogenic beta-glucosidase-like
391	MSTRG.17509	-	Ca6	6.185	-1.276	isoflavone reductase homolog PCBER
392	MSTRG.14435	Ca_05827	Ca6	3.827	-1.286	RING-H2 finger protein ATL20-like
393	MSTRG.17524	Ca_15390	Ca6	1.860	-1.294	DUF241 domain protein

394	MSTRG.16707	Ca_15917	Ca6	4.689	-1.295	cytochrome P450 83B1
395	MSTRG.16985	Ca_20707	Ca6	6.715	-1.301	abscisic acid receptor PYL4-like
396	MSTRG.15287	Ca_05177	Ca6	5.908	-1.324	stress up-regulated Nod 19 protein
397	MSTRG.17278	Ca_21197	Ca6	7.164	-1.353	probable glutathione S-transferase
398	MSTRG.15136	-	Ca6	4.113	-1.357	transmembrane protein, putative
399	MSTRG.16558	Ca_22054	Ca6	4.852	-1.375	RALF-like protein
400	MSTRG.15593	Ca_06384	Ca6	3.699	-1.388	protein trichome birefringence-like 38
401	MSTRG.17274	Ca_16294	Ca6	0.931	-1.420	scarecrow-like protein 14
402	MSTRG.17520	Ca_15386	Ca6	1.624	-1.460	DUF241 domain protein
403	MSTRG.17465	Ca_13651	Ca6	8.821	-1.498	non-symbiotic hemoglobin 1
404	MSTRG.16181	Ca_16684	Ca6	5.661	-1.630	receptor-like cytoplasmic kinase 176 isoform X1
405	MSTRG.15590	Ca_06380	Ca6	5.240	-1.677	phospholipase A1-IIgamma
406	MSTRG.15447	Ca_22015	Ca6	2.959	-1.772	G-type lectin S-receptor-like serine/threonine-protein kinase B120
407	MSTRG.15704	Ca_06488	Ca6	5.353	-1.945	plastid movement impaired protein
408	MSTRG.16596	Ca_15792	Ca6	3.444	-1.958	protein BEARSKIN2-like
409	MSTRG.16555	Ca_22055	Ca6	3.133	-2.070	MDIS1-interacting receptor like kinase 2-like
410	MSTRG.13984	Ca_13249	Ca6	3.955	-2.092	uncharacterized serine-rich protein C215.13
411	MSTRG.15216	Ca_05112	Ca6	3.532	-2.219	isoflavone 2'-hydroxylase
412	MSTRG.16966	Ca_23440	Ca6	-0.218	-3.214	UPF0481 protein At3g47200-like
413	MSTRG.14544	Ca_05720	Ca6	5.844	-4.897	thaumatin-like pathogenesis-related protein 4-like precursor
414	MSTRG.18374	Ca_06660	Ca7	2.197	3.144	protein NRT1/ PTR FAMILY 6.2
415	MSTRG.18704	Ca_12765	Ca7	-0.103	3.003	ethylene-responsive transcription factor ERF038-like
416	MSTRG.17900	Ca_03201	Ca7	2.526	2.734	transmembrane protein, putative
417	MSTRG.19977	Ca_16195	Ca7	0.680	2.632	uncharacterized protein LOC101490868 isoform X1
418	MSTRG.18546	Ca_13159	Ca7	1.204	2.490	agamous-like MADS-box protein AGL65 isoform X1
419	MSTRG.20502	-	Ca7	3.580	2.289	protein piccolo-like
420	MSTRG.18066	Ca_03041	Ca7	2.987	2.212	cell wall / vacuolar inhibitor of fructosidase 1-like
421	MSTRG.19314	Ca_12345	Ca7	3.791	2.036	E3 ubiquitin-protein ligase WAVH1-like
422	MSTRG.20407	Ca_21371	Ca7	3.737	2.034	protein YLS3-like
423	MSTRG.18550	Ca_13155	Ca7	5.855	1.919	GDSL esterase/lipase At1g74460-like
424	MSTRG.18641	Ca_17318	Ca7	0.790	1.868	WAT1-related protein At3g28050-like
425	MSTRG.17704	Ca_03370	Ca7	0.765	1.842	senescence regulator
426	MSTRG.19392	Ca_14493	Ca7	6.143	1.815	polygalacturonase 1 beta-like protein 3
427	MSTRG.19748	Ca_23327	Ca7	1.358	1.767	Dehydration-responsive element-binding protein 3
428	MSTRG.17858	Ca_03237	Ca7	4.519	1.767	probable receptor-like serine/threonine-protein kinase At5g57670
429	MSTRG.18011	Ca_03094	Ca7	5.328	1.736	pectin acetylesterase 10-like
430	MSTRG.18935	Ca_09232	Ca7	6.384	1.697	GDSL esterase/lipase At2g23540
431	MSTRG.18763	Ca_12825	Ca7	5.066	1.690	two-component response regulator-like APRR2
432	MSTRG.20452	Ca_15742	Ca7	8.086	1.675	putative START-like domain-containing protein
433	MSTRG.18784	Ca_12847	Ca7	-0.094	1.614	ferredoxin C 2, chloroplastic
434	MSTRG.18933	Ca_09236	Ca7	5.749	1.558	salicylic acid-binding protein 2
435	MSTRG.18351	Ca_06683	Ca7	3.601	1.535	thylakoid lumenal 16.5 kDa protein, chloroplastic
436	MSTRG.18531	Ca_13173	Ca7	3.967	1.530	protein IMPAIRED IN BABA-INDUCED STERILITY 1
437	MSTRG.17963	Ca_03140	Ca7	1.371	1.461	DUF1677 family protein

438	MSTRG.19906	Ca_10009	Ca7	8.245	1.435	auxin-binding protein ABP19a
439	MSTRG.19389	-	Ca7	1.107	1.416	probable protein phosphatase 2C 39 isoform X3
440	MSTRG.19452	Ca_14559	Ca7	2.936	1.414	metalloendoproteinase 2-MMP-like
441	MSTRG.18458	Ca_06589	Ca7	4.349	1.366	calcium sensing receptor, chloroplastic
442	MSTRG.17624	Ca_20237	Ca7	5.135	1.335	pollen Ole e I family allergen
443	MSTRG.18791	Ca_09379	Ca7	4.016	1.321	basic helix loop helix (bHLH) DNA-binding family protein
444	MSTRG.18061	Ca_03042	Ca7	4.873	1.295	invertase inhibitor-like protein
445	MSTRG.20135	Ca_13740	Ca7	5.065	1.274	cytochrome P450 86A8
446	MSTRG.19088	Ca_09932	Ca7	3.597	1.208	UPF0548 protein At2g17695
447	MSTRG.19779	Ca_10131	Ca7	6.201	1.198	stem 28 kDa glycoprotein
448	MSTRG.18292	Ca_06731	Ca7	3.623	1.198	heparanase-like protein 3
449	MSTRG.20163	Ca_13780	Ca7	6.329	1.193	remorin-like
450	MSTRG.18542	Ca_13162	Ca7	6.141	1.170	ribulose-phosphate 3-epimerase, chloroplastic
451	MSTRG.18748	Ca_12811	Ca7	4.967	1.155	BOI-related E3 ubiquitin-protein ligase 1 isoform X1
452	MSTRG.17789	Ca_03294	Ca7	6.291	1.135	WAT1-related protein At4g28040
453	MSTRG.17625	Ca_20236	Ca7	4.283	1.130	acyl carrier protein 3, mitochondrial
454	MSTRG.18094	Ca_03009	Ca7	4.728	1.087	probable bifunctional TENA-E protein
455	MSTRG.19383	Ca_14480	Ca7	2.700	1.036	transmembrane protein, putative
456	MSTRG.19538	Ca_23631	Ca7	7.466	-1.142	indole-3-acetic acid-amido synthetase GH3.6
457	MSTRG.18211	Ca_06803	Ca7	7.956	-1.183	protein DMP2-like
458	MSTRG.18927	Ca_09239	Ca7	6.628	-1.228	L-ascorbate oxidase homolog
459	MSTRG.18745	Ca_12808	Ca7	6.871	-1.298	beta-amylase 3, chloroplastic
460	MSTRG.19904	Ca_10012	Ca7	3.521	-1.348	growth-regulating factor 5
461	MSTRG.18666	Ca_17294	Ca7	3.387	-1.478	triose phosphate/phosphate translocator, non-green plastid, chloroplastic
462	MSTRG.17910	Ca_03188	Ca7	4.452	-1.492	pathogen-associated molecular patterns-induced protein A70
463	MSTRG.17870	Ca_03224	Ca7	3.695	-1.622	DUF4228 domain protein
464	MSTRG.18354	Ca_06679	Ca7	2.797	-1.632	equilibrative nucleotide transporter 8
465	MSTRG.18949	Ca_16020	Ca7	1.661	-1.659	DUF4228 domain protein
466	MSTRG.17978	Ca_03124	Ca7	2.267	-1.761	pectinesterase inhibitor 3
467	MSTRG.19738	Ca_11697	Ca7	3.460	-1.874	beta-amyrin 11-oxidase-like
468	MSTRG.20484	-	Ca7	2.138	-1.891	glycosyltransferase family 4 protein
469	MSTRG.18229	Ca_06784	Ca7	3.872	-1.892	binding protein
470	MSTRG.20252	-	Ca7	1.672	-2.329	cytochrome P450 704C1-like
471	MSTRG.19236	Ca_15845	Ca7	6.483	-2.616	CTP synthase-like
472	MSTRG.19903	Ca_10011	Ca7	3.835	-3.012	germin-like protein subfamily 3 member 1
473	MSTRG.19109	-	Ca7	1.356	-3.040	dirigent protein 19-like
474	MSTRG.19737	Ca_11698	Ca7	2.103	-3.491	beta-amyrin 11-oxidase-like
475	MSTRG.19669	-	Ca7	-0.088	-4.252	gag-pol polyprotein
476	MSTRG.20566	Ca_11914	Ca8	-0.386	3.211	putative Late embryogenesis abundant protein, LEA5-type
477	MSTRG.21643	Ca_19746	Ca8	4.605	2.056	alpha-galactosidase-like isoform X2
478	MSTRG.20845	Ca_02336	Ca8	2.276	1.462	VAN3-binding protein
479	MSTRG.20897	Ca_02282	Ca8	3.774	1.395	peroxidase 20
480	MSTRG.21270	Ca_23578	Ca8	4.818	1.346	thiosulfate sulfurtransferase 16, chloroplastic-like isoform X2
481	MSTRG.20640	Ca_11845	Ca8	6.415	1.345	non-specific lipid-transfer protein-like protein At2g13820

482	MSTRG.20941	Ca_02236	Ca8	2.824	1.299	galactomannan galactosyltransferase 1-like
483	MSTRG.21830	Ca_13001	Ca8	4.071	1.289	transmembrane protein, putative
484	MSTRG.21426	Ca_10604	Ca8	4.067	1.224	histone-lysine N-methyltransferase ASHR2
485	MSTRG.20948	Ca_02229	Ca8	6.888	1.105	ADP-ribosylation factor-like protein 8a
486	MSTRG.20846	Ca_02335	Ca8	4.134	1.098	phosphatidylserine decarboxylase proenzyme 1, mitochondrial
487	MSTRG.21543	Ca_11538	Ca8	3.013	1.008	protein BRICK 1
488	MSTRG.21220	Ca_01965	Ca8	3.675	-1.225	vacuolar protein
489	MSTRG.21225	Ca_01961	Ca8	3.456	-1.362	protein NUCLEAR FUSION DEFECTIVE 4-like
490	MSTRG.21505	Ca_11501	Ca8	6.563	-1.384	cinnamoyl-CoA reductase-like SNL6
491	MSTRG.21711	Ca_23843	Ca8	1.796	-1.488	TMV resistance protein N
492	MSTRG.20774	Ca_02410	Ca8	1.628	-1.513	protein DETOXIFICATION 49
493	MSTRG.21551	Ca_11546	Ca8	5.127	-1.521	probable mannitol dehydrogenase
494	MSTRG.21928	Ca_17872	Ca8	3.814	-1.561	2-oxoglutarate-Fe(II) type oxidoreductase hxnY-like isoform X1
495	MSTRG.21282	Ca_23585	Ca8	5.211	-1.996	lysine histidine transporter-like 8
496	MSTRG.21859	Ca_12980	Ca8	2.679	-2.121	probable sulfate transporter 3.5
497	MSTRG.21862	Ca_12972	Ca8	1.003	-2.399	Aldehyde dehydrogenase family 2 member C4
498	MSTRG.21043	Ca_02137	Ca8	6.402	-2.492	patatin-like protein 1
499	MSTRG.20598	Ca_11885	Ca8	3.513	-2.825	2-hydroxyisoflavanone dehydratase
500	MSTRG.20599	-	Ca8	-0.461	-3.073	2-hydroxyisoflavanone dehydratase-like
501	MSTRG.20990	Ca_02185	Ca8	1.047	-3.329	cytochrome P450 81E8-like
502	MSTRG.22037	-	scaffold1006	4.774	-1.378	nucleotide-diphospho-sugar transferase family protein
503	MSTRG.22025	-	scaffold1006	0.752	-2.297	probable cyclic nucleotide-gated ion channel 20, chloroplastic isoform X2
504	MSTRG.22243	-	scaffold109_1	1.619	1.702	RING-H2 finger protein ATL52-like
505	MSTRG.22297	Ca_26366	scaffold1145	4.894	-1.378	glycosyltransferase family 2 protein
506	MSTRG.22390	Ca_22967	scaffold12	1.901	1.824	ABC transporter A family member 7-like protein
507	MSTRG.22455	Ca_21437	scaffold128	3.811	1.365	protein PYRICULARIA ORYZAE RESISTANCE 21-like
508	MSTRG.22493	-	scaffold1301_1	4.306	3.779	heavy metal-associated isoprenylated plant protein 24
509	MSTRG.22550	Ca_19763	scaffold1324	4.009	1.659	E3 ubiquitin-protein ligase ATL6-like
510	MSTRG.22571	Ca_19787	scaffold1324	4.048	1.590	probable methyltransferase PMT16
511	MSTRG.22578	-	scaffold134	1.256	2.185	transmembrane protein, putative
512	MSTRG.22590	Ca_22590	scaffold134	3.541	-2.491	G-type lectin S-receptor-like serine/threonine-protein kinase
513	MSTRG.22691	-	scaffold1348_1	4.451	2.783	probable pectate lyase 18
514	MSTRG.22638	-	scaffold1348_1	1.948	1.328	BAG family molecular chaperone regulator 1-like isoform X1
515	MSTRG.22741	Ca_21993	scaffold1351	4.204	1.158	probable pectate lyase 12
516	MSTRG.22792	-	scaffold1417	1.071	2.257	hypothetical protein GLYMA_19G093700
517	MSTRG.22830	Ca_23660	scaffold1439	2.668	1.277	uncharacterized protein LOC101503058 isoform X1
518	MSTRG.22870	Ca_24090	scaffold1504	1.060	3.024	cysteine/histidine-rich C1 domain protein
519	MSTRG.22904	Ca_23862	scaffold1545	3.254	2.776	protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 7-like
520	MSTRG.22919	Ca_21064	scaffold157	6.635	1.183	isoliquiritigenin 2'-O-methyltransferase-like
521	MSTRG.22932	Ca_21083	scaffold157	-0.075	-1.850	glucan endo-1,3-beta-glucosidase 8
522	MSTRG.22943	-	scaffold1580	0.808	2.735	---NA---
523	MSTRG.22959	Ca_20809	scaffold1580	1.754	1.425	Ankyrin repeat-containing protein
524	MSTRG.22997	Ca_24188	scaffold1659	1.981	2.149	protein PELPK1
525	MSTRG.23096	Ca_21708	scaffold174	3.236	1.032	transmembrane protein, putative

526	MSTRG.23246	Ca_24715	scaffold1918	5.054	-1.903	trehalose-phosphate phosphatase A
527	MSTRG.23254	Ca_25164	scaffold193	3.231	-1.794	receptor-like protein EIX2
528	MSTRG.23292	Ca_25214	scaffold1964	2.810	-2.071	mitochondrial phosphate carrier protein 3, mitochondrial-like
529	MSTRG.23346	Ca_26673	scaffold1991	5.428	1.259	chromosome condensation regulator RCC1 repeat protein
530	MSTRG.23345	Ca_24935	scaffold2	-2.589	-7.480	protein transport Sec1a
531	MSTRG.23359	Ca_26286	scaffold2027	3.169	1.784	GDSL esterase/lipase At2g03980-like
532	MSTRG.23374	Ca_26067	scaffold2036	5.905	1.334	omega-hydroxypalmitate O-feruloyl transferase
533	MSTRG.23402	-	scaffold206	3.516	-3.312	uncharacterized protein LOC106766073
534	MSTRG.23474	Ca_27612	scaffold221	6.518	1.115	oxalate--CoA ligase-like
535	MSTRG.23536	Ca_26079	scaffold235	5.805	-2.481	probable trehalose-phosphate phosphatase C
536	MSTRG.23575	-	scaffold2373	5.581	2.000	BURP domain-containing protein BNM2A-like
537	MSTRG.23615	Ca_22270	scaffold242	4.287	1.245	remorin 4.1
538	MSTRG.23656	Ca_22991	scaffold2575	3.497	1.407	protein ABA DEFICIENT 4, chloroplastic-like isoform X2
539	MSTRG.23685	Ca_21869	scaffold2617	4.103	1.699	UDP-glycosyltransferase 1
540	MSTRG.23719	Ca_26034	scaffold2720	2.974	-1.966	probable pectinesterase/pectinesterase inhibitor 33
541	MSTRG.23792	Ca_20600	scaffold284	7.728	-1.488	nitrate reductase [NADH] 2
542	MSTRG.23907	Ca_25903	scaffold305	5.714	1.397	glycerol-3-phosphate 2-O-acyltransferase 6
543	MSTRG.23932	-	scaffold308_2	3.484	1.116	uncharacterized protein LOC101489918
544	MSTRG.23954	Ca_21808	scaffold314	3.732	1.296	ABC transporter G family member 23
545	MSTRG.23963	-	scaffold314	0.131	-3.054	---NA---
546	MSTRG.24182	Ca_25858	scaffold36	4.409	2.067	triacylglycerol lipase 2
547	MSTRG.24282	Ca_23555	scaffold396	2.151	1.896	Heptahelical transmembrane protein 2
548	MSTRG.24435	-	scaffold421_2	2.246	-1.422	zinc ion-binding protein
549	MSTRG.24449	Ca_26259	scaffold435	3.627	1.270	disease resistance response protein
550	MSTRG.24562	Ca_23568	scaffold48	1.733	-1.256	putative calcium-transporting ATPase 11, plasma membrane-type
551	MSTRG.24723	Ca_23286	scaffold537	5.549	2.264	expansin-B3
552	MSTRG.24758	Ca_23922	scaffold545	2.801	-2.054	mitochondrial uncoupling protein 1
553	MSTRG.24836	-	scaffold5792	3.394	1.035	DExH-box ATP-dependent RNA helicase DExH15 chloroplastic
554	MSTRG.24968	-	scaffold6458	1.827	-3.191	digestive organ expansion factor-like protein
555	MSTRG.25044	Ca_23199	scaffold682	6.301	1.115	oxalate--CoA ligase-like
556	MSTRG.25099	Ca_23807	scaffold731	5.592	-1.242	lysine histidine transporter 1
557	MSTRG.25151	Ca_23410	scaffold775	8.882	-2.353	Pectinesterase 2
558	MSTRG.25179	Ca_27918	scaffold7887	3.908	1.589	protein trichome birefringence-like 19
559	MSTRG.25285	Ca_24203	scaffold864	5.393	1.537	GDSL esterase/lipase At1g74460
560	MSTRG.25345	Ca_22178	scaffold88	4.758	3.674	methylecgonone reductase-like
561	MSTRG.25410	-	scaffold895	4.352	1.517	glycoside hydrolase family 1 protein
562	MSTRG.25496	Ca_25673	scaffold924	1.227	1.834	UDP-glycosyltransferase 1
563	MSTRG.25493	-	scaffold924	0.286	-2.393	heavy metal-associated isoprenylated plant protein 39
564	MSTRG.25587	Ca_21401	scaffold98	2.326	-1.662	DUF4228 domain protein

Supplementary Table 8: PRR resistance genes in PRR resistant breeding line 04067-81-2-1-1 (Bc-C) differently expressed under control condition compared to PRR susceptible genotype Rupali

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)
1	MSTRG.2	-	C11044824	1.436	1.586
2	MSTRG.7	-	C11047824	-0.992	7.697
3	MSTRG.6	-	C11048020	-0.407	6.172
4	MSTRG.55	-	C11086496	3.924	-2.118
5	MSTRG.61	-	C11096254	-0.047	2.288
6	MSTRG.71	-	C11103858	-0.133	5.559
7	MSTRG.78	Ca_27990	C11107558	-4.665	-6.447
8	MSTRG.89	Ca_27884	C11124530	2.244	-1.220
9	MSTRG.95	Ca_28135	C11132160	0.898	-1.214
10	MSTRG.101	-	C11137434	0.305	-1.542
11	MSTRG.105	Ca_27911	C11140974	0.260	1.924
12	MSTRG.133	Ca_27905	C11159552	0.195	1.307
13	MSTRG.136	-	C11161176	4.213	1.504
14	MSTRG.148	-	C11165420	-0.323	-9.438
15	MSTRG.156	-	C11165890	-2.650	-3.892
16	MSTRG.164	Ca_27556	C11172910	4.687	-1.187
17	MSTRG.174	Ca_28257	C11177172	4.151	1.105
18	MSTRG.2521	-	Ca1	0.388	-8.573
19	MSTRG.2282	Ca_18302	Ca1	0.862	-7.670
20	MSTRG.2269	Ca_18312	Ca1	-1.715	-6.991
21	MSTRG.1062	-	Ca1	-4.378	-6.957
22	MSTRG.2568	-	Ca1	0.391	-6.333
23	MSTRG.2495	Ca_19441	Ca1	1.593	-6.117
24	MSTRG.2713	-	Ca1	-1.934	-6.051
25	MSTRG.2519	-	Ca1	2.093	-5.931
26	MSTRG.513	Ca_00310	Ca1	2.493	-5.857
27	MSTRG.2569	-	Ca1	-1.829	-5.845
28	MSTRG.2736	-	Ca1	-1.526	-5.786
29	MSTRG.2981	-	Ca1	-2.358	-5.697
30	MSTRG.2661	-	Ca1	-0.972	-5.538
31	MSTRG.2558	-	Ca1	1.980	-5.434
32	MSTRG.2235	-	Ca1	-1.048	-4.963
33	MSTRG.2365	-	Ca1	-1.528	-4.632
34	MSTRG.2829	-	Ca1	-1.175	-4.523
35	MSTRG.2936	Ca_21552	Ca1	-1.451	-4.313

36	MSTRG.2832	-	Ca1	-0.953	-4.185
37	MSTRG.2935	-	Ca1	1.559	-4.002
38	MSTRG.2738	Ca_25799	Ca1	-1.016	-3.764
39	MSTRG.2234	-	Ca1	-0.470	-3.762
40	MSTRG.2504	-	Ca1	-2.240	-3.317
41	MSTRG.2861	Ca_13532	Ca1	2.948	-3.202
42	MSTRG.2454	-	Ca1	1.995	-2.995
43	MSTRG.1002	Ca_07992	Ca1	-0.233	-2.893
44	MSTRG.2694	-	Ca1	8.317	-2.730
45	MSTRG.2224	-	Ca1	0.843	-2.607
46	MSTRG.2417	-	Ca1	0.792	-2.555
47	MSTRG.1260	Ca_02785	Ca1	0.585	-2.275
48	MSTRG.2817	-	Ca1	-0.826	-2.226
49	MSTRG.2286	Ca_25078	Ca1	4.267	-2.206
50	MSTRG.1321	Ca_02716	Ca1	0.566	-2.183
51	MSTRG.438	Ca_00232	Ca1	1.167	-2.105
52	MSTRG.2204	Ca_22350	Ca1	0.202	-2.036
53	MSTRG.1985	-	Ca1	-0.019	-2.035
54	MSTRG.2451	Ca_22454	Ca1	5.007	-1.992
55	MSTRG.2436	Ca_22469	Ca1	1.531	-1.990
56	MSTRG.2581	Ca_21824	Ca1	1.566	-1.978
57	MSTRG.346	Ca_00144	Ca1	2.336	-1.922
58	MSTRG.2478	-	Ca1	1.609	-1.836
59	MSTRG.2481	Ca_26129	Ca1	2.253	-1.815
60	MSTRG.2595	Ca_21844	Ca1	4.725	-1.754
61	MSTRG.1792	Ca_07045	Ca1	1.914	-1.716
62	MSTRG.2770	-	Ca1	-0.501	-1.632
63	MSTRG.806	Ca_00614	Ca1	1.042	-1.610
64	MSTRG.2695	Ca_18459	Ca1	-0.557	-1.605
65	MSTRG.2703	-	Ca1	0.560	-1.562
66	MSTRG.858	Ca_00679	Ca1	4.002	-1.538
67	MSTRG.2559	Ca_21686	Ca1	1.140	-1.538
68	MSTRG.2585	Ca_21834	Ca1	3.719	-1.528
69	MSTRG.1540	-	Ca1	2.723	-1.517
70	MSTRG.2274	Ca_18308	Ca1	2.093	-1.510
71	MSTRG.536	Ca_00332	Ca1	2.183	-1.500
72	MSTRG.2881	Ca_26558	Ca1	0.441	-1.440

73	MSTRG.1254	Ca_02789	Ca1	2.867	-1.432
74	MSTRG.829	Ca_00647	Ca1	2.031	-1.421
75	MSTRG.789	Ca_00599	Ca1	4.672	-1.419
76	MSTRG.2256	Ca_18328	Ca1	2.953	-1.415
77	MSTRG.2257	-	Ca1	-0.426	-1.411
78	MSTRG.370	Ca_00164	Ca1	6.365	-1.353
79	MSTRG.2961	Ca_12939	Ca1	3.652	-1.343
80	MSTRG.596	Ca_00391	Ca1	2.262	-1.315
81	MSTRG.1436	Ca_02610	Ca1	4.038	-1.262
82	MSTRG.2622	Ca_13969	Ca1	3.688	-1.261
83	MSTRG.2307	Ca_18599	Ca1	3.151	-1.257
84	MSTRG.2680	-	Ca1	2.522	-1.242
85	MSTRG.581	-	Ca1	1.103	-1.206
86	MSTRG.1189	Ca_02857	Ca1	4.532	-1.203
87	MSTRG.2259	Ca_18325	Ca1	0.374	-1.202
88	MSTRG.286	Ca_00092	Ca1	-0.445	-1.200
89	MSTRG.1322	-	Ca1	0.768	-1.200
90	MSTRG.1723	Ca_07108	Ca1	0.575	-1.181
91	MSTRG.2300	Ca_18588	Ca1	3.907	-1.171
92	MSTRG.2987	Ca_12914	Ca1	6.806	-1.171
93	MSTRG.1105	Ca_02940	Ca1	1.761	-1.141
94	MSTRG.2702	-	Ca1	0.599	-1.139
95	MSTRG.397	Ca_00188	Ca1	4.461	-1.135
96	MSTRG.2693	Ca_18460	Ca1	13.442	-1.127
97	MSTRG.283	Ca_00089	Ca1	2.871	-1.123
98	MSTRG.2620	Ca_13970	Ca1	2.124	-1.117
99	MSTRG.198	Ca_00004	Ca1	2.035	-1.096
100	MSTRG.830	Ca_00648	Ca1	2.837	-1.096
101	MSTRG.743	Ca_00551	Ca1	7.698	-1.096
102	MSTRG.1928	Ca_06901	Ca1	0.699	-1.071
103	MSTRG.1473	Ca_02568	Ca1	5.053	-1.069
104	MSTRG.2324	-	Ca1	2.678	-1.011
105	MSTRG.2992	Ca_12908	Ca1	4.693	1.042
106	MSTRG.997	Ca_07988	Ca1	5.582	1.045
107	MSTRG.2118	-	Ca1	1.319	1.054
108	MSTRG.376	Ca_00171	Ca1	5.530	1.067
109	MSTRG.197	-	Ca1	2.291	1.069

110	MSTRG.486	Ca_00281	Ca1	3.724	1.075
111	MSTRG.1755	-	Ca1	5.201	1.076
112	MSTRG.485	-	Ca1	1.374	1.098
113	MSTRG.514	Ca_00311	Ca1	5.132	1.115
114	MSTRG.2290	Ca_18581	Ca1	2.941	1.122
115	MSTRG.2786	-	Ca1	-0.167	1.138
116	MSTRG.2745	-	Ca1	3.553	1.140
117	MSTRG.2394	Ca_18504	Ca1	5.545	1.156
118	MSTRG.861	Ca_00682	Ca1	4.937	1.156
119	MSTRG.962	Ca_07957	Ca1	2.023	1.169
120	MSTRG.2339	Ca_20295	Ca1	1.993	1.176
121	MSTRG.2691	Ca_18464	Ca1	6.613	1.177
122	MSTRG.1273	Ca_02773	Ca1	1.451	1.199
123	MSTRG.2233	Ca_19292	Ca1	4.247	1.202
124	MSTRG.2822	-	Ca1	1.694	1.208
125	MSTRG.555	Ca_00351	Ca1	3.318	1.229
126	MSTRG.1335	Ca_02701	Ca1	5.788	1.293
127	MSTRG.1566	Ca_02472	Ca1	2.560	1.309
128	MSTRG.1461	-	Ca1	2.143	1.320
129	MSTRG.377	-	Ca1	2.047	1.327
130	MSTRG.586	Ca_00378	Ca1	3.557	1.340
131	MSTRG.2288	Ca_18578	Ca1	4.850	1.356
132	MSTRG.2678	Ca_18449	Ca1	1.131	1.363
133	MSTRG.1055	Ca_08045	Ca1	3.696	1.373
134	MSTRG.1671	Ca_14129	Ca1	7.259	1.374
135	MSTRG.2272	Ca_18313	Ca1	1.753	1.377
136	MSTRG.2232	Ca_19294	Ca1	5.155	1.383
137	MSTRG.1741	-	Ca1	3.161	1.402
138	MSTRG.2740	-	Ca1	-0.797	1.404
139	MSTRG.630	Ca_00428	Ca1	2.004	1.407
140	MSTRG.1601	Ca_14067	Ca1	-0.152	1.410
141	MSTRG.2054	Ca_14725	Ca1	4.293	1.433
142	MSTRG.412	Ca_00207	Ca1	2.749	1.448
143	MSTRG.1607	-	Ca1	3.449	1.452
144	MSTRG.961	Ca_07956	Ca1	6.026	1.457
145	MSTRG.2662	Ca_18440	Ca1	1.966	1.460
146	MSTRG.937	-	Ca1	0.044	1.473

147	MSTRG.907	Ca_07899	Ca1	3.951	1.547
148	MSTRG.2514	Ca_25476	Ca1	5.516	1.564
149	MSTRG.3010	Ca_12885	Ca1	0.397	1.604
150	MSTRG.2194	Ca_20618	Ca1	1.423	1.612
151	MSTRG.2637	Ca_13958	Ca1	3.181	1.635
152	MSTRG.3007	Ca_12888	Ca1	8.522	1.635
153	MSTRG.550	-	Ca1	-0.069	1.637
154	MSTRG.746	Ca_00559	Ca1	4.591	1.649
155	MSTRG.305	Ca_00107	Ca1	-0.347	1.694
156	MSTRG.2701	Ca_18472	Ca1	2.175	1.699
157	MSTRG.2227	-	Ca1	-0.314	1.718
158	MSTRG.410	Ca_00205	Ca1	1.282	1.733
159	MSTRG.675	Ca_00482	Ca1	4.482	1.737
160	MSTRG.2110	Ca_17347	Ca1	4.655	1.755
161	MSTRG.639	Ca_00437	Ca1	3.717	1.789
162	MSTRG.2790	-	Ca1	-0.934	1.806
163	MSTRG.2189	Ca_20626	Ca1	2.838	1.827
164	MSTRG.1442	Ca_02605	Ca1	2.416	1.841
165	MSTRG.1008	Ca_07996	Ca1	7.677	1.888
166	MSTRG.1549	-	Ca1	2.582	1.901
167	MSTRG.2941	-	Ca1	4.958	1.938
168	MSTRG.2278	Ca_18303	Ca1	1.406	1.945
169	MSTRG.1045	Ca_08031	Ca1	5.160	2.000
170	MSTRG.200	-	Ca1	0.328	2.020
171	MSTRG.2950	Ca_12950	Ca1	4.318	2.028
172	MSTRG.1680	Ca_14144	Ca1	4.985	2.106
173	MSTRG.2679	Ca_18450	Ca1	2.789	2.156
174	MSTRG.1830	Ca_07000	Ca1	1.361	2.182
175	MSTRG.2834	Ca_13562	Ca1	5.237	2.272
176	MSTRG.2980	-	Ca1	0.100	2.307
177	MSTRG.1410	Ca_02630	Ca1	3.104	2.649
178	MSTRG.2986	Ca_12915	Ca1	-0.577	2.761
179	MSTRG.2908	-	Ca1	-2.458	2.869
180	MSTRG.777	-	Ca1	2.814	2.895
181	MSTRG.2192	Ca_20624	Ca1	3.370	2.905
182	MSTRG.577	-	Ca1	-0.867	2.974
183	MSTRG.549	Ca_00345	Ca1	2.258	3.059

184	MSTRG.1907	-	Ca1	-0.993	3.104
185	MSTRG.1561	-	Ca1	-0.489	3.149
186	MSTRG.2640	Ca_13939	Ca1	3.021	3.242
187	MSTRG.2610	Ca_23542	Ca1	3.243	3.336
188	MSTRG.2122	Ca_08869	Ca1	1.001	3.385
189	MSTRG.2129	-	Ca1	0.608	3.414
190	MSTRG.1906	Ca_06919	Ca1	-0.835	3.417
191	MSTRG.1059	-	Ca1	-0.163	3.497
192	MSTRG.2460	-	Ca1	0.727	3.511
193	MSTRG.2552	-	Ca1	1.654	3.558
194	MSTRG.2825	Ca_13567	Ca1	3.102	3.587
195	MSTRG.552	-	Ca1	2.723	3.609
196	MSTRG.2714	-	Ca1	4.366	3.638
197	MSTRG.471	Ca_00264	Ca1	1.257	3.680
198	MSTRG.2715	Ca_18485	Ca1	8.362	3.686
199	MSTRG.1558	Ca_02477	Ca1	-0.298	3.721
200	MSTRG.2119	Ca_17339	Ca1	4.374	3.954
201	MSTRG.1993	-	Ca1	-0.752	3.997
202	MSTRG.470	Ca_00263	Ca1	2.194	4.184
203	MSTRG.2183	Ca_20633	Ca1	-0.466	4.204
204	MSTRG.1548	Ca_02491	Ca1	3.682	4.363
205	MSTRG.466	Ca_00258	Ca1	3.954	4.381
206	MSTRG.2429	-	Ca1	-2.402	4.562
207	MSTRG.2485	-	Ca1	-2.876	4.580
208	MSTRG.2100	-	Ca1	-2.457	4.668
209	MSTRG.2549	Ca_26097	Ca1	-1.698	4.821
210	MSTRG.543	Ca_00340	Ca1	2.350	5.064
211	MSTRG.902	Ca_07897	Ca1	-1.317	5.115
212	MSTRG.2463	Ca_21847	Ca1	0.807	5.759
213	MSTRG.2489	-	Ca1	-3.315	6.004
214	MSTRG.2541	-	Ca1	-4.199	6.094
215	MSTRG.2970	-	Ca1	-2.402	6.528
216	MSTRG.2487	-	Ca1	-2.920	6.557
217	MSTRG.2364	Ca_25066	Ca1	-0.152	6.962
218	MSTRG.3018	-	Ca1	-2.967	6.964
219	MSTRG.201	-	Ca1	-1.496	7.079
220	MSTRG.2551	Ca_26100	Ca1	-2.300	7.306

221	MSTRG.289	-	Ca1	-3.966	7.548
222	MSTRG.2488	-	Ca1	-3.961	8.296
223	MSTRG.2506	Ca_25472	Ca1	-3.311	8.823
224	MSTRG.2434	Ca_24388	Ca1	-3.566	8.897
225	MSTRG.2710	-	Ca1	-3.638	8.976
226	MSTRG.1344	Ca_02690	Ca1	-0.527	10.094
227	MSTRG.3412	-	Ca2	-2.924	-6.545
228	MSTRG.3969	-	Ca2	-2.074	-4.982
229	MSTRG.4471	-	Ca2	-1.110	-3.309
230	MSTRG.4446	Ca_16100	Ca2	1.058	-2.628
231	MSTRG.4627	-	Ca2	0.231	-2.575
232	MSTRG.4395	Ca_14332	Ca2	0.604	-2.386
233	MSTRG.4628	Ca_10285	Ca2	5.022	-2.382
234	MSTRG.3170	Ca_12587	Ca2	6.982	-2.227
235	MSTRG.4677	Ca_10238	Ca2	5.002	-2.071
236	MSTRG.3168	Ca_12588	Ca2	6.745	-1.940
237	MSTRG.4558	Ca_12429	Ca2	4.128	-1.852
238	MSTRG.3390	-	Ca2	3.679	-1.848
239	MSTRG.5008	Ca_09817	Ca2	5.719	-1.729
240	MSTRG.4572	-	Ca2	2.116	-1.619
241	MSTRG.4949	-	Ca2	0.189	-1.548
242	MSTRG.4553	Ca_12434	Ca2	-0.777	-1.537
243	MSTRG.3976	-	Ca2	0.528	-1.507
244	MSTRG.4993	-	Ca2	3.976	-1.454
245	MSTRG.3878	Ca_11634	Ca2	0.209	-1.398
246	MSTRG.4361	-	Ca2	1.345	-1.397
247	MSTRG.3117	Ca_12633	Ca2	3.705	-1.355
248	MSTRG.3067	Ca_16983	Ca2	3.024	-1.268
249	MSTRG.3808	Ca_18069	Ca2	2.616	-1.243
250	MSTRG.3807	Ca_18067	Ca2	2.962	-1.179
251	MSTRG.3082	-	Ca2	-1.029	-1.177
252	MSTRG.3394	Ca_21102	Ca2	4.391	-1.155
253	MSTRG.4625	Ca_10290	Ca2	3.687	-1.125
254	MSTRG.5019	Ca_09828	Ca2	0.047	-1.122
255	MSTRG.4952	-	Ca2	1.041	-1.096
256	MSTRG.3136	Ca_12620	Ca2	0.873	-1.093
257	MSTRG.3164	Ca_12593	Ca2	0.654	-1.058

258	MSTRG.4906	Ca_09712	Ca2	0.976	-1.038
259	MSTRG.4840	Ca_16887	Ca2	4.074	1.062
260	MSTRG.3155	Ca_12601	Ca2	6.617	1.074
261	MSTRG.4606	Ca_17819	Ca2	5.934	1.097
262	MSTRG.4658	-	Ca2	5.647	1.103
263	MSTRG.4413	Ca_16139	Ca2	3.968	1.117
264	MSTRG.4492	Ca_12501	Ca2	6.786	1.120
265	MSTRG.3278	Ca_10545	Ca2	5.858	1.130
266	MSTRG.4637	-	Ca2	1.606	1.131
267	MSTRG.4631	Ca_10280	Ca2	4.227	1.151
268	MSTRG.4367	Ca_14360	Ca2	7.057	1.152
269	MSTRG.3386	Ca_21108	Ca2	6.073	1.193
270	MSTRG.4608	Ca_17816	Ca2	1.256	1.226
271	MSTRG.4493	Ca_12500	Ca2	3.143	1.236
272	MSTRG.4427	Ca_16127	Ca2	4.003	1.245
273	MSTRG.4591	Ca_12421	Ca2	7.861	1.260
274	MSTRG.4541	Ca_12448	Ca2	5.250	1.274
275	MSTRG.4656	-	Ca2	-0.063	1.284
276	MSTRG.4674	Ca_10242	Ca2	6.212	1.306
277	MSTRG.4567	Ca_12419	Ca2	5.448	1.373
278	MSTRG.4885	Ca_09692	Ca2	5.095	1.462
279	MSTRG.3651	Ca_22309	Ca2	0.703	1.462
280	MSTRG.3213	Ca_12528	Ca2	8.899	1.485
281	MSTRG.3298	-	Ca2	1.076	1.488
282	MSTRG.4535	Ca_12456	Ca2	1.942	1.513
283	MSTRG.3321	Ca_10504	Ca2	4.804	1.518
284	MSTRG.4378	Ca_14344	Ca2	2.778	1.531
285	MSTRG.4988	Ca_09800	Ca2	6.730	1.538
286	MSTRG.3372	-	Ca2	3.858	1.574
287	MSTRG.3870	-	Ca2	0.097	1.591
288	MSTRG.4751	-	Ca2	5.317	1.621
289	MSTRG.3621	Ca_21470	Ca2	3.407	1.655
290	MSTRG.3433	Ca_14693	Ca2	5.480	1.677
291	MSTRG.3810	Ca_18071	Ca2	5.537	1.736
292	MSTRG.4421	Ca_16136	Ca2	3.158	1.745
293	MSTRG.4566	Ca_12420	Ca2	2.419	1.760
294	MSTRG.3800	Ca_18060	Ca2	4.454	1.776

295	MSTRG.4429	Ca_16126	Ca2	4.576	1.822
296	MSTRG.3630	Ca_21459	Ca2	-0.067	1.829
297	MSTRG.3259	Ca_10561	Ca2	5.158	1.886
298	MSTRG.3726	Ca_17586	Ca2	2.970	1.939
299	MSTRG.3306	Ca_10518	Ca2	2.829	2.153
300	MSTRG.4275	Ca_15646	Ca2	-0.053	2.219
301	MSTRG.3251	-	Ca2	2.624	2.278
302	MSTRG.3936	Ca_22037	Ca2	-1.285	2.327
303	MSTRG.3146	Ca_12610	Ca2	4.465	2.456
304	MSTRG.3482	Ca_19687	Ca2	3.735	2.467
305	MSTRG.3208	Ca_12535	Ca2	-0.467	2.495
306	MSTRG.4926	Ca_09731	Ca2	0.555	2.504
307	MSTRG.4602	Ca_17822	Ca2	1.807	2.832
308	MSTRG.4774	-	Ca2	1.372	2.985
309	MSTRG.4694	Ca_10219	Ca2	-0.149	3.516
310	MSTRG.4612	-	Ca2	-0.719	3.646
311	MSTRG.3467	Ca_14653	Ca2	1.392	3.663
312	MSTRG.4574	-	Ca2	-2.872	3.693
313	MSTRG.4765	-	Ca2	1.484	4.100
314	MSTRG.4016	-	Ca2	-0.352	4.785
315	MSTRG.3779	Ca_18775	Ca2	-3.173	6.656
316	MSTRG.4730	Ca_10186	Ca2	2.826	6.936
317	MSTRG.3772	-	Ca2	-3.078	8.239
318	MSTRG.4757	-	Ca2	-3.046	9.709
319	MSTRG.6227	Ca_08265	Ca3	-2.994	-10.466
320	MSTRG.5313	-	Ca3	-1.236	-8.514
321	MSTRG.5151	-	Ca3	-3.521	-8.335
322	MSTRG.6924	Ca_20879	Ca3	-4.149	-7.962
323	MSTRG.5460	Ca_22692	Ca3	-0.708	-5.742
324	MSTRG.5459	-	Ca3	-1.303	-5.404
325	MSTRG.7556	-	Ca3	-0.814	-5.381
326	MSTRG.7543	Ca_01273	Ca3	-2.029	-4.761
327	MSTRG.5368	Ca_18806	Ca3	0.628	-4.581
328	MSTRG.6963	-	Ca3	-1.764	-4.199
329	MSTRG.6962	-	Ca3	0.016	-3.992
330	MSTRG.6824	-	Ca3	0.732	-3.507
331	MSTRG.5488	-	Ca3	-0.261	-3.308

332	MSTRG.5317	Ca_25280	Ca3	1.306	-2.975
333	MSTRG.6714	-	Ca3	0.854	-2.959
334	MSTRG.6769	Ca_12274	Ca3	2.733	-2.882
335	MSTRG.6614	Ca_07348	Ca3	-0.511	-2.680
336	MSTRG.5510	-	Ca3	-1.109	-2.621
337	MSTRG.5458	-	Ca3	-0.902	-2.560
338	MSTRG.5291	-	Ca3	-0.780	-2.552
339	MSTRG.6615	-	Ca3	0.754	-2.433
340	MSTRG.6903	-	Ca3	-0.547	-2.329
341	MSTRG.5773	Ca_09449	Ca3	-1.503	-2.306
342	MSTRG.6703	-	Ca3	-0.239	-2.305
343	MSTRG.6678	Ca_12188	Ca3	0.848	-2.172
344	MSTRG.6747	-	Ca3	1.534	-2.153
345	MSTRG.6702	-	Ca3	2.097	-2.109
346	MSTRG.5939	-	Ca3	1.452	-2.066
347	MSTRG.5862	Ca_20430	Ca3	0.357	-2.064
348	MSTRG.6831	Ca_11993	Ca3	7.036	-2.058
349	MSTRG.6558	Ca_07298	Ca3	2.079	-2.012
350	MSTRG.7615	-	Ca3	0.878	-1.940
351	MSTRG.6698	-	Ca3	3.306	-1.926
352	MSTRG.7649	Ca_01366	Ca3	1.022	-1.916
353	MSTRG.7431	-	Ca3	1.396	-1.800
354	MSTRG.7617	Ca_01339	Ca3	2.918	-1.797
355	MSTRG.6570	Ca_07309	Ca3	4.154	-1.793
356	MSTRG.6694	Ca_12205	Ca3	2.109	-1.790
357	MSTRG.7424	Ca_01167	Ca3	1.305	-1.742
358	MSTRG.5393	-	Ca3	0.816	-1.738
359	MSTRG.5881	Ca_06279	Ca3	4.397	-1.703
360	MSTRG.6796	Ca_11961	Ca3	-0.830	-1.690
361	MSTRG.6251	-	Ca3	1.169	-1.646
362	MSTRG.7477	Ca_01220	Ca3	4.777	-1.540
363	MSTRG.5324	-	Ca3	0.008	-1.524
364	MSTRG.6788	-	Ca3	-0.554	-1.510
365	MSTRG.7217	Ca_00966	Ca3	3.815	-1.497
366	MSTRG.5149	-	Ca3	0.200	-1.479
367	MSTRG.6433	-	Ca3	3.428	-1.475
368	MSTRG.7467	Ca_01210	Ca3	5.087	-1.417

369	MSTRG.5771	Ca_09447	Ca3	3.281	-1.410
370	MSTRG.6668	Ca_07398	Ca3	1.634	-1.401
371	MSTRG.6607	Ca_07342	Ca3	1.505	-1.396
372	MSTRG.7623	-	Ca3	2.400	-1.339
373	MSTRG.7041	Ca_00790	Ca3	4.298	-1.320
374	MSTRG.7503	Ca_01242	Ca3	0.017	-1.309
375	MSTRG.6707	Ca_12213	Ca3	0.304	-1.300
376	MSTRG.6600	Ca_07338	Ca3	7.356	-1.267
377	MSTRG.7226	Ca_00974	Ca3	0.856	-1.253
378	MSTRG.7097	Ca_00844	Ca3	4.629	-1.229
379	MSTRG.5551	Ca_18266	Ca3	1.065	-1.204
380	MSTRG.5644	-	Ca3	3.567	-1.184
381	MSTRG.7518	Ca_01250	Ca3	3.843	-1.167
382	MSTRG.6975	Ca_00733	Ca3	4.461	-1.165
383	MSTRG.5666	Ca_19321	Ca3	1.189	-1.154
384	MSTRG.6762	Ca_12271	Ca3	3.475	-1.134
385	MSTRG.7460	Ca_01205	Ca3	2.818	-1.101
386	MSTRG.6951	-	Ca3	2.853	-1.089
387	MSTRG.5376	-	Ca3	0.506	-1.075
388	MSTRG.6643	Ca_07376	Ca3	3.087	-1.066
389	MSTRG.6122	Ca_06020	Ca3	2.566	-1.055
390	MSTRG.6771	Ca_12280	Ca3	2.552	-1.052
391	MSTRG.6640	Ca_07373	Ca3	1.824	-1.050
392	MSTRG.6822	Ca_11983	Ca3	3.855	-1.048
393	MSTRG.6803	Ca_11967	Ca3	1.161	-1.033
394	MSTRG.5873	Ca_20417	Ca3	7.693	-1.010
395	MSTRG.6152	Ca_05988	Ca3	7.090	-1.010
396	MSTRG.5491	Ca_22502	Ca3	2.162	-1.009
397	MSTRG.7089	-	Ca3	1.574	-1.005
398	MSTRG.6779	Ca_12288	Ca3	4.775	-1.000
399	MSTRG.7538	-	Ca3	2.617	1.001
400	MSTRG.6759	Ca_12269	Ca3	5.521	1.004
401	MSTRG.5792	-	Ca3	3.174	1.018
402	MSTRG.7537	Ca_01272	Ca3	2.981	1.022
403	MSTRG.7605	Ca_01329	Ca3	0.813	1.031
404	MSTRG.6732	Ca_12239	Ca3	3.202	1.056
405	MSTRG.6906	-	Ca3	0.406	1.065

406	MSTRG.5724	Ca_09400	Ca3	2.358	1.074
407	MSTRG.7304	Ca_01053	Ca3	2.222	1.106
408	MSTRG.7326	-	Ca3	5.271	1.109
409	MSTRG.5100	Ca_22148	Ca3	4.064	1.111
410	MSTRG.5687	-	Ca3	3.660	1.123
411	MSTRG.5600	Ca_23331	Ca3	3.962	1.135
412	MSTRG.5638	Ca_19627	Ca3	0.639	1.138
413	MSTRG.7399	Ca_01137	Ca3	0.623	1.154
414	MSTRG.6136	Ca_06003	Ca3	1.639	1.175
415	MSTRG.5884	Ca_06277	Ca3	5.166	1.184
416	MSTRG.5154	Ca_22383	Ca3	1.358	1.214
417	MSTRG.5987	Ca_06170	Ca3	5.292	1.215
418	MSTRG.6687	Ca_12196	Ca3	4.884	1.225
419	MSTRG.7031	Ca_00778	Ca3	2.778	1.226
420	MSTRG.7647	-	Ca3	1.241	1.228
421	MSTRG.7114	Ca_00867	Ca3	2.338	1.231
422	MSTRG.7662	-	Ca3	2.825	1.241
423	MSTRG.7461	Ca_01207	Ca3	3.845	1.255
424	MSTRG.6800	Ca_11962	Ca3	5.410	1.258
425	MSTRG.5270	Ca_16533	Ca3	4.579	1.271
426	MSTRG.7085	Ca_00833	Ca3	1.540	1.305
427	MSTRG.7639	Ca_01358	Ca3	3.177	1.318
428	MSTRG.6301	Ca_08194	Ca3	1.723	1.322
429	MSTRG.6876	-	Ca3	0.859	1.330
430	MSTRG.7245	-	Ca3	0.767	1.341
431	MSTRG.5045	Ca_22939	Ca3	4.234	1.343
432	MSTRG.7450	Ca_01195	Ca3	2.632	1.360
433	MSTRG.5465	Ca_25322	Ca3	2.439	1.365
434	MSTRG.5602	Ca_21116	Ca3	4.700	1.402
435	MSTRG.6481	Ca_07226	Ca3	3.045	1.403
436	MSTRG.5094	Ca_19393	Ca3	5.095	1.466
437	MSTRG.7062	-	Ca3	2.951	1.467
438	MSTRG.5525	Ca_17045	Ca3	3.801	1.487
439	MSTRG.7426	Ca_01170	Ca3	-0.707	1.490
440	MSTRG.6123	Ca_06014	Ca3	3.538	1.508
441	MSTRG.7362	-	Ca3	3.947	1.585
442	MSTRG.5859	Ca_20433	Ca3	2.173	1.634

443	MSTRG.7620	-	Ca3	1.102	1.663
444	MSTRG.5382	Ca_18820	Ca3	6.540	1.669
445	MSTRG.7156	Ca_00913	Ca3	7.486	1.718
446	MSTRG.7488	Ca_01230	Ca3	6.081	1.734
447	MSTRG.7025	Ca_00776	Ca3	5.371	1.772
448	MSTRG.6818	Ca_11980	Ca3	0.731	1.774
449	MSTRG.5631	Ca_19619	Ca3	4.895	1.793
450	MSTRG.5708	Ca_19354	Ca3	1.482	1.878
451	MSTRG.6952	Ca_00712	Ca3	0.189	1.893
452	MSTRG.5049	Ca_22936	Ca3	3.419	1.900
453	MSTRG.7309	Ca_01059	Ca3	5.019	2.015
454	MSTRG.5803	Ca_09478	Ca3	0.467	2.091
455	MSTRG.5125	-	Ca3	1.106	2.148
456	MSTRG.6980	Ca_00737	Ca3	5.257	2.235
457	MSTRG.6635	-	Ca3	1.463	2.256
458	MSTRG.6895	Ca_12057	Ca3	4.673	2.361
459	MSTRG.5605	Ca_21120	Ca3	1.571	2.559
460	MSTRG.7563	Ca_01292	Ca3	3.693	2.586
461	MSTRG.6691	Ca_12198	Ca3	2.728	2.614
462	MSTRG.5633	Ca_19621	Ca3	2.756	2.753
463	MSTRG.5281	Ca_16514	Ca3	3.081	3.033
464	MSTRG.6610	Ca_07345	Ca3	-0.744	3.278
465	MSTRG.6448	-	Ca3	-0.293	3.442
466	MSTRG.5705	-	Ca3	4.530	3.445
467	MSTRG.6451	Ca_07196	Ca3	2.547	4.183
468	MSTRG.7468	-	Ca3	-3.156	4.315
469	MSTRG.6955	-	Ca3	-1.509	4.532
470	MSTRG.5358	-	Ca3	-2.760	5.697
471	MSTRG.6297	Ca_08196	Ca3	1.834	5.826
472	MSTRG.5432	-	Ca3	-4.057	6.181
473	MSTRG.5300	-	Ca3	-1.899	6.186
474	MSTRG.7013	-	Ca3	-4.043	6.280
475	MSTRG.6482	-	Ca3	-3.545	6.573
476	MSTRG.5730	-	Ca3	-3.213	6.715
477	MSTRG.6652	-	Ca3	-4.357	6.913
478	MSTRG.6544	-	Ca3	1.177	7.568
479	MSTRG.5298	-	Ca3	-3.846	7.786

480	MSTRG.7635	-	Ca3	-2.319	8.465
481	MSTRG.7699	Ca_07670	Ca4	1.014	-11.003
482	MSTRG.9167	-	Ca4	-1.511	-8.789
483	MSTRG.8569	Ca_08374	Ca4	-2.957	-7.310
484	MSTRG.9560	-	Ca4	-4.258	-6.294
485	MSTRG.7670	-	Ca4	-1.145	-5.476
486	MSTRG.10326	-	Ca4	-0.340	-5.323
487	MSTRG.9146	Ca_05635	Ca4	0.682	-4.572
488	MSTRG.8979	Ca_04534	Ca4	3.500	-3.970
489	MSTRG.10909	Ca_10786	Ca4	-1.760	-3.838
490	MSTRG.8829	-	Ca4	-1.644	-3.714
491	MSTRG.8655	-	Ca4	6.220	-3.504
492	MSTRG.10768	-	Ca4	-2.061	-3.480
493	MSTRG.8936	Ca_04492	Ca4	-1.885	-3.478
494	MSTRG.8963	Ca_04518	Ca4	2.476	-3.419
495	MSTRG.9240	-	Ca4	-1.140	-3.382
496	MSTRG.7714	Ca_07686	Ca4	1.129	-3.079
497	MSTRG.8616	Ca_08423	Ca4	2.141	-3.047
498	MSTRG.10111	Ca_14855	Ca4	2.898	-3.007
499	MSTRG.8914	Ca_04473	Ca4	2.570	-2.763
500	MSTRG.10959	-	Ca4	5.386	-2.749
501	MSTRG.8850	Ca_04405	Ca4	6.958	-2.737
502	MSTRG.8654	Ca_08456	Ca4	9.938	-2.341
503	MSTRG.8978	Ca_04533	Ca4	1.955	-2.271
504	MSTRG.8717	-	Ca4	2.337	-2.271
505	MSTRG.9104	Ca_04649	Ca4	4.537	-2.270
506	MSTRG.8553	-	Ca4	-0.202	-2.261
507	MSTRG.8904	Ca_04462	Ca4	4.353	-2.254
508	MSTRG.9022	Ca_04574	Ca4	5.540	-2.250
509	MSTRG.9383	Ca_05399	Ca4	1.595	-2.247
510	MSTRG.9020	-	Ca4	0.853	-2.224
511	MSTRG.7904	Ca_07872	Ca4	-1.608	-2.159
512	MSTRG.7697	Ca_07667	Ca4	0.260	-2.099
513	MSTRG.8422	Ca_03495	Ca4	0.745	-2.098
514	MSTRG.10215	Ca_15105	Ca4	3.523	-2.096
515	MSTRG.8398	Ca_03519	Ca4	-0.171	-2.060
516	MSTRG.8392	Ca_03525	Ca4	-0.456	-1.974

517	MSTRG.9213	Ca_05575	Ca4	2.124	-1.972
518	MSTRG.8186	Ca_03735	Ca4	6.039	-1.956
519	MSTRG.8948	Ca_04504	Ca4	-0.427	-1.895
520	MSTRG.9212	Ca_05576	Ca4	4.700	-1.889
521	MSTRG.10363	Ca_14909	Ca4	2.426	-1.862
522	MSTRG.10239	Ca_13140	Ca4	-0.911	-1.847
523	MSTRG.8856	Ca_04411	Ca4	2.828	-1.844
524	MSTRG.9205	Ca_05578	Ca4	1.979	-1.791
525	MSTRG.9719	-	Ca4	-0.351	-1.786
526	MSTRG.10191	Ca_15134	Ca4	-0.696	-1.781
527	MSTRG.8738	Ca_04309	Ca4	0.716	-1.776
528	MSTRG.9593	-	Ca4	-0.620	-1.719
529	MSTRG.9214	Ca_05574	Ca4	5.819	-1.696
530	MSTRG.8762	Ca_04335	Ca4	3.222	-1.614
531	MSTRG.10347	Ca_14927	Ca4	4.519	-1.613
532	MSTRG.10650	Ca_09136	Ca4	3.397	-1.595
533	MSTRG.8063	Ca_03852	Ca4	2.248	-1.527
534	MSTRG.9446	Ca_18620	Ca4	2.446	-1.521
535	MSTRG.10566	-	Ca4	5.191	-1.508
536	MSTRG.10313	Ca_13069	Ca4	0.688	-1.502
537	MSTRG.9093	Ca_04636	Ca4	10.515	-1.462
538	MSTRG.8957	-	Ca4	-0.281	-1.448
539	MSTRG.8592	-	Ca4	1.797	-1.400
540	MSTRG.7803	Ca_07768	Ca4	2.917	-1.398
541	MSTRG.9928	Ca_14166	Ca4	5.493	-1.358
542	MSTRG.7832	Ca_07799	Ca4	2.662	-1.356
543	MSTRG.8756	Ca_04327	Ca4	1.053	-1.354
544	MSTRG.9098	Ca_04643	Ca4	2.377	-1.352
545	MSTRG.10811	Ca_19262	Ca4	1.006	-1.347
546	MSTRG.7805	Ca_07770	Ca4	3.381	-1.337
547	MSTRG.8170	Ca_03750	Ca4	5.634	-1.332
548	MSTRG.9096	Ca_04642	Ca4	2.898	-1.324
549	MSTRG.9436	Ca_05353	Ca4	4.798	-1.312
550	MSTRG.8561	-	Ca4	-0.032	-1.310
551	MSTRG.9884	Ca_23178	Ca4	1.292	-1.298
552	MSTRG.10009	-	Ca4	-0.307	-1.283
553	MSTRG.8981	Ca_04537	Ca4	4.002	-1.276

554	MSTRG.9664	Ca_19059	Ca4	1.693	-1.263
555	MSTRG.7695	-	Ca4	-2.415	-1.256
556	MSTRG.9215	Ca_05573	Ca4	0.450	-1.238
557	MSTRG.7828	-	Ca4	0.529	-1.222
558	MSTRG.8688	Ca_08492	Ca4	6.248	-1.220
559	MSTRG.10003	Ca_15467	Ca4	4.662	-1.220
560	MSTRG.8377	Ca_03541	Ca4	2.245	-1.196
561	MSTRG.7871	Ca_07835	Ca4	2.720	-1.190
562	MSTRG.8055	Ca_03868	Ca4	3.601	-1.184
563	MSTRG.9763	Ca_14423	Ca4	2.331	-1.167
564	MSTRG.10776	Ca_18357	Ca4	0.804	-1.167
565	MSTRG.9778	Ca_14408	Ca4	0.868	-1.160
566	MSTRG.8652	Ca_08460	Ca4	2.351	-1.151
567	MSTRG.10685	Ca_09167	Ca4	0.377	-1.148
568	MSTRG.7848	Ca_07812	Ca4	4.770	-1.131
569	MSTRG.8139	-	Ca4	1.880	-1.129
570	MSTRG.8659	Ca_08465	Ca4	2.634	-1.124
571	MSTRG.10681	Ca_09164	Ca4	4.668	-1.109
572	MSTRG.9176	Ca_05606	Ca4	7.215	-1.097
573	MSTRG.9216	Ca_05572	Ca4	2.692	-1.088
574	MSTRG.9836	Ca_25308	Ca4	2.668	-1.073
575	MSTRG.9919	Ca_14160	Ca4	0.598	-1.069
576	MSTRG.8397	Ca_03520	Ca4	3.944	-1.068
577	MSTRG.9486	Ca_18657	Ca4	2.971	-1.051
578	MSTRG.7814	Ca_07781	Ca4	1.136	-1.050
579	MSTRG.9000	Ca_04557	Ca4	5.284	-1.039
580	MSTRG.9927	Ca_14170	Ca4	2.423	-1.033
581	MSTRG.10197	Ca_15126	Ca4	4.022	-1.028
582	MSTRG.10498	Ca_10934	Ca4	3.055	-1.014
583	MSTRG.8014	Ca_12148	Ca4	6.550	-1.012
584	MSTRG.8470	Ca_03442	Ca4	8.592	-1.010
585	MSTRG.10662	Ca_09148	Ca4	5.182	1.002
586	MSTRG.10676	Ca_09157	Ca4	8.558	1.011
587	MSTRG.9280	-	Ca4	0.755	1.028
588	MSTRG.10971	Ca_23020	Ca4	2.939	1.034
589	MSTRG.8599	Ca_08406	Ca4	5.176	1.040
590	MSTRG.9796	-	Ca4	0.635	1.061

591	MSTRG.8556	Ca_08363	Ca4	3.162	1.069
592	MSTRG.8268	Ca_03652	Ca4	4.319	1.071
593	MSTRG.10219	Ca_15098	Ca4	4.070	1.076
594	MSTRG.10420	Ca_11021	Ca4	2.865	1.081
595	MSTRG.9894	Ca_23164	Ca4	7.733	1.082
596	MSTRG.9133	Ca_05647	Ca4	3.245	1.111
597	MSTRG.10404	Ca_14865	Ca4	5.661	1.113
598	MSTRG.7706	Ca_07674	Ca4	1.155	1.114
599	MSTRG.9243	Ca_05546	Ca4	1.896	1.118
600	MSTRG.10085	Ca_20019	Ca4	7.332	1.123
601	MSTRG.7942	Ca_12085	Ca4	5.478	1.153
602	MSTRG.8525	-	Ca4	0.729	1.156
603	MSTRG.8530	Ca_08341	Ca4	6.094	1.158
604	MSTRG.10718	Ca_09200	Ca4	2.624	1.161
605	MSTRG.9708	Ca_20130	Ca4	6.429	1.167
606	MSTRG.9062	Ca_04614	Ca4	4.337	1.169
607	MSTRG.9753	-	Ca4	1.630	1.178
608	MSTRG.8194	Ca_03726	Ca4	3.945	1.179
609	MSTRG.9319	Ca_05464	Ca4	5.418	1.181
610	MSTRG.9738	Ca_14458	Ca4	3.237	1.188
611	MSTRG.9048	Ca_04603	Ca4	1.998	1.204
612	MSTRG.10346	Ca_14929	Ca4	9.595	1.208
613	MSTRG.9535	Ca_14000	Ca4	5.456	1.216
614	MSTRG.9010	Ca_04563	Ca4	5.244	1.232
615	MSTRG.9608	Ca_17130	Ca4	4.457	1.251
616	MSTRG.8071	Ca_03845	Ca4	1.798	1.274
617	MSTRG.9349	Ca_05434	Ca4	4.773	1.282
618	MSTRG.10330	Ca_13052	Ca4	4.697	1.295
619	MSTRG.8444	Ca_03471	Ca4	7.966	1.308
620	MSTRG.7669	Ca_07647	Ca4	1.169	1.322
621	MSTRG.9698	Ca_20139	Ca4	3.409	1.367
622	MSTRG.10344	Ca_14931	Ca4	2.923	1.372
623	MSTRG.9946	Ca_14195	Ca4	2.326	1.372
624	MSTRG.7951	Ca_12092	Ca4	3.127	1.373
625	MSTRG.10030	Ca_15498	Ca4	2.360	1.377
626	MSTRG.8051	Ca_03861	Ca4	3.263	1.398
627	MSTRG.7806	Ca_07771	Ca4	0.844	1.407

628	MSTRG.9581	Ca_14048	Ca4	2.828	1.426
629	MSTRG.8112	Ca_03805	Ca4	1.287	1.433
630	MSTRG.9373	Ca_05412	Ca4	5.332	1.459
631	MSTRG.10339	Ca_14936	Ca4	2.646	1.462
632	MSTRG.9199	Ca_05585	Ca4	1.088	1.465
633	MSTRG.10214	Ca_15106	Ca4	-0.120	1.513
634	MSTRG.8129	Ca_03790	Ca4	3.625	1.530
635	MSTRG.10677	-	Ca4	3.085	1.533
636	MSTRG.10359	Ca_14911	Ca4	4.553	1.535
637	MSTRG.9739	-	Ca4	2.492	1.542
638	MSTRG.10418	Ca_23900	Ca4	-0.329	1.560
639	MSTRG.9686	-	Ca4	-0.187	1.582
640	MSTRG.8333	Ca_03587	Ca4	0.982	1.587
641	MSTRG.10651	Ca_09138	Ca4	2.053	1.595
642	MSTRG.8894	Ca_04453	Ca4	1.353	1.604
643	MSTRG.10341	Ca_14935	Ca4	3.394	1.609
644	MSTRG.8885	Ca_04443	Ca4	3.551	1.621
645	MSTRG.9401	-	Ca4	-0.636	1.634
646	MSTRG.8269	-	Ca4	2.237	1.667
647	MSTRG.9123	Ca_05657	Ca4	1.334	1.670
648	MSTRG.7857	Ca_07825	Ca4	1.060	1.724
649	MSTRG.9342	Ca_05441	Ca4	6.697	1.736
650	MSTRG.9831	-	Ca4	3.406	1.788
651	MSTRG.9513	-	Ca4	1.031	1.794
652	MSTRG.10015	-	Ca4	0.554	1.838
653	MSTRG.10905	Ca_10798	Ca4	3.353	1.843
654	MSTRG.8708	-	Ca4	-0.611	1.874
655	MSTRG.9604	Ca_17125	Ca4	4.882	1.881
656	MSTRG.8457	-	Ca4	1.758	1.897
657	MSTRG.10912	-	Ca4	2.453	1.916
658	MSTRG.9136	Ca_05643	Ca4	2.991	1.936
659	MSTRG.9323	Ca_05458	Ca4	2.043	2.023
660	MSTRG.9413	-	Ca4	-1.124	2.028
661	MSTRG.8870	Ca_04426	Ca4	3.639	2.033
662	MSTRG.8469	Ca_03440	Ca4	-1.159	2.042
663	MSTRG.8754	Ca_04324	Ca4	5.632	2.044
664	MSTRG.9994	-	Ca4	0.269	2.051

665	MSTRG.10966	Ca_23014	Ca4	6.129	2.060
666	MSTRG.10311	-	Ca4	-0.176	2.061
667	MSTRG.8742	Ca_04313	Ca4	2.893	2.096
668	MSTRG.8539	-	Ca4	-0.281	2.105
669	MSTRG.9175	-	Ca4	3.712	2.106
670	MSTRG.8069	Ca_03847	Ca4	3.431	2.115
671	MSTRG.10329	Ca_13053	Ca4	2.385	2.191
672	MSTRG.10661	Ca_09144	Ca4	0.679	2.261
673	MSTRG.9569	Ca_14034	Ca4	1.407	2.281
674	MSTRG.8847	Ca_04402	Ca4	-0.416	2.347
675	MSTRG.9528	Ca_13997	Ca4	-1.725	2.375
676	MSTRG.10705	-	Ca4	-1.555	2.385
677	MSTRG.10317	Ca_13068	Ca4	4.661	2.431
678	MSTRG.8941	Ca_04499	Ca4	0.371	2.510
679	MSTRG.8620	Ca_08429	Ca4	2.239	2.552
680	MSTRG.8772	Ca_04343	Ca4	4.838	2.623
681	MSTRG.9933	-	Ca4	2.111	2.630
682	MSTRG.10707	Ca_09186	Ca4	5.142	2.667
683	MSTRG.9301	Ca_05484	Ca4	3.942	2.705
684	MSTRG.7691	Ca_07664	Ca4	3.548	2.715
685	MSTRG.9066	-	Ca4	-2.144	2.746
686	MSTRG.9804	Ca_16561	Ca4	1.739	2.747
687	MSTRG.8437	Ca_03479	Ca4	5.353	2.764
688	MSTRG.9732	-	Ca4	-0.533	2.823
689	MSTRG.8718	-	Ca4	0.248	2.893
690	MSTRG.8455	Ca_03462	Ca4	0.657	2.927
691	MSTRG.7890	-	Ca4	0.579	2.976
692	MSTRG.9444	-	Ca4	1.365	2.988
693	MSTRG.10331	Ca_13051	Ca4	-0.447	3.053
694	MSTRG.8188	-	Ca4	-1.948	3.132
695	MSTRG.10318	Ca_13067	Ca4	4.073	3.288
696	MSTRG.8523	Ca_08338	Ca4	-1.649	3.754
697	MSTRG.9735	Ca_14462	Ca4	0.567	3.904
698	MSTRG.9893	Ca_23165	Ca4	6.208	4.190
699	MSTRG.9416	-	Ca4	-1.650	4.223
700	MSTRG.10240	-	Ca4	3.376	4.304
701	MSTRG.8193	Ca_03727	Ca4	-1.707	4.380

702	MSTRG.9415	-	Ca4	0.554	4.656
703	MSTRG.9480	-	Ca4	-1.004	4.741
704	MSTRG.9479	-	Ca4	-2.043	4.932
705	MSTRG.10340	-	Ca4	0.359	4.940
706	MSTRG.8813	Ca_04377	Ca4	-3.979	5.440
707	MSTRG.10357	Ca_14913	Ca4	-1.090	5.663
708	MSTRG.9330	-	Ca4	-2.726	5.804
709	MSTRG.10309	-	Ca4	-2.515	5.862
710	MSTRG.9333	Ca_05449	Ca4	-0.316	6.174
711	MSTRG.9417	-	Ca4	-1.657	6.524
712	MSTRG.10327	Ca_13055	Ca4	0.630	6.699
713	MSTRG.9086	-	Ca4	-3.206	6.773
714	MSTRG.9392	-	Ca4	0.221	7.511
715	MSTRG.10547	-	Ca4	-3.638	7.683
716	MSTRG.8082	-	Ca4	-2.888	7.907
717	MSTRG.10328	Ca_13054	Ca4	1.215	9.616
718	MSTRG.11072	-	Ca5	-0.148	-9.225
719	MSTRG.11607	-	Ca5	-2.040	-7.910
720	MSTRG.12212	-	Ca5	-0.946	-7.292
721	MSTRG.11070	-	Ca5	-2.213	-5.957
722	MSTRG.11071	-	Ca5	-1.629	-5.435
723	MSTRG.13644	Ca_03951	Ca5	1.006	-4.821
724	MSTRG.11563	-	Ca5	0.301	-3.912
725	MSTRG.13668	-	Ca5	-1.501	-3.234
726	MSTRG.13756	Ca_04061	Ca5	2.537	-3.152
727	MSTRG.13727	Ca_04035	Ca5	0.598	-3.147
728	MSTRG.11562	-	Ca5	0.100	-3.126
729	MSTRG.12209	Ca_04731	Ca5	-0.924	-3.123
730	MSTRG.12211	Ca_04732	Ca5	-0.576	-3.070
731	MSTRG.12454	-	Ca5	1.773	-2.501
732	MSTRG.11242	-	Ca5	-1.045	-2.486
733	MSTRG.13762	-	Ca5	2.660	-2.374
734	MSTRG.11919	-	Ca5	1.322	-2.349
735	MSTRG.11914	Ca_08947	Ca5	4.027	-2.271
736	MSTRG.12016	-	Ca5	1.046	-2.171
737	MSTRG.12515	-	Ca5	-0.721	-2.140
738	MSTRG.11496	-	Ca5	4.840	-2.111

739	MSTRG.11865	Ca_08998	Ca5	0.470	-1.877
740	MSTRG.13055	-	Ca5	-0.545	-1.829
741	MSTRG.12579	Ca_01862	Ca5	2.369	-1.754
742	MSTRG.13468	-	Ca5	-0.625	-1.735
743	MSTRG.12827	Ca_01600	Ca5	1.350	-1.733
744	MSTRG.11890	-	Ca5	-0.013	-1.629
745	MSTRG.12691	Ca_01729	Ca5	1.830	-1.611
746	MSTRG.13889	Ca_04190	Ca5	1.965	-1.580
747	MSTRG.12159	Ca_04687	Ca5	6.755	-1.548
748	MSTRG.11008	Ca_18157	Ca5	4.489	-1.536
749	MSTRG.12885	-	Ca5	0.929	-1.490
750	MSTRG.13645	Ca_03952	Ca5	0.912	-1.486
751	MSTRG.11508	-	Ca5	0.973	-1.479
752	MSTRG.13101	Ca_07459	Ca5	4.810	-1.474
753	MSTRG.13609	Ca_03911	Ca5	4.829	-1.449
754	MSTRG.13239	Ca_07604	Ca5	3.583	-1.373
755	MSTRG.12673	Ca_01749	Ca5	5.024	-1.371
756	MSTRG.13970	Ca_04270	Ca5	4.062	-1.365
757	MSTRG.13744	-	Ca5	1.769	-1.337
758	MSTRG.11011	-	Ca5	2.725	-1.317
759	MSTRG.13018	Ca_01402	Ca5	4.003	-1.303
760	MSTRG.11517	-	Ca5	2.786	-1.297
761	MSTRG.13087	Ca_07447	Ca5	6.597	-1.270
762	MSTRG.11616	Ca_18229	Ca5	3.426	-1.269
763	MSTRG.12132	Ca_16662	Ca5	1.951	-1.269
764	MSTRG.11039	-	Ca5	1.941	-1.256
765	MSTRG.11584	-	Ca5	3.122	-1.247
766	MSTRG.12352	Ca_04863	Ca5	3.356	-1.231
767	MSTRG.12008	Ca_13410	Ca5	2.458	-1.217
768	MSTRG.13936	Ca_04240	Ca5	3.238	-1.211
769	MSTRG.12221	Ca_04742	Ca5	1.038	-1.206
770	MSTRG.13575	Ca_03882	Ca5	3.981	-1.204
771	MSTRG.13046	Ca_07409	Ca5	2.574	-1.196
772	MSTRG.13670	Ca_03976	Ca5	6.026	-1.196
773	MSTRG.11885	Ca_08971	Ca5	6.025	-1.192
774	MSTRG.13719	Ca_04027	Ca5	3.376	-1.191
775	MSTRG.13649	Ca_03955	Ca5	3.567	-1.161

776	MSTRG.12017	Ca_13402	Ca5	3.554	-1.146
777	MSTRG.12361	Ca_04866	Ca5	2.365	-1.145
778	MSTRG.11949	Ca_08904	Ca5	1.749	-1.143
779	MSTRG.11055	Ca_26283	Ca5	1.537	-1.137
780	MSTRG.13365	Ca_11381	Ca5	6.513	-1.137
781	MSTRG.13752	-	Ca5	2.848	-1.135
782	MSTRG.12022	-	Ca5	0.639	-1.131
783	MSTRG.13253	Ca_07623	Ca5	4.109	-1.130
784	MSTRG.13571	Ca_03879	Ca5	6.384	-1.126
785	MSTRG.13821	Ca_04124	Ca5	4.589	-1.122
786	MSTRG.13849	Ca_04153	Ca5	5.463	-1.062
787	MSTRG.13724	Ca_04032	Ca5	0.667	-1.050
788	MSTRG.12054	Ca_13365	Ca5	1.786	-1.045
789	MSTRG.12802	Ca_01620	Ca5	4.522	-1.034
790	MSTRG.12434	Ca_04942	Ca5	8.186	-1.030
791	MSTRG.13321	Ca_19224	Ca5	2.795	-1.027
792	MSTRG.11521	Ca_22481	Ca5	1.387	-1.022
793	MSTRG.12506	Ca_05017	Ca5	6.411	-1.017
794	MSTRG.13478	Ca_12718	Ca5	3.836	-1.011
795	MSTRG.13303	Ca_19240	Ca5	6.701	-1.006
796	MSTRG.12347	Ca_04858	Ca5	6.310	1.016
797	MSTRG.11987	Ca_13432	Ca5	3.676	1.019
798	MSTRG.12574	Ca_01866	Ca5	4.383	1.024
799	MSTRG.13532	Ca_12662	Ca5	5.169	1.049
800	MSTRG.11471	Ca_17917	Ca5	2.214	1.070
801	MSTRG.13536	Ca_12653	Ca5	7.742	1.070
802	MSTRG.11558	Ca_24492	Ca5	4.162	1.072
803	MSTRG.12344	-	Ca5	1.160	1.077
804	MSTRG.12520	Ca_01918	Ca5	1.328	1.123
805	MSTRG.11967	Ca_08886	Ca5	2.783	1.123
806	MSTRG.12253	Ca_04773	Ca5	2.235	1.142
807	MSTRG.12105	Ca_16629	Ca5	7.721	1.158
808	MSTRG.12113	Ca_16640	Ca5	7.172	1.174
809	MSTRG.12019	-	Ca5	2.114	1.181
810	MSTRG.11943	-	Ca5	2.836	1.182
811	MSTRG.12407	Ca_04918	Ca5	4.378	1.186
812	MSTRG.13580	Ca_03888	Ca5	1.609	1.187

813	MSTRG.11821	Ca_09044	Ca5	1.837	1.187
814	MSTRG.11357	-	Ca5	3.555	1.193
815	MSTRG.13189	Ca_07550	Ca5	0.776	1.219
816	MSTRG.13378	Ca_11364	Ca5	-0.588	1.232
817	MSTRG.11118	Ca_24950	Ca5	2.407	1.236
818	MSTRG.11837	Ca_09030	Ca5	10.898	1.246
819	MSTRG.13417	Ca_11331	Ca5	2.137	1.287
820	MSTRG.12251	Ca_04769	Ca5	4.704	1.317
821	MSTRG.12428	Ca_04936	Ca5	2.348	1.326
822	MSTRG.12099	Ca_16626	Ca5	5.454	1.332
823	MSTRG.12535	-	Ca5	4.380	1.358
824	MSTRG.12912	-	Ca5	0.603	1.361
825	MSTRG.11403	Ca_17085	Ca5	3.460	1.362
826	MSTRG.11475	Ca_17926	Ca5	-0.724	1.384
827	MSTRG.11283	Ca_23782	Ca5	3.247	1.385
828	MSTRG.12026	Ca_13396	Ca5	5.071	1.419
829	MSTRG.11776	-	Ca5	0.413	1.504
830	MSTRG.12861	Ca_01564	Ca5	3.716	1.519
831	MSTRG.12908	Ca_01515	Ca5	7.142	1.531
832	MSTRG.13507	Ca_12684	Ca5	4.633	1.548
833	MSTRG.11795	Ca_15613	Ca5	2.243	1.587
834	MSTRG.13398	Ca_11349	Ca5	2.702	1.595
835	MSTRG.13556	-	Ca5	0.409	1.651
836	MSTRG.12922	Ca_01498	Ca5	-0.059	1.670
837	MSTRG.11812	Ca_15625	Ca5	3.364	1.687
838	MSTRG.12002	Ca_13414	Ca5	0.246	1.809
839	MSTRG.13801	Ca_04106	Ca5	4.016	1.831
840	MSTRG.11666	Ca_20083	Ca5	3.433	1.860
841	MSTRG.13623	Ca_03929	Ca5	1.137	1.909
842	MSTRG.12393	Ca_04900	Ca5	2.974	1.987
843	MSTRG.13671	Ca_03977	Ca5	3.392	2.021
844	MSTRG.11415	Ca_17071	Ca5	1.883	2.074
845	MSTRG.11083	-	Ca5	-0.585	2.227
846	MSTRG.12976	Ca_01445	Ca5	4.133	2.304
847	MSTRG.12372	Ca_04881	Ca5	4.716	2.305
848	MSTRG.12931	Ca_01491	Ca5	3.215	2.306
849	MSTRG.13770	Ca_04075	Ca5	2.267	2.307

850	MSTRG.13573	Ca_03883	Ca5	6.875	2.325
851	MSTRG.11274	Ca_19988	Ca5	1.879	2.334
852	MSTRG.13552	Ca_12639	Ca5	6.280	2.410
853	MSTRG.13195	Ca_07557	Ca5	0.703	2.414
854	MSTRG.11920	Ca_08932	Ca5	-1.084	2.442
855	MSTRG.11388	Ca_17116	Ca5	0.904	2.503
856	MSTRG.13271	Ca_07638	Ca5	1.374	2.516
857	MSTRG.11917	-	Ca5	1.309	2.549
858	MSTRG.11285	Ca_23783	Ca5	1.255	2.572
859	MSTRG.13733	Ca_04038	Ca5	0.543	2.586
860	MSTRG.11016	Ca_18168	Ca5	-1.302	2.624
861	MSTRG.12011	Ca_13408	Ca5	1.886	2.640
862	MSTRG.13130	-	Ca5	-0.142	2.699
863	MSTRG.13742	Ca_04048	Ca5	-0.666	3.411
864	MSTRG.11349	Ca_23746	Ca5	4.453	3.414
865	MSTRG.11203	-	Ca5	0.464	4.265
866	MSTRG.12074	Ca_13344	Ca5	-0.254	4.329
867	MSTRG.12445	Ca_04955	Ca5	1.255	4.763
868	MSTRG.11505	Ca_17955	Ca5	0.812	4.972
869	MSTRG.12131	-	Ca5	-2.057	5.304
870	MSTRG.11546	-	Ca5	-3.773	5.435
871	MSTRG.13648	-	Ca5	-0.798	5.859
872	MSTRG.11184	-	Ca5	-2.271	6.026
873	MSTRG.13818	-	Ca5	-0.640	6.229
874	MSTRG.13740	-	Ca5	-3.220	6.791
875	MSTRG.11185	-	Ca5	-1.844	7.392
876	MSTRG.13602	-	Ca5	-1.272	7.466
877	MSTRG.16458	Ca_15171	Ca6	-3.339	-10.280
878	MSTRG.17326	-	Ca6	-2.871	-10.257
879	MSTRG.16749	-	Ca6	-5.005	-9.885
880	MSTRG.16664	-	Ca6	-0.679	-8.947
881	MSTRG.16304	Ca_25967	Ca6	0.334	-8.726
882	MSTRG.17182	-	Ca6	-0.845	-8.700
883	MSTRG.17295	-	Ca6	-0.743	-8.599
884	MSTRG.15846	Ca_16333	Ca6	1.136	-8.392
885	MSTRG.16918	-	Ca6	-0.172	-8.215
886	MSTRG.16654	Ca_19804	Ca6	-1.215	-7.896

887	MSTRG.17113	Ca_19190	Ca6	2.426	-7.893
888	MSTRG.16990	-	Ca6	-1.664	-7.689
889	MSTRG.17007	-	Ca6	-0.996	-7.286
890	MSTRG.14997	Ca_08561	Ca6	-4.149	-7.078
891	MSTRG.16706	-	Ca6	-1.051	-6.992
892	MSTRG.16451	-	Ca6	-1.869	-6.953
893	MSTRG.16414	-	Ca6	-2.211	-6.716
894	MSTRG.16386	-	Ca6	-1.940	-6.586
895	MSTRG.17337	-	Ca6	-1.065	-5.473
896	MSTRG.17103	Ca_13435	Ca6	-2.059	-5.408
897	MSTRG.16675	-	Ca6	1.112	-5.222
898	MSTRG.16793	Ca_23239	Ca6	3.162	-5.018
899	MSTRG.16342	-	Ca6	0.882	-4.992
900	MSTRG.16825	-	Ca6	-0.557	-4.798
901	MSTRG.17230	Ca_18906	Ca6	3.279	-4.335
902	MSTRG.17085	Ca_13451	Ca6	-0.272	-4.219
903	MSTRG.16715	Ca_15924	Ca6	-1.522	-4.167
904	MSTRG.16476	-	Ca6	-0.455	-4.071
905	MSTRG.17086	Ca_13450	Ca6	-1.496	-3.638
906	MSTRG.16064	Ca_11096	Ca6	3.160	-3.543
907	MSTRG.16556	-	Ca6	0.590	-3.445
908	MSTRG.16273	Ca_14581	Ca6	5.832	-3.364
909	MSTRG.17338	-	Ca6	-0.170	-3.152
910	MSTRG.17292	Ca_21219	Ca6	1.721	-3.131
911	MSTRG.16597	Ca_15786	Ca6	-0.552	-3.081
912	MSTRG.16474	-	Ca6	0.114	-3.054
913	MSTRG.17608	-	Ca6	-0.287	-2.998
914	MSTRG.15565	Ca_06354	Ca6	1.517	-2.744
915	MSTRG.15819	Ca_16361	Ca6	2.411	-2.735
916	MSTRG.16966	Ca_23440	Ca6	-0.218	-2.715
917	MSTRG.14635	Ca_16935	Ca6	0.055	-2.677
918	MSTRG.14634	Ca_16934	Ca6	-0.104	-2.670
919	MSTRG.16397	Ca_16454	Ca6	-1.388	-2.655
920	MSTRG.15229	-	Ca6	-0.765	-2.630
921	MSTRG.17137	-	Ca6	-0.516	-2.609
922	MSTRG.15307	-	Ca6	2.321	-2.599
923	MSTRG.16068	Ca_11088	Ca6	3.829	-2.595

924	MSTRG.16263	Ca_14588	Ca6	0.390	-2.538
925	MSTRG.16965	-	Ca6	3.324	-2.533
926	MSTRG.16673	Ca_19788	Ca6	-1.049	-2.530
927	MSTRG.16344	Ca_17465	Ca6	3.239	-2.517
928	MSTRG.16868	-	Ca6	0.249	-2.426
929	MSTRG.16376	Ca_24059	Ca6	3.063	-2.363
930	MSTRG.16065	Ca_11089	Ca6	4.361	-2.356
931	MSTRG.16746	Ca_21597	Ca6	0.789	-2.311
932	MSTRG.15308	Ca_05195	Ca6	3.916	-2.206
933	MSTRG.17217	Ca_18885	Ca6	8.032	-2.182
934	MSTRG.16459	Ca_15174	Ca6	-0.669	-2.161
935	MSTRG.15422	-	Ca6	-1.110	-2.159
936	MSTRG.15892	Ca_19862	Ca6	4.503	-2.128
937	MSTRG.16418	Ca_16474	Ca6	0.550	-2.120
938	MSTRG.16819	-	Ca6	3.175	-2.096
939	MSTRG.16309	-	Ca6	4.507	-2.092
940	MSTRG.14437	-	Ca6	4.902	-2.054
941	MSTRG.16359	Ca_17455	Ca6	4.754	-1.986
942	MSTRG.17334	-	Ca6	1.925	-1.918
943	MSTRG.15723	Ca_06505	Ca6	5.600	-1.910
944	MSTRG.16219	Ca_16727	Ca6	4.266	-1.872
945	MSTRG.15887	Ca_19869	Ca6	0.224	-1.871
946	MSTRG.14071	Ca_13329	Ca6	2.757	-1.845
947	MSTRG.17590	Ca_18859	Ca6	-0.323	-1.769
948	MSTRG.16438	Ca_16494	Ca6	2.311	-1.755
949	MSTRG.16980	-	Ca6	1.174	-1.723
950	MSTRG.16799	-	Ca6	-0.505	-1.720
951	MSTRG.16210	Ca_16716	Ca6	5.104	-1.668
952	MSTRG.15709	-	Ca6	-0.270	-1.653
953	MSTRG.16133	Ca_11028	Ca6	0.161	-1.648
954	MSTRG.17091	Ca_13443	Ca6	2.758	-1.635
955	MSTRG.15467	-	Ca6	-0.136	-1.630
956	MSTRG.16911	Ca_17751	Ca6	-1.442	-1.626
957	MSTRG.17126	Ca_19170	Ca6	-0.644	-1.624
958	MSTRG.15805	Ca_16375	Ca6	0.708	-1.525
959	MSTRG.16116	Ca_11045	Ca6	3.820	-1.516
960	MSTRG.15962	Ca_11225	Ca6	7.578	-1.512

961	MSTRG.15525	-	Ca6	1.540	-1.471
962	MSTRG.17251	Ca_16269	Ca6	0.451	-1.435
963	MSTRG.17300	Ca_19013	Ca6	5.355	-1.424
964	MSTRG.14469	Ca_05797	Ca6	4.457	-1.399
965	MSTRG.15386	-	Ca6	4.808	-1.373
966	MSTRG.16708	Ca_15918	Ca6	3.173	-1.366
967	MSTRG.16187	Ca_16695	Ca6	4.580	-1.366
968	MSTRG.15017	Ca_08538	Ca6	4.459	-1.363
969	MSTRG.17006	-	Ca6	6.072	-1.361
970	MSTRG.15385	Ca_05277	Ca6	7.496	-1.339
971	MSTRG.16162	Ca_24014	Ca6	3.676	-1.324
972	MSTRG.16217	Ca_16725	Ca6	2.331	-1.322
973	MSTRG.14040	Ca_13303	Ca6	1.857	-1.315
974	MSTRG.17236	-	Ca6	1.699	-1.300
975	MSTRG.17418	-	Ca6	1.485	-1.292
976	MSTRG.14717	Ca_09628	Ca6	1.352	-1.281
977	MSTRG.16611	-	Ca6	0.396	-1.268
978	MSTRG.17095	Ca_13441	Ca6	1.783	-1.259
979	MSTRG.16803	Ca_23252	Ca6	3.349	-1.247
980	MSTRG.17177	-	Ca6	5.146	-1.247
981	MSTRG.15951	Ca_11236	Ca6	3.066	-1.237
982	MSTRG.14752	Ca_09594	Ca6	6.295	-1.227
983	MSTRG.16382	Ca_24054	Ca6	2.190	-1.216
984	MSTRG.14695	Ca_09649	Ca6	4.049	-1.213
985	MSTRG.15529	Ca_06315	Ca6	6.885	-1.213
986	MSTRG.14177	Ca_10364	Ca6	2.857	-1.213
987	MSTRG.14546	Ca_05719	Ca6	5.732	-1.183
988	MSTRG.15768	Ca_06554	Ca6	3.876	-1.178
989	MSTRG.16530	Ca_22233	Ca6	1.505	-1.172
990	MSTRG.15682	Ca_06465	Ca6	3.384	-1.167
991	MSTRG.15746	-	Ca6	2.714	-1.161
992	MSTRG.14270	-	Ca6	0.027	-1.160
993	MSTRG.14372	Ca_05889	Ca6	0.776	-1.152
994	MSTRG.15126	Ca_05023	Ca6	0.929	-1.146
995	MSTRG.14559	Ca_05704	Ca6	-0.397	-1.141
996	MSTRG.15960	Ca_11228	Ca6	2.636	-1.141
997	MSTRG.17005	Ca_20726	Ca6	9.249	-1.140

998	MSTRG.14909	Ca_08655	Ca6	2.058	-1.114
999	MSTRG.17449	Ca_13662	Ca6	0.762	-1.108
1000	MSTRG.15475	Ca_19667	Ca6	3.291	-1.098
1001	MSTRG.16571	-	Ca6	2.440	-1.080
1002	MSTRG.14547	Ca_05718	Ca6	2.478	-1.067
1003	MSTRG.16816	-	Ca6	3.598	-1.049
1004	MSTRG.16738	Ca_15950	Ca6	6.270	-1.022
1005	MSTRG.16149	Ca_24163	Ca6	3.969	-1.017
1006	MSTRG.16943	Ca_17714	Ca6	2.819	-1.012
1007	MSTRG.14199	-	Ca6	2.261	-1.006
1008	MSTRG.15370	Ca_05262	Ca6	6.021	-1.006
1009	MSTRG.15228	Ca_05124	Ca6	-0.161	-1.002
1010	MSTRG.16975	Ca_24609	Ca6	3.645	1.011
1011	MSTRG.15593	Ca_06384	Ca6	3.699	1.013
1012	MSTRG.15653	-	Ca6	2.611	1.018
1013	MSTRG.16104	Ca_11059	Ca6	5.877	1.020
1014	MSTRG.17464	-	Ca6	0.814	1.024
1015	MSTRG.14761	Ca_09586	Ca6	0.904	1.025
1016	MSTRG.14645	Ca_16945	Ca6	5.142	1.029
1017	MSTRG.15098	-	Ca6	2.939	1.034
1018	MSTRG.16181	Ca_16684	Ca6	5.661	1.034
1019	MSTRG.14865	Ca_16741	Ca6	7.226	1.036
1020	MSTRG.15900	Ca_11292	Ca6	4.312	1.041
1021	MSTRG.17491	-	Ca6	5.369	1.045
1022	MSTRG.16423	Ca_16480	Ca6	4.675	1.046
1023	MSTRG.13984	Ca_13249	Ca6	3.955	1.046
1024	MSTRG.15918	Ca_11271	Ca6	0.936	1.047
1025	MSTRG.14021	Ca_13282	Ca6	9.708	1.051
1026	MSTRG.14193	Ca_10384	Ca6	3.075	1.062
1027	MSTRG.16786	Ca_21944	Ca6	11.051	1.070
1028	MSTRG.15172	Ca_05071	Ca6	6.749	1.084
1029	MSTRG.16657	Ca_19802	Ca6	7.235	1.090
1030	MSTRG.17277	Ca_21196	Ca6	7.477	1.090
1031	MSTRG.14480	Ca_05787	Ca6	4.553	1.097
1032	MSTRG.14493	Ca_05779	Ca6	8.234	1.121
1033	MSTRG.15802	Ca_16379	Ca6	4.362	1.138
1034	MSTRG.15848	-	Ca6	1.833	1.152

1035	MSTRG.15447	Ca_22015	Ca6	2.959	1.157
1036	MSTRG.17240	Ca_18917	Ca6	12.049	1.159
1037	MSTRG.16777	Ca_23160	Ca6	1.731	1.194
1038	MSTRG.14434	-	Ca6	1.906	1.218
1039	MSTRG.15298	Ca_05187	Ca6	2.119	1.222
1040	MSTRG.15818	Ca_16360	Ca6	4.338	1.228
1041	MSTRG.14189	Ca_10375	Ca6	2.968	1.234
1042	MSTRG.16502	Ca_15222	Ca6	4.060	1.251
1043	MSTRG.16088	-	Ca6	1.229	1.258
1044	MSTRG.15693	Ca_06479	Ca6	4.672	1.260
1045	MSTRG.14164	Ca_10350	Ca6	3.948	1.262
1046	MSTRG.17283	Ca_21208	Ca6	2.571	1.267
1047	MSTRG.15810	-	Ca6	0.849	1.268
1048	MSTRG.14323	Ca_05937	Ca6	3.874	1.273
1049	MSTRG.15852	Ca_16327	Ca6	2.214	1.276
1050	MSTRG.15282	Ca_05172	Ca6	1.941	1.295
1051	MSTRG.15341	Ca_05233	Ca6	5.680	1.312
1052	MSTRG.15853	Ca_16325	Ca6	4.343	1.319
1053	MSTRG.16195	Ca_16706	Ca6	2.676	1.337
1054	MSTRG.17065	Ca_13472	Ca6	5.860	1.342
1055	MSTRG.15079	Ca_20491	Ca6	2.632	1.368
1056	MSTRG.17522	Ca_15388	Ca6	0.833	1.388
1057	MSTRG.16555	Ca_22055	Ca6	3.133	1.397
1058	MSTRG.16025	Ca_11131	Ca6	8.237	1.414
1059	MSTRG.17066	-	Ca6	-0.017	1.415
1060	MSTRG.17524	Ca_15390	Ca6	1.860	1.418
1061	MSTRG.15545	Ca_06334	Ca6	-0.505	1.428
1062	MSTRG.16059	Ca_11101	Ca6	5.206	1.441
1063	MSTRG.16974	Ca_24607	Ca6	4.037	1.443
1064	MSTRG.17286	Ca_21212	Ca6	3.963	1.449
1065	MSTRG.13988	Ca_13252	Ca6	0.920	1.473
1066	MSTRG.16489	-	Ca6	-1.024	1.549
1067	MSTRG.15403	Ca_05303	Ca6	2.285	1.594
1068	MSTRG.17232	Ca_18910	Ca6	1.351	1.598
1069	MSTRG.17520	Ca_15386	Ca6	1.624	1.611
1070	MSTRG.15323	Ca_05208	Ca6	4.788	1.633
1071	MSTRG.16540	Ca_22072	Ca6	4.372	1.665

1072	MSTRG.16938	-	Ca6	-0.337	1.670
1073	MSTRG.17279	-	Ca6	0.051	1.673
1074	MSTRG.16209	Ca_16717	Ca6	3.993	1.693
1075	MSTRG.17284	-	Ca6	-0.602	1.702
1076	MSTRG.17154	Ca_17522	Ca6	3.031	1.706
1077	MSTRG.15596	Ca_06386	Ca6	2.374	1.728
1078	MSTRG.14489	-	Ca6	2.642	1.739
1079	MSTRG.16596	Ca_15792	Ca6	3.444	1.748
1080	MSTRG.14770	Ca_09578	Ca6	6.351	1.754
1081	MSTRG.17073	Ca_13462	Ca6	4.438	1.809
1082	MSTRG.15570	Ca_06359	Ca6	1.503	1.811
1083	MSTRG.17525	Ca_15391	Ca6	0.258	1.853
1084	MSTRG.17609	-	Ca6	1.351	1.913
1085	MSTRG.15624	-	Ca6	4.822	1.915
1086	MSTRG.17571	Ca_18876	Ca6	-0.005	1.916
1087	MSTRG.15146	Ca_05042	Ca6	0.838	1.926
1088	MSTRG.16234	-	Ca6	3.679	1.955
1089	MSTRG.17521	Ca_15387	Ca6	0.601	1.969
1090	MSTRG.14098	Ca_10297	Ca6	0.561	2.042
1091	MSTRG.15721	-	Ca6	0.747	2.073
1092	MSTRG.16937	-	Ca6	-0.190	2.129
1093	MSTRG.14748	-	Ca6	-0.418	2.133
1094	MSTRG.16023	-	Ca6	0.691	2.229
1095	MSTRG.14570	Ca_05688	Ca6	0.637	2.243
1096	MSTRG.16069	Ca_11087	Ca6	5.167	2.244
1097	MSTRG.17305	Ca_19018	Ca6	0.003	2.289
1098	MSTRG.17034	-	Ca6	0.902	2.330
1099	MSTRG.17269	Ca_16286	Ca6	1.823	2.337
1100	MSTRG.17509	-	Ca6	6.185	2.356
1101	MSTRG.16148	Ca_24166	Ca6	1.173	2.382
1102	MSTRG.17488	Ca_13632	Ca6	6.002	2.399
1103	MSTRG.15995	-	Ca6	0.569	2.447
1104	MSTRG.15665	Ca_06452	Ca6	9.299	2.517
1105	MSTRG.17519	Ca_15385	Ca6	-0.009	2.546
1106	MSTRG.17581	-	Ca6	-2.074	2.549
1107	MSTRG.16766	Ca_23152	Ca6	5.713	2.571
1108	MSTRG.15139	Ca_05033	Ca6	4.595	2.611

1109	MSTRG.17611	-	Ca6	0.253	2.630
1110	MSTRG.17605	Ca_18846	Ca6	2.402	2.655
1111	MSTRG.16235	-	Ca6	0.536	2.710
1112	MSTRG.17246	Ca_16265	Ca6	1.563	2.732
1113	MSTRG.17204	Ca_22926	Ca6	1.544	2.819
1114	MSTRG.15997	Ca_11189	Ca6	2.198	2.873
1115	MSTRG.15240	Ca_05132	Ca6	3.585	2.929
1116	MSTRG.15178	-	Ca6	0.584	3.048
1117	MSTRG.17144	-	Ca6	-1.617	3.070
1118	MSTRG.17465	Ca_13651	Ca6	8.821	3.075
1119	MSTRG.16253	Ca_14604	Ca6	2.615	3.149
1120	MSTRG.17202	Ca_22925	Ca6	2.292	3.209
1121	MSTRG.13994	-	Ca6	0.119	3.435
1122	MSTRG.16467	Ca_15179	Ca6	-1.265	3.462
1123	MSTRG.15181	Ca_05078	Ca6	0.882	3.463
1124	MSTRG.15460	-	Ca6	0.449	3.693
1125	MSTRG.17518	Ca_15382	Ca6	-2.522	3.717
1126	MSTRG.17102	-	Ca6	-2.858	4.023
1127	MSTRG.15124	-	Ca6	0.232	4.133
1128	MSTRG.16910	-	Ca6	-0.910	4.929
1129	MSTRG.15258	Ca_05148	Ca6	0.226	5.048
1130	MSTRG.15796	-	Ca6	-2.318	5.447
1131	MSTRG.15894	Ca_19857	Ca6	-2.475	5.520
1132	MSTRG.16665	-	Ca6	-3.918	5.800
1133	MSTRG.15996	-	Ca6	-3.576	6.215
1134	MSTRG.17009	-	Ca6	-3.411	6.316
1135	MSTRG.17532	-	Ca6	-4.324	6.668
1136	MSTRG.16230	-	Ca6	-3.598	6.737
1137	MSTRG.17008	-	Ca6	-4.380	6.844
1138	MSTRG.16979	-	Ca6	-3.588	6.871
1139	MSTRG.17109	Ca_19194	Ca6	-1.586	6.907
1140	MSTRG.15847	-	Ca6	-2.932	7.173
1141	MSTRG.15833	-	Ca6	-2.574	7.952
1142	MSTRG.16624	-	Ca6	-2.901	8.070
1143	MSTRG.16572	-	Ca6	-3.198	8.200
1144	MSTRG.17517	Ca_15380	Ca6	-3.162	8.300
1145	MSTRG.17489	-	Ca6	-0.544	9.382

1146	MSTRG.17231	Ca_18908	Ca6	-0.392	10.077
1147	MSTRG.19962	-	Ca7	-4.072	-8.557
1148	MSTRG.18788	-	Ca7	-1.336	-7.960
1149	MSTRG.20530	-	Ca7	-3.661	-7.349
1150	MSTRG.19453	-	Ca7	-1.782	-6.439
1151	MSTRG.20391	-	Ca7	0.544	-5.704
1152	MSTRG.19672	-	Ca7	-1.255	-4.643
1153	MSTRG.17674	Ca_03396	Ca7	-1.848	-4.569
1154	MSTRG.19528	-	Ca7	-1.370	-4.276
1155	MSTRG.18484	Ca_13222	Ca7	1.887	-4.125
1156	MSTRG.18157	Ca_02952	Ca7	-0.272	-3.914
1157	MSTRG.17733	-	Ca7	2.431	-3.875
1158	MSTRG.18116	Ca_02987	Ca7	6.978	-3.798
1159	MSTRG.19980	-	Ca7	-1.764	-3.577
1160	MSTRG.17869	-	Ca7	-0.509	-3.202
1161	MSTRG.18117	Ca_02986	Ca7	7.308	-2.901
1162	MSTRG.18779	-	Ca7	-2.059	-2.843
1163	MSTRG.20501	-	Ca7	0.073	-2.775
1164	MSTRG.18796	Ca_09372	Ca7	0.827	-2.428
1165	MSTRG.19951	Ca_16173	Ca7	2.084	-2.415
1166	MSTRG.19983	-	Ca7	1.207	-2.397
1167	MSTRG.17704	Ca_03370	Ca7	0.765	-2.193
1168	MSTRG.19218	Ca_15861	Ca7	4.348	-2.181
1169	MSTRG.18133	Ca_02970	Ca7	0.589	-2.179
1170	MSTRG.20400	-	Ca7	-1.139	-2.070
1171	MSTRG.19063	-	Ca7	1.259	-2.001
1172	MSTRG.20440	-	Ca7	1.168	-1.940
1173	MSTRG.20216	-	Ca7	-0.071	-1.802
1174	MSTRG.19675	Ca_11767	Ca7	3.243	-1.755
1175	MSTRG.17684	-	Ca7	1.296	-1.735
1176	MSTRG.17836	Ca_03261	Ca7	5.230	-1.684
1177	MSTRG.18249	Ca_06767	Ca7	0.451	-1.622
1178	MSTRG.19003	Ca_16073	Ca7	1.037	-1.615
1179	MSTRG.19292	-	Ca7	0.911	-1.567
1180	MSTRG.20238	-	Ca7	-0.331	-1.535
1181	MSTRG.18845	-	Ca7	-0.776	-1.408
1182	MSTRG.18497	-	Ca7	1.076	-1.382

1183	MSTRG.17775	Ca_03305	Ca7	3.959	-1.307
1184	MSTRG.18949	Ca_16020	Ca7	1.661	-1.292
1185	MSTRG.19610	Ca_18948	Ca7	2.178	-1.284
1186	MSTRG.18119	Ca_02983	Ca7	5.733	-1.262
1187	MSTRG.18387	Ca_06650	Ca7	0.002	-1.253
1188	MSTRG.18782	Ca_12848	Ca7	0.269	-1.252
1189	MSTRG.17928	Ca_03171	Ca7	1.864	-1.233
1190	MSTRG.17906	Ca_03196	Ca7	2.485	-1.207
1191	MSTRG.18759	Ca_12822	Ca7	2.628	-1.186
1192	MSTRG.17793	Ca_03292	Ca7	1.598	-1.180
1193	MSTRG.17769	Ca_03310	Ca7	5.933	-1.173
1194	MSTRG.20135	Ca_13740	Ca7	5.065	-1.163
1195	MSTRG.20013	Ca_20980	Ca7	4.159	-1.141
1196	MSTRG.20137	Ca_13742	Ca7	4.719	-1.135
1197	MSTRG.20461	Ca_15745	Ca7	6.045	-1.127
1198	MSTRG.19392	Ca_14493	Ca7	6.143	-1.127
1199	MSTRG.18546	Ca_13159	Ca7	1.204	-1.127
1200	MSTRG.18824	Ca_09346	Ca7	1.321	-1.118
1201	MSTRG.19551	Ca_16253	Ca7	1.270	-1.086
1202	MSTRG.19586	Ca_26609	Ca7	1.699	-1.086
1203	MSTRG.18841	Ca_09325	Ca7	7.436	-1.071
1204	MSTRG.19613	Ca_18947	Ca7	4.400	-1.067
1205	MSTRG.19545	Ca_23639	Ca7	-0.030	-1.037
1206	MSTRG.17963	Ca_03140	Ca7	1.371	-1.027
1207	MSTRG.19272	Ca_22125	Ca7	7.748	-1.025
1208	MSTRG.17956	Ca_03148	Ca7	4.261	-1.018
1209	MSTRG.18112	Ca_02991	Ca7	2.966	-1.015
1210	MSTRG.18344	Ca_06686	Ca7	7.093	-1.009
1211	MSTRG.18240	Ca_06777	Ca7	1.531	-1.008
1212	MSTRG.17680	Ca_03392	Ca7	4.343	-1.005
1213	MSTRG.18783	Ca_12847	Ca7	3.657	-1.005
1214	MSTRG.17983	Ca_03121	Ca7	2.208	1.025
1215	MSTRG.20502	-	Ca7	3.580	1.030
1216	MSTRG.17837	Ca_03254	Ca7	2.029	1.042
1217	MSTRG.17875	Ca_03227	Ca7	5.909	1.049
1218	MSTRG.19382	Ca_12416	Ca7	5.864	1.066
1219	MSTRG.18509	Ca_13195	Ca7	1.897	1.074

1220	MSTRG.19484	Ca_26245	Ca7	3.185	1.093
1221	MSTRG.18827	Ca_09343	Ca7	4.688	1.100
1222	MSTRG.18767	Ca_12828	Ca7	6.590	1.138
1223	MSTRG.20065	Ca_17648	Ca7	4.922	1.162
1224	MSTRG.20145	Ca_13759	Ca7	3.066	1.221
1225	MSTRG.17763	-	Ca7	1.040	1.233
1226	MSTRG.19781	Ca_10128	Ca7	0.398	1.241
1227	MSTRG.19095	-	Ca7	3.015	1.253
1228	MSTRG.19049	Ca_09969	Ca7	5.388	1.269
1229	MSTRG.19928	Ca_16151	Ca7	4.173	1.273
1230	MSTRG.17889	Ca_03208	Ca7	2.700	1.277
1231	MSTRG.19237	Ca_15844	Ca7	5.407	1.277
1232	MSTRG.19968	Ca_16186	Ca7	7.073	1.284
1233	MSTRG.18437	Ca_06606	Ca7	5.847	1.325
1234	MSTRG.20022	Ca_17607	Ca7	2.475	1.360
1235	MSTRG.19273	-	Ca7	2.020	1.392
1236	MSTRG.20370	-	Ca7	0.151	1.403
1237	MSTRG.18590	-	Ca7	2.455	1.427
1238	MSTRG.18317	-	Ca7	1.685	1.434
1239	MSTRG.17632	Ca_20231	Ca7	0.397	1.451
1240	MSTRG.19857	-	Ca7	2.498	1.456
1241	MSTRG.19051	Ca_09970	Ca7	2.955	1.502
1242	MSTRG.19194	Ca_15884	Ca7	2.922	1.513
1243	MSTRG.18585	Ca_15333	Ca7	7.533	1.569
1244	MSTRG.18210	-	Ca7	3.954	1.569
1245	MSTRG.19967	Ca_16185	Ca7	7.330	1.625
1246	MSTRG.19671	-	Ca7	3.999	1.649
1247	MSTRG.20164	Ca_13781	Ca7	4.523	1.652
1248	MSTRG.18229	Ca_06784	Ca7	3.872	1.666
1249	MSTRG.19318	Ca_12348	Ca7	4.185	1.673
1250	MSTRG.18346	Ca_06685	Ca7	0.703	1.682
1251	MSTRG.18589	Ca_15322	Ca7	6.497	1.689
1252	MSTRG.19096	Ca_09920	Ca7	4.184	1.694
1253	MSTRG.18144	Ca_02960	Ca7	2.457	1.713
1254	MSTRG.17780	Ca_03301	Ca7	3.277	1.736
1255	MSTRG.19808	Ca_10100	Ca7	2.824	1.767
1256	MSTRG.19319	Ca_12340	Ca7	2.058	1.797

1257	MSTRG.20079	-	Ca7	0.833	1.799
1258	MSTRG.20252	-	Ca7	1.672	1.812
1259	MSTRG.20006	Ca_20988	Ca7	1.945	1.813
1260	MSTRG.18224	-	Ca7	2.416	1.817
1261	MSTRG.20004	Ca_20989	Ca7	4.625	1.886
1262	MSTRG.18483	Ca_13223	Ca7	4.421	1.902
1263	MSTRG.17756	Ca_03319	Ca7	-0.037	1.926
1264	MSTRG.19738	Ca_11697	Ca7	3.460	1.985
1265	MSTRG.19604	Ca_18940	Ca7	1.954	2.014
1266	MSTRG.18733	Ca_12797	Ca7	8.944	2.073
1267	MSTRG.19463	-	Ca7	-0.630	2.133
1268	MSTRG.19737	Ca_11698	Ca7	2.103	2.234
1269	MSTRG.20302	Ca_20261	Ca7	2.945	2.240
1270	MSTRG.20369	-	Ca7	1.642	2.303
1271	MSTRG.17978	Ca_03124	Ca7	2.267	2.388
1272	MSTRG.20438	-	Ca7	-1.414	2.514
1273	MSTRG.17829	Ca_03258	Ca7	1.839	2.534
1274	MSTRG.17688	-	Ca7	3.624	2.629
1275	MSTRG.18007	Ca_03099	Ca7	1.455	2.630
1276	MSTRG.18769	Ca_12830	Ca7	5.046	2.712
1277	MSTRG.17681	Ca_03390	Ca7	3.368	2.737
1278	MSTRG.19679	-	Ca7	-0.333	2.771
1279	MSTRG.17815	-	Ca7	2.726	2.832
1280	MSTRG.17870	-	Ca7	3.695	2.860
1281	MSTRG.19504	-	Ca7	4.212	2.868
1282	MSTRG.20410	Ca_15698	Ca7	4.453	2.876
1283	MSTRG.17924	Ca_03175	Ca7	5.513	2.890
1284	MSTRG.18923	Ca_09243	Ca7	6.086	2.898
1285	MSTRG.18702	-	Ca7	-2.974	3.126
1286	MSTRG.18981	Ca_16053	Ca7	0.409	3.446
1287	MSTRG.19669	-	Ca7	-0.088	3.998
1288	MSTRG.17975	Ca_03126	Ca7	0.930	4.365
1289	MSTRG.17669	Ca_03399	Ca7	3.161	4.449
1290	MSTRG.17854	-	Ca7	-0.997	4.842
1291	MSTRG.20171	Ca_13797	Ca7	-1.231	4.886
1292	MSTRG.17974	Ca_03127	Ca7	-0.579	5.085
1293	MSTRG.19670	-	Ca7	-0.480	5.206

1294	MSTRG.18685	-	Ca7	-2.921	5.268
1295	MSTRG.19667	-	Ca7	-1.705	5.413
1296	MSTRG.19645	Ca_11789	Ca7	2.840	6.153
1297	MSTRG.19824	-	Ca7	-4.370	6.719
1298	MSTRG.19650	-	Ca7	-4.129	7.555
1299	MSTRG.21788	-	Ca8	-3.361	-9.758
1300	MSTRG.21422	-	Ca8	-1.683	-8.457
1301	MSTRG.21777	-	Ca8	-1.794	-7.778
1302	MSTRG.21192	-	Ca8	-1.440	-7.480
1303	MSTRG.21370	Ca_10628	Ca8	3.192	-5.497
1304	MSTRG.21278	-	Ca8	1.550	-5.265
1305	MSTRG.21773	-	Ca8	-0.993	-5.008
1306	MSTRG.21774	-	Ca8	-0.915	-4.102
1307	MSTRG.21325	Ca_10704	Ca8	2.596	-3.716
1308	MSTRG.21280	Ca_23584	Ca8	-1.004	-3.470
1309	MSTRG.21157	Ca_02024	Ca8	1.614	-3.365
1310	MSTRG.21271	-	Ca8	0.006	-2.956
1311	MSTRG.21921	-	Ca8	-0.542	-2.955
1312	MSTRG.21787	Ca_13034	Ca8	2.521	-2.929
1313	MSTRG.20817	Ca_02363	Ca8	-0.076	-2.893
1314	MSTRG.21090	Ca_02094	Ca8	-0.898	-2.619
1315	MSTRG.20614	Ca_11869	Ca8	2.880	-2.514
1316	MSTRG.20639	Ca_11846	Ca8	6.119	-2.054
1317	MSTRG.20906	Ca_02274	Ca8	1.585	-1.989
1318	MSTRG.21068	Ca_02114	Ca8	0.477	-1.989
1319	MSTRG.20764	Ca_02420	Ca8	8.640	-1.981
1320	MSTRG.20918	-	Ca8	1.471	-1.920
1321	MSTRG.20638	Ca_11847	Ca8	1.881	-1.881
1322	MSTRG.20713	Ca_15031	Ca8	1.292	-1.836
1323	MSTRG.21322	Ca_10708	Ca8	5.800	-1.813
1324	MSTRG.21784	Ca_13035	Ca8	3.493	-1.784
1325	MSTRG.20712	Ca_15034	Ca8	3.222	-1.769
1326	MSTRG.21299	Ca_10732	Ca8	0.709	-1.742
1327	MSTRG.21305	Ca_10724	Ca8	1.592	-1.722
1328	MSTRG.21987	Ca_15550	Ca8	-1.666	-1.698
1329	MSTRG.21362	-	Ca8	0.894	-1.627
1330	MSTRG.20705	Ca_15041	Ca8	-0.364	-1.416

1331	MSTRG.21172	Ca_02009	Ca8	2.303	-1.393
1332	MSTRG.21245	Ca_01942	Ca8	3.609	-1.326
1333	MSTRG.20640	Ca_11845	Ca8	6.415	-1.315
1334	MSTRG.21832	Ca_12999	Ca8	0.180	-1.313
1335	MSTRG.21270	Ca_23578	Ca8	4.818	-1.311
1336	MSTRG.21950	-	Ca8	0.815	-1.132
1337	MSTRG.21125	Ca_02060	Ca8	1.848	-1.116
1338	MSTRG.21437	Ca_10594	Ca8	6.943	-1.115
1339	MSTRG.21136	Ca_02045	Ca8	1.382	-1.102
1340	MSTRG.20585	Ca_11898	Ca8	5.496	-1.100
1341	MSTRG.21169	-	Ca8	1.845	-1.071
1342	MSTRG.21352	Ca_10677	Ca8	3.754	-1.070
1343	MSTRG.21045	-	Ca8	1.846	-1.059
1344	MSTRG.21742	Ca_20118	Ca8	1.280	-1.058
1345	MSTRG.21267	Ca_01923	Ca8	4.719	-1.037
1346	MSTRG.21186	Ca_01996	Ca8	3.910	-1.035
1347	MSTRG.21330	Ca_10697	Ca8	4.222	-1.014
1348	MSTRG.21705	Ca_16791	Ca8	3.771	-1.006
1349	MSTRG.21127	Ca_02059	Ca8	0.017	-1.003
1350	MSTRG.20801	Ca_02381	Ca8	4.310	1.005
1351	MSTRG.21603	Ca_18429	Ca8	4.105	1.005
1352	MSTRG.21529	Ca_11524	Ca8	7.587	1.028
1353	MSTRG.21439	Ca_11432	Ca8	0.167	1.045
1354	MSTRG.21837	-	Ca8	1.472	1.047
1355	MSTRG.21671	-	Ca8	2.314	1.059
1356	MSTRG.20912	-	Ca8	0.738	1.084
1357	MSTRG.20694	Ca_15053	Ca8	0.632	1.104
1358	MSTRG.20931	-	Ca8	-0.076	1.105
1359	MSTRG.21311	Ca_10716	Ca8	3.216	1.128
1360	MSTRG.21829	Ca_13002	Ca8	6.134	1.159
1361	MSTRG.21056	Ca_02128	Ca8	5.279	1.165
1362	MSTRG.21222	Ca_01963	Ca8	3.587	1.169
1363	MSTRG.20841	Ca_02339	Ca8	2.709	1.190
1364	MSTRG.20914	Ca_02264	Ca8	2.792	1.204
1365	MSTRG.21494	Ca_11488	Ca8	2.800	1.220
1366	MSTRG.21354	-	Ca8	2.266	1.260
1367	MSTRG.21258	Ca_01930	Ca8	6.560	1.277

1368	MSTRG.21446	Ca_11443	Ca8	5.155	1.279
1369	MSTRG.21850	-	Ca8	5.208	1.326
1370	MSTRG.20971	Ca_02206	Ca8	3.480	1.343
1371	MSTRG.21395	Ca_10643	Ca8	1.823	1.386
1372	MSTRG.21008	Ca_02170	Ca8	4.854	1.433
1373	MSTRG.21368	-	Ca8	2.057	1.442
1374	MSTRG.20774	Ca_02410	Ca8	1.628	1.452
1375	MSTRG.21608	Ca_18433	Ca8	5.451	1.456
1376	MSTRG.21711	Ca_23843	Ca8	1.796	1.465
1377	MSTRG.21869	-	Ca8	0.495	1.477
1378	MSTRG.21818	Ca_13010	Ca8	7.545	1.489
1379	MSTRG.21913	-	Ca8	4.150	1.547
1380	MSTRG.21754	Ca_22732	Ca8	2.778	1.570
1381	MSTRG.20975	Ca_02196	Ca8	4.077	1.580
1382	MSTRG.21423	Ca_10608	Ca8	1.860	1.585
1383	MSTRG.21149	Ca_02031	Ca8	3.626	1.590
1384	MSTRG.21859	Ca_12980	Ca8	2.679	1.602
1385	MSTRG.21276	Ca_23582	Ca8	1.680	1.607
1386	MSTRG.20936	Ca_02241	Ca8	0.600	1.609
1387	MSTRG.21285	-	Ca8	0.009	1.673
1388	MSTRG.21381	Ca_10657	Ca8	-0.422	1.692
1389	MSTRG.21012	Ca_02167	Ca8	3.975	1.698
1390	MSTRG.20766	Ca_02422	Ca8	1.450	1.716
1391	MSTRG.21159	Ca_02019	Ca8	6.975	1.739
1392	MSTRG.21944	Ca_15504	Ca8	4.281	1.755
1393	MSTRG.21102	Ca_02082	Ca8	0.413	1.899
1394	MSTRG.21551	Ca_11546	Ca8	5.127	2.019
1395	MSTRG.20998	Ca_02176	Ca8	0.698	2.038
1396	MSTRG.20740	-	Ca8	-0.168	2.072
1397	MSTRG.21908	Ca_17891	Ca8	2.547	2.089
1398	MSTRG.21065	Ca_02117	Ca8	3.844	2.145
1399	MSTRG.20738	Ca_02445	Ca8	2.622	2.178
1400	MSTRG.21183	Ca_01998	Ca8	1.810	2.205
1401	MSTRG.21840	-	Ca8	0.059	2.240
1402	MSTRG.20707	Ca_15040	Ca8	3.252	2.248
1403	MSTRG.20901	Ca_02279	Ca8	3.812	2.273
1404	MSTRG.21552	Ca_11547	Ca8	0.122	2.302

1405	MSTRG.21116	Ca_02070	Ca8	2.978	2.406
1406	MSTRG.20789	Ca_02397	Ca8	5.379	2.414
1407	MSTRG.21301	Ca_10730	Ca8	1.774	2.478
1408	MSTRG.21566	-	Ca8	-0.202	2.494
1409	MSTRG.21399	-	Ca8	-1.135	2.572
1410	MSTRG.20598	Ca_11885	Ca8	3.513	2.586
1411	MSTRG.20708	Ca_15039	Ca8	1.322	2.588
1412	MSTRG.21768	Ca_13048	Ca8	3.117	2.780
1413	MSTRG.21541	Ca_11536	Ca8	0.704	2.794
1414	MSTRG.20758	Ca_02428	Ca8	0.159	2.925
1415	MSTRG.21383	Ca_10655	Ca8	-1.442	2.994
1416	MSTRG.21043	Ca_02137	Ca8	6.402	3.236
1417	MSTRG.21361	-	Ca8	0.657	3.481
1418	MSTRG.21147	-	Ca8	-1.393	3.541
1419	MSTRG.21363	-	Ca8	0.200	3.589
1420	MSTRG.20599	-	Ca8	-0.461	4.377
1421	MSTRG.21448	-	Ca8	-3.008	4.789
1422	MSTRG.20825	Ca_02358	Ca8	4.397	5.582
1423	MSTRG.21450	-	Ca8	-2.860	5.593
1424	MSTRG.21094	Ca_02088	Ca8	2.659	6.042
1425	MSTRG.20779	-	Ca8	-2.954	6.615
1426	MSTRG.21452	-	Ca8	-2.585	6.739
1427	MSTRG.21738	Ca_20106	Ca8	0.475	6.860
1428	MSTRG.21358	-	Ca8	-2.457	7.910
1429	MSTRG.21451	-	Ca8	-3.559	8.634
1430	MSTRG.21449	-	Ca8	-3.531	9.388
1431	MSTRG.22057	-	scaffold1006	4.833	1.449
1432	MSTRG.22051	-	scaffold1010	-3.633	-6.128
1433	MSTRG.22053	-	scaffold1010	-1.617	4.800
1434	MSTRG.22067	Ca_28086	scaffold10227	4.025	1.504
1435	MSTRG.22147	-	scaffold1052	4.707	-1.691
1436	MSTRG.22149	-	scaffold1052	-2.764	5.264
1437	MSTRG.22157	Ca_25316	scaffold1055	5.054	1.672
1438	MSTRG.22195	-	scaffold1067	-0.275	-2.633
1439	MSTRG.22204	-	scaffold1089	1.038	2.874
1440	MSTRG.22206	Ca_24273	scaffold1089	4.630	2.969
1441	MSTRG.22220	-	scaffold109_1	4.328	1.010

1442	MSTRG.22227	-	scaffold109_1	1.160	1.889
1443	MSTRG.22234	-	scaffold109_1	2.362	2.598
1444	MSTRG.22216	Ca_27968	scaffold1095	0.926	-1.051
1445	MSTRG.22258	-	scaffold1107	-1.277	3.459
1446	MSTRG.22268	Ca_27287	scaffold1114	-1.656	-3.248
1447	MSTRG.22270	Ca_24640	scaffold1115	6.189	1.228
1448	MSTRG.22272	-	scaffold1116	-3.444	5.978
1449	MSTRG.22289	Ca_25662	scaffold1131	-2.369	6.050
1450	MSTRG.22292	Ca_25666	scaffold1131	-2.017	6.648
1451	MSTRG.22297	Ca_26366	scaffold1145	4.894	1.164
1452	MSTRG.22301	Ca_22323	scaffold1151	-1.092	3.458
1453	MSTRG.22320	-	scaffold1176_2	1.712	1.067
1454	MSTRG.22332	Ca_22947	scaffold118	1.004	6.677
1455	MSTRG.22364	-	scaffold1195	1.638	1.149
1456	MSTRG.22383	-	scaffold1197	0.015	-2.545
1457	MSTRG.22390	Ca_22967	scaffold12	1.901	-1.302
1458	MSTRG.22409	Ca_24666	scaffold1202	6.366	-3.334
1459	MSTRG.22423	-	scaffold123	2.078	-1.030
1460	MSTRG.22425	-	scaffold1231	-2.993	2.190
1461	MSTRG.22437	-	scaffold1259	0.951	1.615
1462	MSTRG.22441	-	scaffold1275	0.881	-1.328
1463	MSTRG.22464	-	scaffold128	-3.632	-7.942
1464	MSTRG.22463	-	scaffold128	-4.293	-7.289
1465	MSTRG.22450	-	scaffold128	-3.572	-6.044
1466	MSTRG.22449	-	scaffold128	-0.862	-5.046
1467	MSTRG.22460	-	scaffold128	3.694	-3.554
1468	MSTRG.22462	Ca_21449	scaffold128	7.865	-1.987
1469	MSTRG.22468	Ca_21511	scaffold1281	5.958	1.081
1470	MSTRG.22516	-	scaffold1301_1	-0.462	-9.134
1471	MSTRG.22514	-	scaffold1301_1	-4.213	-7.553
1472	MSTRG.22493	-	scaffold1301_1	4.306	-1.279
1473	MSTRG.22556	-	scaffold1324	1.659	-1.332
1474	MSTRG.22564	Ca_19776	scaffold1324	5.203	-1.108
1475	MSTRG.22571	Ca_19787	scaffold1324	4.048	5.801
1476	MSTRG.22583	-	scaffold134	0.376	-1.037
1477	MSTRG.22577	Ca_22580	scaffold134	5.055	1.385
1478	MSTRG.22590	Ca_22590	scaffold134	3.541	1.547

1479	MSTRG.22634	-	scaffold1348_1	6.884	-3.850
1480	MSTRG.22635	-	scaffold1348_1	4.101	1.125
1481	MSTRG.22695	-	scaffold1348_1	5.603	1.542
1482	MSTRG.22696	-	scaffold1348_1	-0.044	2.181
1483	MSTRG.22707	-	scaffold1348_1	7.654	2.640
1484	MSTRG.22739	Ca_21989	scaffold1351	4.816	1.384
1485	MSTRG.22769	-	scaffold1382	-2.645	4.937
1486	MSTRG.22796	-	scaffold1417	-1.451	-5.963
1487	MSTRG.22790	-	scaffold1417	0.462	-2.067
1488	MSTRG.22801	-	scaffold1417	1.532	-1.049
1489	MSTRG.22845	Ca_26807	scaffold1467	3.095	-2.470
1490	MSTRG.22846	-	scaffold1467	-0.043	-2.378
1491	MSTRG.22857	-	scaffold1483	4.505	-1.040
1492	MSTRG.22854	-	scaffold1490	0.772	-5.572
1493	MSTRG.22871	Ca_24096	scaffold1504	-1.792	-4.003
1494	MSTRG.22878	-	scaffold1506	0.589	1.877
1495	MSTRG.22893	-	scaffold1543	0.934	-2.461
1496	MSTRG.22934	Ca_21087	scaffold157	6.551	1.070
1497	MSTRG.22927	Ca_21077	scaffold157	-0.744	1.657
1498	MSTRG.22937	Ca_27018	scaffold1575	-0.510	-4.798
1499	MSTRG.22980	-	scaffold1633	-2.573	4.138
1500	MSTRG.22984	-	scaffold1633	-3.470	6.692
1501	MSTRG.23012	-	scaffold167	0.039	-2.273
1502	MSTRG.23015	-	scaffold167	-0.395	-2.084
1503	MSTRG.23048	-	scaffold1703	-2.563	8.754
1504	MSTRG.23053	Ca_27772	scaffold1706	0.599	-1.773
1505	MSTRG.23069	Ca_25726	scaffold1710	3.348	2.630
1506	MSTRG.23100	Ca_21711	scaffold174	0.879	-6.191
1507	MSTRG.23180	Ca_26998	scaffold1825	-2.149	6.480
1508	MSTRG.23194	-	scaffold1844	2.492	3.193
1509	MSTRG.23212	-	scaffold186	1.611	-1.068
1510	MSTRG.23214	Ca_24799	scaffold186	4.089	1.474
1511	MSTRG.23226	Ca_25353	scaffold1867	-1.577	-4.160
1512	MSTRG.23223	-	scaffold1867	2.657	-1.051
1513	MSTRG.23262	-	scaffold193	-2.188	-7.728
1514	MSTRG.23261	-	scaffold193	-1.602	-4.628
1515	MSTRG.23254	Ca_25164	scaffold193	3.231	1.194

1516	MSTRG.23282	Ca_26462	scaffold1959	-0.157	-3.458
1517	MSTRG.23300	-	scaffold198	-2.946	9.687
1518	MSTRG.23319	-	scaffold1981	-2.664	3.975
1519	MSTRG.23367	-	scaffold2033	-2.455	3.081
1520	MSTRG.23404	-	scaffold206	-1.367	2.759
1521	MSTRG.23412	Ca_21896	scaffold210	2.435	-1.637
1522	MSTRG.23417	Ca_21901	scaffold210	4.236	-1.215
1523	MSTRG.23411	Ca_21894	scaffold210	1.286	2.354
1524	MSTRG.23428	Ca_24892	scaffold212	2.709	-1.557
1525	MSTRG.23445	-	scaffold2152	0.476	-3.496
1526	MSTRG.23483	-	scaffold223	-2.811	3.908
1527	MSTRG.23538	Ca_24344	scaffold2356	6.922	-2.177
1528	MSTRG.23545	-	scaffold2356	-0.959	7.655
1529	MSTRG.23578	-	scaffold2373	0.218	1.303
1530	MSTRG.23573	Ca_27075	scaffold2373	-1.049	1.840
1531	MSTRG.23576	-	scaffold2378	-3.138	6.128
1532	MSTRG.23600	Ca_25869	scaffold2415	5.217	1.048
1533	MSTRG.23643	Ca_26665	scaffold2557	-2.981	4.039
1534	MSTRG.23645	-	scaffold2560	3.986	2.050
1535	MSTRG.23649	Ca_26161	scaffold2569	1.178	1.797
1536	MSTRG.23706	Ca_27756	scaffold2678	3.803	-1.650
1537	MSTRG.23707	Ca_27757	scaffold2678	3.868	-1.581
1538	MSTRG.23713	-	scaffold2711	-1.220	-2.685
1539	MSTRG.23719	Ca_26034	scaffold2720	2.974	1.738
1540	MSTRG.23725	-	scaffold2728	3.302	-6.074
1541	MSTRG.23735	-	scaffold2734	-0.114	3.118
1542	MSTRG.23742	-	scaffold275	-0.469	-2.524
1543	MSTRG.23754	-	scaffold2763	0.877	-5.690
1544	MSTRG.23775	-	scaffold2837	0.263	-1.458
1545	MSTRG.23792	Ca_20600	scaffold284	7.728	3.396
1546	MSTRG.23793	-	scaffold284	-3.570	8.888
1547	MSTRG.23801	-	scaffold2850	-0.848	8.486
1548	MSTRG.23831	-	scaffold287	-1.647	-3.608
1549	MSTRG.23813	-	scaffold287	1.048	-1.066
1550	MSTRG.23835	-	scaffold290	-1.481	-7.428
1551	MSTRG.23868	Ca_20540	scaffold296	0.006	-9.873
1552	MSTRG.23861	Ca_20532	scaffold296	3.239	1.294

1553	MSTRG.23898	-	scaffold3016	-1.746	-7.427
1554	MSTRG.23903	Ca_25899	scaffold305	-2.266	-5.281
1555	MSTRG.23904	-	scaffold305	3.483	-2.965
1556	MSTRG.23905	-	scaffold305	-0.854	-2.424
1557	MSTRG.23908	Ca_25904	scaffold305	0.496	2.846
1558	MSTRG.23948	-	scaffold314	-0.293	-2.437
1559	MSTRG.23963	-	scaffold314	0.131	2.452
1560	MSTRG.23987	Ca_24182	scaffold3170	4.602	1.651
1561	MSTRG.23991	Ca_24185	scaffold3170	-0.531	1.903
1562	MSTRG.24007	-	scaffold3254_2	3.526	1.031
1563	MSTRG.24025	-	scaffold3254_2	3.246	1.564
1564	MSTRG.24038	Ca_25759	scaffold332	0.557	-6.932
1565	MSTRG.24039	Ca_25706	scaffold3321	1.148	1.180
1566	MSTRG.24045	Ca_28178	scaffold3337	-3.264	3.870
1567	MSTRG.24044	-	scaffold3337	-4.268	7.761
1568	MSTRG.24051	-	scaffold335	1.190	-1.882
1569	MSTRG.24069	Ca_21291	scaffold336	1.218	-4.537
1570	MSTRG.24088	-	scaffold3397	-0.231	1.352
1571	MSTRG.24087	-	scaffold3397	-2.545	1.445
1572	MSTRG.24104	-	scaffold342	0.355	-3.528
1573	MSTRG.24109	-	scaffold342	-0.665	-3.398
1574	MSTRG.24106	-	scaffold342	-0.321	-2.256
1575	MSTRG.24142	-	scaffold346_1	-0.596	-2.139
1576	MSTRG.24139	-	scaffold346_1	0.236	-1.020
1577	MSTRG.24143	-	scaffold346_1	3.384	1.404
1578	MSTRG.24136	-	scaffold346_1	3.265	1.615
1579	MSTRG.24141	-	scaffold346_1	-3.002	7.890
1580	MSTRG.24152	Ca_24505	scaffold349	0.517	-7.299
1581	MSTRG.24151	Ca_24504	scaffold349	1.927	-2.049
1582	MSTRG.24149	Ca_24496	scaffold349	3.478	-1.268
1583	MSTRG.24189	-	scaffold362	-1.115	-7.827
1584	MSTRG.24192	Ca_24991	scaffold362	2.927	-7.619
1585	MSTRG.24201	-	scaffold3654	-4.030	-7.011
1586	MSTRG.24227	Ca_26156	scaffold379	3.193	1.272
1587	MSTRG.24236	Ca_23621	scaffold38	4.159	2.819
1588	MSTRG.24244	-	scaffold3817	-3.827	8.563
1589	MSTRG.24257	Ca_27767	scaffold387	-2.079	-6.018

1590	MSTRG.24251	Ca_27766	scaffold387	-2.473	-4.786
1591	MSTRG.24256	-	scaffold387	1.878	-2.199
1592	MSTRG.24255	Ca_27532	scaffold3934	-3.016	4.187
1593	MSTRG.24267	Ca_24514	scaffold395	-2.945	-5.909
1594	MSTRG.24275	Ca_24520	scaffold395	6.156	-1.065
1595	MSTRG.24280	-	scaffold396	-4.098	-7.685
1596	MSTRG.24281	-	scaffold396	-4.288	-6.741
1597	MSTRG.24282	Ca_23555	scaffold396	2.151	-2.530
1598	MSTRG.24276	-	scaffold396	-1.729	-2.335
1599	MSTRG.24298	-	scaffold398	-0.798	-1.870
1600	MSTRG.24299	-	scaffold398	-0.907	-1.687
1601	MSTRG.24325	-	scaffold40	0.891	-1.014
1602	MSTRG.24332	Ca_19001	scaffold40	0.207	1.157
1603	MSTRG.24346	Ca_24360	scaffold404	2.683	1.228
1604	MSTRG.24368	-	scaffold411	-3.194	-5.690
1605	MSTRG.24369	-	scaffold411	-3.934	5.304
1606	MSTRG.24385	Ca_26397	scaffold419	0.653	1.844
1607	MSTRG.24386	-	scaffold419	-2.998	4.326
1608	MSTRG.24403	-	scaffold420	-3.412	-7.728
1609	MSTRG.24401	-	scaffold420	0.383	-4.642
1610	MSTRG.24402	-	scaffold420	-0.472	-3.428
1611	MSTRG.24433	-	scaffold421_1	-1.749	6.492
1612	MSTRG.24449	Ca_26259	scaffold435	3.627	-1.384
1613	MSTRG.24450	Ca_26260	scaffold435	-0.963	1.708
1614	MSTRG.24455	Ca_27838	scaffold4387	1.762	-1.836
1615	MSTRG.24462	Ca_25414	scaffold44	-3.495	6.844
1616	MSTRG.24471	-	scaffold4462	0.227	-9.937
1617	MSTRG.24479	-	scaffold450	-2.924	5.596
1618	MSTRG.24497	Ca_22614	scaffold451	5.348	1.500
1619	MSTRG.24490	Ca_22603	scaffold451	1.426	1.833
1620	MSTRG.24549	-	scaffold4773	-4.454	5.999
1621	MSTRG.24622	-	scaffold4978	-1.076	-3.899
1622	MSTRG.24626	Ca_25362	scaffold498	1.039	1.822
1623	MSTRG.24654	-	scaffold513	-4.154	6.321
1624	MSTRG.24664	-	scaffold5226	0.526	1.698
1625	MSTRG.24667	Ca_26390	scaffold527	1.069	-1.095
1626	MSTRG.24758	Ca_23922	scaffold545	2.801	-1.192

1627	MSTRG.24788	Ca_19945	scaffold553	3.283	1.187
1628	MSTRG.24772	Ca_19924	scaffold553	0.799	2.096
1629	MSTRG.24810	Ca_23125	scaffold562	6.043	-2.114
1630	MSTRG.24812	Ca_23129	scaffold562	5.538	2.985
1631	MSTRG.24811	-	scaffold562	-2.188	4.006
1632	MSTRG.24820	Ca_27413	scaffold5687	3.215	1.675
1633	MSTRG.24825	-	scaffold5739	-0.358	1.913
1634	MSTRG.24830	-	scaffold575	-4.061	-7.416
1635	MSTRG.24849	-	scaffold589	-1.448	-3.042
1636	MSTRG.24851	-	scaffold590	0.313	-1.858
1637	MSTRG.24853	-	scaffold590	5.246	-1.409
1638	MSTRG.24850	-	scaffold590	0.689	1.571
1639	MSTRG.24852	-	scaffold590	-1.441	2.120
1640	MSTRG.24861	-	scaffold5902	0.293	3.233
1641	MSTRG.24863	-	scaffold593	-0.221	-5.561
1642	MSTRG.24886	-	scaffold599	-0.570	-1.990
1643	MSTRG.24901	-	scaffold6181	-2.246	2.875
1644	MSTRG.24956	-	scaffold642	0.321	-2.785
1645	MSTRG.24951	Ca_19118	scaffold642	6.471	-1.682
1646	MSTRG.24962	-	scaffold645	-0.421	-9.588
1647	MSTRG.24964	-	scaffold645	-2.162	-5.114
1648	MSTRG.24968	-	scaffold6458	1.827	1.044
1649	MSTRG.24970	Ca_27555	scaffold6458	0.764	2.683
1650	MSTRG.24987	-	scaffold661	-0.923	-1.203
1651	MSTRG.24993	-	scaffold661	-0.794	4.836
1652	MSTRG.25001	-	scaffold6704	-1.997	-4.556
1653	MSTRG.25012	Ca_20156	scaffold674	1.046	6.433
1654	MSTRG.25031	-	scaffold682	-3.410	-5.273
1655	MSTRG.25038	Ca_23193	scaffold682	3.291	-1.567
1656	MSTRG.25046	-	scaffold686	-0.588	-1.439
1657	MSTRG.25068	Ca_24965	scaffold716	0.374	3.787
1658	MSTRG.25072	Ca_27654	scaffold72	0.697	-1.866
1659	MSTRG.25077	-	scaffold720	-3.810	8.070
1660	MSTRG.25097	Ca_28149	scaffold728	2.404	1.073
1661	MSTRG.25140	-	scaffold766	-1.786	2.329
1662	MSTRG.25155	-	scaffold775	-2.218	-6.467
1663	MSTRG.25149	-	scaffold775	0.476	-6.034

1664	MSTRG.25161	-	scaffold7765	0.062	-2.910
1665	MSTRG.25164	Ca_27351	scaffold7800	2.318	1.524
1666	MSTRG.25168	Ca_27195	scaffold783	4.884	2.324
1667	MSTRG.25177	-	scaffold787	-0.025	1.589
1668	MSTRG.25209	-	scaffold811	-0.500	-1.352
1669	MSTRG.25255	-	scaffold845	0.716	-2.339
1670	MSTRG.25258	-	scaffold847	-0.703	-2.827
1671	MSTRG.25333	-	scaffold876	-1.722	6.556
1672	MSTRG.25377	Ca_26670	scaffold886	3.847	-1.491
1673	MSTRG.25383	-	scaffold887_1	3.229	1.021
1674	MSTRG.25405	-	scaffold895	2.733	1.445
1675	MSTRG.25404	-	scaffold895	3.390	1.773
1676	MSTRG.25424	-	scaffold9	-0.960	-4.813
1677	MSTRG.25445	-	scaffold913	0.115	-8.162
1678	MSTRG.25446	Ca_23217	scaffold913	8.776	1.453
1679	MSTRG.25440	-	scaffold913	-2.429	6.751
1680	MSTRG.25441	-	scaffold913	-2.971	7.875
1681	MSTRG.25480	Ca_21060	scaffold916	5.211	1.010
1682	MSTRG.25541	Ca_26911	scaffold953	1.660	2.014
1683	MSTRG.25544	-	scaffold96	-1.156	-8.661
1684	MSTRG.25551	Ca_24084	scaffold96	0.546	-1.840
1685	MSTRG.25567	-	scaffold960	2.555	-2.629
1686	MSTRG.25585	-	scaffold98	1.427	1.229
1687	MSTRG.25571	-	scaffold98	-0.593	1.701
1688	MSTRG.25568	-	scaffold98	0.632	1.780
1689	MSTRG.25579	Ca_21391	scaffold98	5.866	2.316
1690	MSTRG.25595	-	scaffold983	-0.576	1.285

Supplementary Table 9: PRR resistance genes in PRR resistant breeding line 04067-81-2-1-1 (Bc-C) differently expressed under control condition compared to PRR moderately resistant genotype Yorker

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)
1	MSTRG.7699	Ca_07670	Ca4	1.014	-11.128
2	MSTRG.23868	Ca_20540	scaffold296	0.006	-10.080
3	MSTRG.24471	-	scaffold4462	0.227	-10.048
4	MSTRG.21024	-	Ca8	0.003	-9.975
5	MSTRG.148	-	C11165420	-0.323	-9.766
6	MSTRG.24962	-	scaffold645	-0.421	-9.305
7	MSTRG.2521	-	Ca1	0.388	-9.109
8	MSTRG.24189	-	scaffold362	-1.115	-9.042
9	MSTRG.4070	-	Ca2	-3.794	-8.861
10	MSTRG.11072	-	Ca5	-0.148	-8.674
11	MSTRG.15846	Ca_16333	Ca6	1.136	-8.659
12	MSTRG.16918	-	Ca6	-0.172	-8.603
13	MSTRG.16304	Ca_25967	Ca6	0.334	-8.581
14	MSTRG.25445	-	scaffold913	0.115	-8.564
15	MSTRG.22516	-	scaffold1301_1	-0.462	-8.388
16	MSTRG.17295	-	Ca6	-0.743	-8.385
17	MSTRG.17113	Ca_19190	Ca6	2.426	-8.298
18	MSTRG.17182	-	Ca6	-0.845	-8.212
19	MSTRG.11148	-	Ca5	-3.734	-8.046
20	MSTRG.16654	Ca_19804	Ca6	-1.215	-7.846
21	MSTRG.18788	-	Ca7	-1.336	-7.796
22	MSTRG.2282	Ca_18302	Ca1	0.862	-7.684
23	MSTRG.22989	Ca_26203	scaffold1633	-4.209	-7.630
24	MSTRG.17007	-	Ca6	-0.996	-7.570
25	MSTRG.16990	-	Ca6	-1.664	-7.557
26	MSTRG.25544	-	scaffold96	-1.156	-7.548
27	MSTRG.9720	-	Ca4	-3.448	-7.415
28	MSTRG.5313	-	Ca3	-1.236	-7.401
29	MSTRG.24152	Ca_24505	scaffold349	0.517	-7.395
30	MSTRG.16706	-	Ca6	-1.051	-7.285
31	MSTRG.21422	-	Ca8	-1.683	-7.246
32	MSTRG.21777	-	Ca8	-1.794	-7.236
33	MSTRG.23903	Ca_25899	scaffold305	-2.266	-7.145
34	MSTRG.562	-	Ca1	-3.834	-7.078
35	MSTRG.16451	-	Ca6	-1.869	-6.997

36	MSTRG.23898	-	scaffold3016	-1.746	-6.975
37	MSTRG.24716	-	scaffold537	1.281	-6.892
38	MSTRG.11110	-	Ca5	-3.892	-6.871
39	MSTRG.10100	Ca_22449	Ca4	-1.634	-6.788
40	MSTRG.25155	-	scaffold775	-2.218	-6.749
41	MSTRG.22473	Ca_21520	scaffold1281	-1.380	-6.678
42	MSTRG.2269	Ca_18312	Ca1	-1.715	-6.630
43	MSTRG.22796	-	scaffold1417	-1.451	-6.580
44	MSTRG.12212	-	Ca5	-0.946	-6.554
45	MSTRG.23633	-	scaffold2516	-3.782	-6.466
46	MSTRG.16414	-	Ca6	-2.211	-6.456
47	MSTRG.513	Ca_00310	Ca1	2.493	-6.399
48	MSTRG.7543	Ca_01273	Ca3	-2.029	-6.372
49	MSTRG.24156	-	scaffold3497	-3.054	-6.363
50	MSTRG.24257	Ca_27767	scaffold387	-2.079	-6.354
51	MSTRG.2568	-	Ca1	0.391	-6.281
52	MSTRG.21192	-	Ca8	-1.440	-6.271
53	MSTRG.22854	-	scaffold1490	0.772	-6.239
54	MSTRG.24192	Ca_24991	scaffold362	2.927	-6.171
55	MSTRG.3134	Ca_12619	Ca2	-4.201	-6.162
56	MSTRG.16966	Ca_23440	Ca6	-0.218	-6.131
57	MSTRG.20391	-	Ca7	0.544	-6.124
58	MSTRG.17337	-	Ca6	-1.065	-6.098
59	MSTRG.2558	-	Ca1	1.980	-6.032
60	MSTRG.23100	Ca_21711	scaffold174	0.879	-6.030
61	MSTRG.11607	-	Ca5	-2.040	-6.024
62	MSTRG.8110	Ca_03807	Ca4	1.255	-5.888
63	MSTRG.23725	-	scaffold2728	3.302	-5.856
64	MSTRG.25001	-	scaffold6704	-1.997	-5.815
65	MSTRG.16386	-	Ca6	-1.940	-5.738
66	MSTRG.16675	-	Ca6	1.112	-5.736
67	MSTRG.21370	Ca_10628	Ca8	3.192	-5.696
68	MSTRG.2170	Ca_22106	Ca1	-1.733	-5.565
69	MSTRG.25149	-	scaffold775	0.476	-5.564
70	MSTRG.16793	Ca_23239	Ca6	3.162	-5.494
71	MSTRG.12177	-	Ca5	-3.398	-5.380
72	MSTRG.7670	-	Ca4	-1.145	-5.342

73	MSTRG.17344	-	Ca6	-1.532	-5.315
74	MSTRG.2981	-	Ca1	-2.358	-5.310
75	MSTRG.21278	-	Ca8	1.550	-5.284
76	MSTRG.16342	-	Ca6	0.882	-5.175
77	MSTRG.9146	Ca_05635	Ca4	0.682	-5.134
78	MSTRG.11421	-	Ca5	-3.376	-5.072
79	MSTRG.2519	-	Ca1	2.093	-5.034
80	MSTRG.22937	Ca_27018	scaffold1575	-0.510	-5.014
81	MSTRG.10287	Ca_13096	Ca4	4.033	-4.990
82	MSTRG.11071	-	Ca5	-1.629	-4.907
83	MSTRG.17103	Ca_13435	Ca6	-2.059	-4.893
84	MSTRG.2661	-	Ca1	-0.972	-4.867
85	MSTRG.23812	Ca_25387	scaffold287	0.409	-4.864
86	MSTRG.5994	Ca_06159	Ca3	-1.906	-4.863
87	MSTRG.19528	-	Ca7	-1.370	-4.855
88	MSTRG.13644	Ca_03951	Ca5	1.006	-4.833
89	MSTRG.5368	Ca_18806	Ca3	0.628	-4.815
90	MSTRG.4446	Ca_16100	Ca2	1.058	-4.713
91	MSTRG.17230	Ca_18906	Ca6	3.279	-4.665
92	MSTRG.2569	-	Ca1	-1.829	-4.621
93	MSTRG.24964	-	scaffold645	-2.162	-4.563
94	MSTRG.2235	-	Ca1	-1.048	-4.501
95	MSTRG.8555	Ca_08362	Ca4	1.390	-4.499
96	MSTRG.23226	Ca_25353	scaffold1867	-1.577	-4.437
97	MSTRG.24863	-	scaffold593	-0.221	-4.253
98	MSTRG.21325	Ca_10704	Ca8	2.596	-4.219
99	MSTRG.3969	-	Ca2	-2.074	-4.205
100	MSTRG.2832	-	Ca1	-0.953	-4.187
101	MSTRG.18157	Ca_02952	Ca7	-0.272	-4.142
102	MSTRG.9240	-	Ca4	-1.140	-4.127
103	MSTRG.10325	Ca_13056	Ca4	0.559	-4.114
104	MSTRG.16808	Ca_23256	Ca6	-0.811	-4.097
105	MSTRG.17426	-	Ca6	-1.702	-4.084
106	MSTRG.24038	Ca_25759	scaffold332	0.557	-4.035
107	MSTRG.7556	-	Ca3	-0.814	-4.027
108	MSTRG.25330	-	scaffold876	0.290	-4.018
109	MSTRG.2894	-	Ca1	-1.492	-4.009

110	MSTRG.23282	Ca_26462	scaffold1959	-0.157	-3.926
111	MSTRG.2829	-	Ca1	-1.175	-3.845
112	MSTRG.25276	-	scaffold855	-1.168	-3.773
113	MSTRG.17733	-	Ca7	2.431	-3.771
114	MSTRG.22634	-	scaffold1348_1	6.884	-3.770
115	MSTRG.17674	Ca_03396	Ca7	-1.848	-3.717
116	MSTRG.21280	Ca_23584	Ca8	-1.004	-3.704
117	MSTRG.16715	Ca_15924	Ca6	-1.522	-3.690
118	MSTRG.23904	-	scaffold305	3.483	-3.671
119	MSTRG.16476	-	Ca6	-0.455	-3.577
120	MSTRG.6286	Ca_08205	Ca3	3.486	-3.558
121	MSTRG.16673	Ca_19788	Ca6	-1.049	-3.504
122	MSTRG.8936	Ca_04492	Ca4	-1.885	-3.486
123	MSTRG.24014	-	scaffold3254_2	-1.468	-3.473
124	MSTRG.25161	-	scaffold7765	0.062	-3.470
125	MSTRG.2417	-	Ca1	0.792	-3.461
126	MSTRG.16556	-	Ca6	0.590	-3.439
127	MSTRG.8398	Ca_03519	Ca4	-0.171	-3.409
128	MSTRG.8435	Ca_03482	Ca4	4.852	-3.391
129	MSTRG.23035	-	scaffold1687	0.658	-3.354
130	MSTRG.18209	-	Ca7	0.896	-3.339
131	MSTRG.16273	Ca_14581	Ca6	5.832	-3.332
132	MSTRG.22460	-	scaffold128	3.694	-3.319
133	MSTRG.2365	-	Ca1	-1.528	-3.311
134	MSTRG.17274	Ca_16294	Ca6	0.931	-3.306
135	MSTRG.4627	-	Ca2	0.231	-3.285
136	MSTRG.15963	-	Ca6	1.711	-3.281
137	MSTRG.8588	Ca_08397	Ca4	3.438	-3.245
138	MSTRG.9593	-	Ca4	-0.620	-3.223
139	MSTRG.13727	Ca_04035	Ca5	0.598	-3.200
140	MSTRG.6824	-	Ca3	0.732	-3.197
141	MSTRG.16064	Ca_11096	Ca6	3.160	-3.160
142	MSTRG.21862	Ca_12972	Ca8	1.003	-3.138
143	MSTRG.13756	Ca_04061	Ca5	2.537	-3.106
144	MSTRG.8589	Ca_08398	Ca4	3.295	-3.103
145	MSTRG.15214	-	Ca6	3.573	-3.090
146	MSTRG.16926	-	Ca6	-2.107	-3.087

147	MSTRG.16376	Ca_24059	Ca6	3.063	-3.082
148	MSTRG.2234	-	Ca1	-0.470	-3.070
149	MSTRG.438	Ca_00232	Ca1	1.167	-3.061
150	MSTRG.25219	-	scaffold812	0.125	-3.027
151	MSTRG.8850	Ca_04405	Ca4	6.958	-3.008
152	MSTRG.555	Ca_00351	Ca1	3.318	-2.990
153	MSTRG.15526	-	Ca6	-1.054	-2.979
154	MSTRG.15962	Ca_11225	Ca6	7.578	-2.976
155	MSTRG.17338	-	Ca6	-0.170	-2.970
156	MSTRG.13238	-	Ca5	2.221	-2.961
157	MSTRG.15509	Ca_06299	Ca6	4.231	-2.948
158	MSTRG.9414	Ca_05372	Ca4	-0.041	-2.933
159	MSTRG.15913	-	Ca6	-0.461	-2.899
160	MSTRG.24104	-	scaffold342	0.355	-2.882
161	MSTRG.2694	-	Ca1	8.317	-2.879
162	MSTRG.2721	-	Ca1	-1.741	-2.877
163	MSTRG.655	Ca_00464	Ca1	-0.222	-2.857
164	MSTRG.14544	Ca_05720	Ca6	5.844	-2.852
165	MSTRG.24849	-	scaffold589	-1.448	-2.846
166	MSTRG.21528	-	Ca8	-1.752	-2.833
167	MSTRG.2224	-	Ca1	0.843	-2.822
168	MSTRG.17239	Ca_18916	Ca6	3.960	-2.815
169	MSTRG.12008	Ca_13410	Ca5	2.458	-2.813
170	MSTRG.14545	-	Ca6	3.512	-2.741
171	MSTRG.11988	Ca_13431	Ca5	5.163	-2.740
172	MSTRG.17482	Ca_13637	Ca6	5.555	-2.737
173	MSTRG.24402	-	scaffold420	-0.472	-2.731
174	MSTRG.25567	-	scaffold960	2.555	-2.727
175	MSTRG.6614	Ca_07348	Ca3	-0.511	-2.717
176	MSTRG.5819	Ca_09495	Ca3	2.203	-2.685
177	MSTRG.16965	-	Ca6	3.324	-2.683
178	MSTRG.24109	-	scaffold342	-0.665	-2.665
179	MSTRG.23445	-	scaffold2152	0.476	-2.654
180	MSTRG.23034	-	scaffold1687	0.204	-2.641
181	MSTRG.15307	-	Ca6	2.321	-2.630
182	MSTRG.20906	Ca_02274	Ca8	1.585	-2.622
183	MSTRG.16819	-	Ca6	3.175	-2.611

184	MSTRG.6310	-	Ca3	-0.823	-2.606
185	MSTRG.9286	Ca_05500	Ca4	0.447	-2.605
186	MSTRG.23713	-	scaffold2711	-1.220	-2.590
187	MSTRG.9104	Ca_04649	Ca4	4.537	-2.579
188	MSTRG.17916	Ca_03183	Ca7	0.095	-2.571
189	MSTRG.22893	-	scaffold1543	0.934	-2.567
190	MSTRG.15308	Ca_05195	Ca6	3.916	-2.561
191	MSTRG.18779	-	Ca7	-2.059	-2.560
192	MSTRG.3199	Ca_12556	Ca2	1.378	-2.560
193	MSTRG.2738	Ca_25799	Ca1	-1.016	-2.552
194	MSTRG.9020	-	Ca4	0.853	-2.524
195	MSTRG.6831	Ca_11993	Ca3	7.036	-2.494
196	MSTRG.11914	Ca_08947	Ca5	4.027	-2.479
197	MSTRG.15283	Ca_05173	Ca6	3.343	-2.473
198	MSTRG.2436	Ca_22469	Ca1	1.531	-2.473
199	MSTRG.15819	Ca_16361	Ca6	2.411	-2.470
200	MSTRG.10229	-	Ca4	1.693	-2.468
201	MSTRG.16344	Ca_17465	Ca6	3.239	-2.455
202	MSTRG.21202	Ca_01984	Ca8	1.056	-2.435
203	MSTRG.24256	-	scaffold387	1.878	-2.430
204	MSTRG.9398	-	Ca4	1.065	-2.430
205	MSTRG.24951	Ca_19118	scaffold642	6.471	-2.428
206	MSTRG.23012	-	scaffold167	0.039	-2.407
207	MSTRG.16219	Ca_16727	Ca6	4.266	-2.401
208	MSTRG.16309	-	Ca6	4.507	-2.390
209	MSTRG.16892	-	Ca6	-1.938	-2.390
210	MSTRG.9022	Ca_04574	Ca4	5.540	-2.387
211	MSTRG.8377	Ca_03541	Ca4	2.245	-2.381
212	MSTRG.20371	-	Ca7	-1.145	-2.379
213	MSTRG.6714	-	Ca3	0.854	-2.373
214	MSTRG.16474	-	Ca6	0.114	-2.364
215	MSTRG.20638	Ca_11847	Ca8	1.881	-2.359
216	MSTRG.16438	Ca_16494	Ca6	2.311	-2.347
217	MSTRG.2555	-	Ca1	0.600	-2.337
218	MSTRG.23015	-	scaffold167	-0.395	-2.337
219	MSTRG.23538	Ca_24344	scaffold2356	6.922	-2.331
220	MSTRG.6698	-	Ca3	3.306	-2.327

221	MSTRG.10123	-	Ca4	0.191	-2.325
222	MSTRG.1321	Ca_02716	Ca1	0.566	-2.324
223	MSTRG.17334	-	Ca6	1.925	-2.324
224	MSTRG.16151	Ca_24160	Ca6	1.237	-2.317
225	MSTRG.15216	-	Ca6	3.532	-2.315
226	MSTRG.6769	Ca_12274	Ca3	2.733	-2.312
227	MSTRG.20990	Ca_02185	Ca8	1.047	-2.309
228	MSTRG.16210	Ca_16716	Ca6	5.104	-2.297
229	MSTRG.11713	-	Ca5	-0.884	-2.295
230	MSTRG.21271	-	Ca8	0.006	-2.292
231	MSTRG.8616	Ca_08423	Ca4	2.141	-2.269
232	MSTRG.16478	Ca_15198	Ca6	2.383	-2.266
233	MSTRG.5149	-	Ca3	0.200	-2.266
234	MSTRG.14469	Ca_05797	Ca6	4.457	-2.245
235	MSTRG.15213	Ca_05110	Ca6	9.202	-2.239
236	MSTRG.24956	-	scaffold642	0.321	-2.229
237	MSTRG.24455	Ca_27838	scaffold4387	1.762	-2.225
238	MSTRG.10809	-	Ca4	0.538	-2.197
239	MSTRG.24758	Ca_23922	scaffold545	2.801	-2.197
240	MSTRG.23536	Ca_26079	scaffold235	5.805	-2.177
241	MSTRG.7230	Ca_00977	Ca3	3.381	-2.168
242	MSTRG.6495	Ca_07234	Ca3	5.627	-2.152
243	MSTRG.16418	Ca_16474	Ca6	0.550	-2.151
244	MSTRG.2286	Ca_25078	Ca1	4.267	-2.150
245	MSTRG.2585	Ca_21834	Ca1	3.719	-2.149
246	MSTRG.24142	-	scaffold346_1	-0.596	-2.149
247	MSTRG.23742	-	scaffold275	-0.469	-2.137
248	MSTRG.19063	-	Ca7	1.259	-2.129
249	MSTRG.1588	Ca_02452	Ca1	2.130	-2.126
250	MSTRG.24151	Ca_24504	scaffold349	1.927	-2.124
251	MSTRG.453	Ca_00247	Ca1	-0.092	-2.114
252	MSTRG.6015	Ca_06140	Ca3	-0.669	-2.090
253	MSTRG.2663	-	Ca1	-0.209	-2.086
254	MSTRG.2961	Ca_12939	Ca1	3.652	-2.085
255	MSTRG.17137	-	Ca6	-0.516	-2.084
256	MSTRG.19704	Ca_11733	Ca7	-0.633	-2.079
257	MSTRG.20639	Ca_11846	Ca8	6.119	-2.075

258	MSTRG.12435	Ca_04943	Ca5	3.330	-2.070
259	MSTRG.1565	-	Ca1	0.999	-2.056
260	MSTRG.23552	-	scaffold2371	1.102	-2.055
261	MSTRG.3968	-	Ca2	0.750	-2.045
262	MSTRG.16955	-	Ca6	-0.135	-2.041
263	MSTRG.8717	-	Ca4	2.337	-2.038
264	MSTRG.17641	Ca_20221	Ca7	0.139	-2.031
265	MSTRG.19570	-	Ca7	-0.180	-2.019
266	MSTRG.8904	Ca_04462	Ca4	4.353	-2.015
267	MSTRG.2861	Ca_13532	Ca1	2.948	-2.013
268	MSTRG.16263	Ca_14588	Ca6	0.390	-2.011
269	MSTRG.9166	Ca_05616	Ca4	4.239	-2.005
270	MSTRG.15723	Ca_06505	Ca6	5.600	-1.995
271	MSTRG.18949	Ca_16020	Ca7	1.661	-1.994
272	MSTRG.17953	Ca_03151	Ca7	2.610	-1.993
273	MSTRG.12028	Ca_13394	Ca5	1.098	-1.993
274	MSTRG.12460	Ca_04971	Ca5	-0.191	-1.979
275	MSTRG.8186	Ca_03735	Ca4	6.039	-1.977
276	MSTRG.19009	Ca_23032	Ca7	3.392	-1.977
277	MSTRG.8063	Ca_03852	Ca4	2.248	-1.976
278	MSTRG.6094	-	Ca3	-3.080	-1.970
279	MSTRG.16120	Ca_11041	Ca6	1.630	-1.967
280	MSTRG.5667	-	Ca3	-0.268	-1.955
281	MSTRG.6702	-	Ca3	2.097	-1.947
282	MSTRG.7803	Ca_07768	Ca4	2.917	-1.942
283	MSTRG.4558	Ca_12429	Ca2	4.128	-1.941
284	MSTRG.15887	Ca_19869	Ca6	0.224	-1.938
285	MSTRG.18815	Ca_09355	Ca7	1.964	-1.938
286	MSTRG.2478	-	Ca1	1.609	-1.933
287	MSTRG.13762	-	Ca5	2.660	-1.932
288	MSTRG.5862	Ca_20430	Ca3	0.357	-1.930
289	MSTRG.7782	Ca_07754	Ca4	2.908	-1.927
290	MSTRG.20707	Ca_15040	Ca8	3.252	-1.917
291	MSTRG.9835	-	Ca4	-1.374	-1.914
292	MSTRG.5008	Ca_09817	Ca2	5.719	-1.912
293	MSTRG.14437	-	Ca6	4.902	-1.909
294	MSTRG.11559	Ca_24493	Ca5	-0.171	-1.897

295	MSTRG.17919	-	Ca7	-0.197	-1.897
296	MSTRG.23246	Ca_24715	scaffold1918	5.054	-1.894
297	MSTRG.17171	Ca_17540	Ca6	1.974	-1.877
298	MSTRG.17608	-	Ca6	-0.287	-1.871
299	MSTRG.20764	Ca_02420	Ca8	8.640	-1.870
300	MSTRG.681	Ca_00488	Ca1	1.355	-1.848
301	MSTRG.1981	Ca_22779	Ca1	7.814	-1.843
302	MSTRG.14351	Ca_05908	Ca6	7.134	-1.837
303	MSTRG.19904	Ca_10012	Ca7	3.521	-1.836
304	MSTRG.8692	-	Ca4	2.342	-1.834
305	MSTRG.8592	-	Ca4	1.797	-1.831
306	MSTRG.24851	-	scaffold590	0.313	-1.818
307	MSTRG.19983	-	Ca7	1.207	-1.816
308	MSTRG.440	Ca_00234	Ca1	3.874	-1.813
309	MSTRG.7551	Ca_01281	Ca3	1.275	-1.808
310	MSTRG.17292	Ca_21219	Ca6	1.721	-1.803
311	MSTRG.1117	Ca_02929	Ca1	3.826	-1.801
312	MSTRG.13889	Ca_04190	Ca5	1.965	-1.797
313	MSTRG.8920	Ca_04477	Ca4	1.082	-1.793
314	MSTRG.15960	Ca_11228	Ca6	2.636	-1.793
315	MSTRG.17660	Ca_03409	Ca7	1.244	-1.780
316	MSTRG.12159	Ca_04687	Ca5	6.755	-1.777
317	MSTRG.24991	-	scaffold661	-0.814	-1.774
318	MSTRG.2951	Ca_12948	Ca1	7.134	-1.771
319	MSTRG.1281	Ca_02766	Ca1	3.525	-1.769
320	MSTRG.6796	Ca_11961	Ca3	-0.830	-1.769
321	MSTRG.24106	-	scaffold342	-0.321	-1.750
322	MSTRG.23948	-	scaffold314	-0.293	-1.750
323	MSTRG.18247	Ca_06769	Ca7	7.110	-1.747
324	MSTRG.17097	Ca_13440	Ca6	4.719	-1.747
325	MSTRG.16359	Ca_17455	Ca6	4.754	-1.745
326	MSTRG.8963	Ca_04518	Ca4	2.476	-1.721
327	MSTRG.13821	Ca_04124	Ca5	4.589	-1.720
328	MSTRG.17091	Ca_13443	Ca6	2.758	-1.720
329	MSTRG.1041	Ca_08034	Ca1	6.607	-1.714
330	MSTRG.17684	-	Ca7	1.296	-1.709
331	MSTRG.20515	-	Ca7	0.736	-1.697

332	MSTRG.7354	Ca_01099	Ca3	5.199	-1.697
333	MSTRG.17164	Ca_17532	Ca6	3.308	-1.689
334	MSTRG.15704	Ca_06488	Ca6	5.353	-1.687
335	MSTRG.7649	Ca_01366	Ca3	1.022	-1.686
336	MSTRG.7615	-	Ca3	0.878	-1.685
337	MSTRG.17217	Ca_18885	Ca6	8.032	-1.683
338	MSTRG.7431	-	Ca3	1.396	-1.672
339	MSTRG.16571	-	Ca6	2.440	-1.667
340	MSTRG.21129	Ca_02055	Ca8	5.988	-1.666
341	MSTRG.1138	Ca_02911	Ca1	1.793	-1.663
342	MSTRG.22517	Ca_26764	scaffold1309	0.321	-1.660
343	MSTRG.4151	-	Ca2	1.566	-1.654
344	MSTRG.20614	Ca_11869	Ca8	2.880	-1.648
345	MSTRG.9430	-	Ca4	0.531	-1.645
346	MSTRG.14940	Ca_08619	Ca6	3.640	-1.643
347	MSTRG.17918	Ca_03182	Ca7	4.451	-1.639
348	MSTRG.17002	-	Ca6	0.678	-1.632
349	MSTRG.7923	Ca_12068	Ca4	6.002	-1.626
350	MSTRG.6002	Ca_06155	Ca3	-0.053	-1.625
351	MSTRG.17236	-	Ca6	1.699	-1.625
352	MSTRG.13253	Ca_07623	Ca5	4.109	-1.618
353	MSTRG.17300	Ca_19013	Ca6	5.355	-1.602
354	MSTRG.13970	Ca_04270	Ca5	4.062	-1.602
355	MSTRG.25377	Ca_26670	scaffold886	3.847	-1.597
356	MSTRG.18666	Ca_17294	Ca7	3.387	-1.588
357	MSTRG.18133	Ca_02970	Ca7	0.589	-1.579
358	MSTRG.16116	Ca_11045	Ca6	3.820	-1.579
359	MSTRG.11008	Ca_18157	Ca5	4.489	-1.565
360	MSTRG.16316	-	Ca6	-0.009	-1.562
361	MSTRG.22393	Ca_22983	scaffold12	-0.135	-1.559
362	MSTRG.2257	-	Ca1	-0.426	-1.555
363	MSTRG.12507	Ca_05018	Ca5	8.855	-1.553
364	MSTRG.25301	Ca_27390	scaffold869	2.253	-1.551
365	MSTRG.6600	Ca_07338	Ca3	7.356	-1.550
366	MSTRG.3976	-	Ca2	0.528	-1.547
367	MSTRG.13764	Ca_04067	Ca5	3.466	-1.546
368	MSTRG.5939	-	Ca3	1.452	-1.546

369	MSTRG.21784	Ca_13035	Ca8	3.493	-1.544
370	MSTRG.23435	-	scaffold2152	0.209	-1.537
371	MSTRG.22216	Ca_27968	scaffold1095	0.926	-1.532
372	MSTRG.101	-	C11137434	0.305	-1.529
373	MSTRG.21513	-	Ca8	-0.114	-1.527
374	MSTRG.21305	Ca_10724	Ca8	1.592	-1.526
375	MSTRG.12454	-	Ca5	1.773	-1.525
376	MSTRG.1120	Ca_02925	Ca1	2.011	-1.523
377	MSTRG.14234	Ca_10424	Ca6	-0.091	-1.521
378	MSTRG.6975	Ca_00733	Ca3	4.461	-1.517
379	MSTRG.11011	-	Ca5	2.725	-1.507
380	MSTRG.11407	Ca_17081	Ca5	6.235	-1.505
381	MSTRG.19675	Ca_11767	Ca7	3.243	-1.505
382	MSTRG.12081	-	Ca5	-0.107	-1.495
383	MSTRG.22556	-	scaffold1324	1.659	-1.494
384	MSTRG.2074	Ca_17387	Ca1	8.254	-1.492
385	MSTRG.22462	Ca_21449	scaffold128	7.865	-1.492
386	MSTRG.8659	Ca_08465	Ca4	2.634	-1.488
387	MSTRG.430	-	Ca1	-1.065	-1.487
388	MSTRG.14735	Ca_09609	Ca6	4.092	-1.484
389	MSTRG.20500	-	Ca7	-0.656	-1.484
390	MSTRG.7301	Ca_01050	Ca3	3.182	-1.483
391	MSTRG.11496	-	Ca5	4.840	-1.480
392	MSTRG.22868	Ca_28063	scaffold1498	0.106	-1.477
393	MSTRG.15709	-	Ca6	-0.270	-1.475
394	MSTRG.55	-	C11086496	3.924	-1.466
395	MSTRG.13565	Ca_03876	Ca5	6.166	-1.460
396	MSTRG.13645	Ca_03952	Ca5	0.912	-1.453
397	MSTRG.8170	Ca_03750	Ca4	5.634	-1.452
398	MSTRG.19916	Ca_10000	Ca7	4.351	-1.451
399	MSTRG.19669	-	Ca7	-0.088	-1.449
400	MSTRG.6640	Ca_07373	Ca3	1.824	-1.445
401	MSTRG.2001	Ca_14783	Ca1	1.459	-1.441
402	MSTRG.9446	Ca_18620	Ca4	2.446	-1.439
403	MSTRG.20238	-	Ca7	-0.331	-1.438
404	MSTRG.2620	Ca_13970	Ca1	2.124	-1.438
405	MSTRG.17233	Ca_18911	Ca6	6.437	-1.434

406	MSTRG.11938	Ca_08913	Ca5	2.015	-1.429
407	MSTRG.17141	Ca_17510	Ca6	3.760	-1.416
408	MSTRG.16019	Ca_11133	Ca6	2.888	-1.414
409	MSTRG.13091	Ca_07450	Ca5	0.197	-1.413
410	MSTRG.11971	Ca_08880	Ca5	4.710	-1.409
411	MSTRG.1087	Ca_08086	Ca1	2.021	-1.408
412	MSTRG.11941	Ca_08911	Ca5	2.104	-1.402
413	MSTRG.16733	Ca_15947	Ca6	-0.278	-1.402
414	MSTRG.24853	-	scaffold590	5.246	-1.398
415	MSTRG.2695	Ca_18459	Ca1	-0.557	-1.398
416	MSTRG.6314	Ca_08179	Ca3	3.106	-1.397
417	MSTRG.549	Ca_00345	Ca1	2.258	-1.393
418	MSTRG.16941	Ca_17723	Ca6	2.311	-1.389
419	MSTRG.11293	Ca_20495	Ca5	5.522	-1.385
420	MSTRG.9093	Ca_04636	Ca4	10.515	-1.382
421	MSTRG.7623	-	Ca3	2.400	-1.379
422	MSTRG.8055	Ca_03868	Ca4	3.601	-1.376
423	MSTRG.21032	Ca_02146	Ca8	3.753	-1.376
424	MSTRG.2595	Ca_21844	Ca1	4.725	-1.372
425	MSTRG.21058	Ca_02124	Ca8	1.697	-1.370
426	MSTRG.6	-	C11048020	-0.407	-1.367
427	MSTRG.19308	-	Ca7	-0.605	-1.364
428	MSTRG.20137	Ca_13742	Ca7	4.719	-1.362
429	MSTRG.6747	-	Ca3	1.534	-1.361
430	MSTRG.23386	Ca_26619	scaffold2040	9.830	-1.358
431	MSTRG.25038	Ca_23193	scaffold682	3.291	-1.357
432	MSTRG.9884	Ca_23178	Ca4	1.292	-1.354
433	MSTRG.10849	-	Ca4	4.352	-1.352
434	MSTRG.7518	Ca_01250	Ca3	3.843	-1.345
435	MSTRG.16338	Ca_17470	Ca6	4.023	-1.342
436	MSTRG.6607	Ca_07342	Ca3	1.505	-1.338
437	MSTRG.6368	Ca_08124	Ca3	5.017	-1.337
438	MSTRG.21225	Ca_01961	Ca8	3.456	-1.336
439	MSTRG.14138	-	Ca6	0.184	-1.333
440	MSTRG.2451	Ca_22454	Ca1	5.007	-1.333
441	MSTRG.13852	Ca_04158	Ca5	2.293	-1.333
442	MSTRG.2454	-	Ca1	1.995	-1.331

443	MSTRG.2087	Ca_17370	Ca1	3.032	-1.330
444	MSTRG.11031	Ca_18182	Ca5	2.990	-1.328
445	MSTRG.13456	Ca_12740	Ca5	1.951	-1.327
446	MSTRG.13302	Ca_11408	Ca5	5.880	-1.327
447	MSTRG.10252	Ca_13131	Ca4	8.429	-1.325
448	MSTRG.582	Ca_00374	Ca1	7.096	-1.323
449	MSTRG.2300	Ca_18588	Ca1	3.907	-1.321
450	MSTRG.24139	-	scaffold346_1	0.236	-1.316
451	MSTRG.6668	Ca_07398	Ca3	1.634	-1.315
452	MSTRG.12691	Ca_01729	Ca5	1.830	-1.312
453	MSTRG.9139	Ca_05641	Ca4	5.557	-1.312
454	MSTRG.1645	Ca_14111	Ca1	2.795	-1.307
455	MSTRG.6646	Ca_07380	Ca3	3.380	-1.302
456	MSTRG.16980	-	Ca6	1.174	-1.299
457	MSTRG.10628	-	Ca4	2.949	-1.297
458	MSTRG.3390	-	Ca2	3.679	-1.294
459	MSTRG.10144	Ca_14822	Ca4	1.305	-1.290
460	MSTRG.17943	Ca_03159	Ca7	0.959	-1.289
461	MSTRG.8623	-	Ca4	2.163	-1.285
462	MSTRG.24484	-	scaffold451	0.056	-1.284
463	MSTRG.19480	Ca_19509	Ca7	3.840	-1.284
464	MSTRG.4628	Ca_10285	Ca2	5.022	-1.275
465	MSTRG.17872	Ca_03226	Ca7	4.001	-1.275
466	MSTRG.1160	Ca_02885	Ca1	5.733	-1.274
467	MSTRG.5161	Ca_22375	Ca3	1.784	-1.273
468	MSTRG.6382	Ca_08107	Ca3	4.856	-1.265
469	MSTRG.5597	Ca_23335	Ca3	0.038	-1.264
470	MSTRG.9058	Ca_04610	Ca4	5.317	-1.263
471	MSTRG.2297	Ca_18585	Ca1	6.209	-1.260
472	MSTRG.8253	Ca_03670	Ca4	4.443	-1.259
473	MSTRG.397	Ca_00188	Ca1	4.461	-1.255
474	MSTRG.15525	-	Ca6	1.540	-1.254
475	MSTRG.22147	-	scaffold1052	4.707	-1.254
476	MSTRG.7848	Ca_07812	Ca4	4.770	-1.251
477	MSTRG.2133	Ca_08856	Ca1	3.716	-1.249
478	MSTRG.12106	Ca_16633	Ca5	4.033	-1.247
479	MSTRG.17005	Ca_20726	Ca6	9.249	-1.246

480	MSTRG.16801	Ca_23250	Ca6	5.288	-1.244
481	MSTRG.15892	Ca_19862	Ca6	4.503	-1.243
482	MSTRG.12594	Ca_01845	Ca5	4.732	-1.243
483	MSTRG.25486	Ca_22841	scaffold919	-0.159	-1.242
484	MSTRG.18119	Ca_02983	Ca7	5.733	-1.242
485	MSTRG.24043	-	scaffold3323	0.758	-1.239
486	MSTRG.14677	Ca_09665	Ca6	5.413	-1.238
487	MSTRG.14565	Ca_05697	Ca6	0.914	-1.237
488	MSTRG.789	Ca_00599	Ca1	4.672	-1.237
489	MSTRG.13205	Ca_07569	Ca5	3.096	-1.229
490	MSTRG.9000	Ca_04557	Ca4	5.284	-1.228
491	MSTRG.15669	Ca_06456	Ca6	1.692	-1.225
492	MSTRG.2307	Ca_18599	Ca1	3.151	-1.219
493	MSTRG.17298	Ca_19011	Ca6	6.381	-1.219
494	MSTRG.6602	Ca_07339	Ca3	8.507	-1.219
495	MSTRG.24077	-	scaffold3397	4.131	-1.216
496	MSTRG.15053	Ca_20467	Ca6	5.286	-1.211
497	MSTRG.20135	Ca_13740	Ca7	5.065	-1.210
498	MSTRG.15189	Ca_05087	Ca6	2.735	-1.209
499	MSTRG.20640	Ca_11845	Ca8	6.415	-1.201
500	MSTRG.13303	Ca_19240	Ca5	6.701	-1.195
501	MSTRG.4705	Ca_10210	Ca2	6.434	-1.192
502	MSTRG.4361	-	Ca2	1.345	-1.190
503	MSTRG.21937	Ca_17860	Ca8	0.401	-1.188
504	MSTRG.24634	-	scaffold498	-0.007	-1.188
505	MSTRG.17704	Ca_03370	Ca7	0.765	-1.186
506	MSTRG.21176	Ca_02004	Ca8	4.042	-1.184
507	MSTRG.802	Ca_00611	Ca1	8.233	-1.181
508	MSTRG.6433	-	Ca3	3.428	-1.177
509	MSTRG.22158	Ca_25317	scaffold1055	3.233	-1.176
510	MSTRG.13121	-	Ca5	2.606	-1.175
511	MSTRG.22997	Ca_24188	scaffold1659	1.981	-1.174
512	MSTRG.4531	Ca_12460	Ca2	1.527	-1.173
513	MSTRG.619	Ca_00414	Ca1	2.999	-1.172
514	MSTRG.17278	Ca_21197	Ca6	7.164	-1.170
515	MSTRG.7	-	C11047824	-0.992	-1.167
516	MSTRG.2693	Ca_18460	Ca1	13.442	-1.166

517	MSTRG.9205	Ca_05578	Ca4	1.979	-1.166
518	MSTRG.6967	Ca_00727	Ca3	2.691	-1.166
519	MSTRG.13462	Ca_12733	Ca5	5.949	-1.165
520	MSTRG.23461	Ca_25017	scaffold2166	3.490	-1.160
521	MSTRG.14692	Ca_09651	Ca6	2.216	-1.158
522	MSTRG.21068	Ca_02114	Ca8	0.477	-1.157
523	MSTRG.6798	-	Ca3	5.729	-1.153
524	MSTRG.16740	-	Ca6	0.629	-1.153
525	MSTRG.16708	Ca_15918	Ca6	3.173	-1.148
526	MSTRG.9484	Ca_18656	Ca4	4.752	-1.146
527	MSTRG.1367	Ca_02669	Ca1	5.310	-1.146
528	MSTRG.24485	Ca_22598	scaffold451	-0.173	-1.146
529	MSTRG.7477	Ca_01220	Ca3	4.777	-1.146
530	MSTRG.17709	Ca_03364	Ca7	1.309	-1.146
531	MSTRG.4488	Ca_12504	Ca2	1.597	-1.144
532	MSTRG.21437	Ca_10594	Ca8	6.943	-1.144
533	MSTRG.1391	Ca_02649	Ca1	3.755	-1.142
534	MSTRG.11364	-	Ca5	0.146	-1.139
535	MSTRG.21166	Ca_02013	Ca8	3.468	-1.134
536	MSTRG.751	Ca_00568	Ca1	0.836	-1.132
537	MSTRG.23127	Ca_23936	scaffold1751	0.822	-1.129
538	MSTRG.22564	Ca_19776	scaffold1324	5.203	-1.128
539	MSTRG.21949	Ca_15509	Ca8	3.083	-1.127
540	MSTRG.2481	Ca_26129	Ca1	2.253	-1.127
541	MSTRG.14811	Ca_09539	Ca6	3.584	-1.125
542	MSTRG.20837	Ca_02343	Ca8	3.611	-1.123
543	MSTRG.1758	Ca_07074	Ca1	4.033	-1.122
544	MSTRG.8139	-	Ca4	1.880	-1.121
545	MSTRG.15601	Ca_06390	Ca6	7.414	-1.115
546	MSTRG.10525	Ca_10900	Ca4	0.342	-1.115
547	MSTRG.19050	Ca_09968	Ca7	3.986	-1.114
548	MSTRG.2256	Ca_18328	Ca1	2.953	-1.114
549	MSTRG.2172	Ca_22105	Ca1	5.531	-1.113
550	MSTRG.10268	Ca_13108	Ca4	4.386	-1.112
551	MSTRG.4806	Ca_15268	Ca2	5.283	-1.112
552	MSTRG.12973	-	Ca5	2.100	-1.112
553	MSTRG.21950	-	Ca8	0.815	-1.112

554	MSTRG.24216	-	scaffold374	1.206	-1.112
555	MSTRG.5969	-	Ca3	3.852	-1.111
556	MSTRG.15028	Ca_08527	Ca6	3.069	-1.110
557	MSTRG.20660	Ca_11826	Ca8	8.171	-1.110
558	MSTRG.548	Ca_00344	Ca1	2.490	-1.110
559	MSTRG.3807	Ca_18067	Ca2	2.962	-1.109
560	MSTRG.11655	Ca_21153	Ca5	3.510	-1.108
561	MSTRG.18038	Ca_03068	Ca7	8.739	-1.103
562	MSTRG.4317	Ca_15688	Ca2	2.647	-1.102
563	MSTRG.21425	Ca_10607	Ca8	1.887	-1.100
564	MSTRG.17068	Ca_13466	Ca6	6.950	-1.100
565	MSTRG.8979	Ca_04534	Ca4	3.500	-1.099
566	MSTRG.10099	Ca_22448	Ca4	3.295	-1.095
567	MSTRG.21136	Ca_02045	Ca8	1.382	-1.093
568	MSTRG.7385	Ca_01127	Ca3	5.275	-1.092
569	MSTRG.13196	Ca_07559	Ca5	4.929	-1.089
570	MSTRG.1924	Ca_06905	Ca1	5.603	-1.088
571	MSTRG.19481	-	Ca7	4.913	-1.087
572	MSTRG.12502	Ca_05011	Ca5	4.078	-1.087
573	MSTRG.16807	Ca_23255	Ca6	4.498	-1.085
574	MSTRG.14326	Ca_05934	Ca6	2.900	-1.079
575	MSTRG.13811	Ca_04114	Ca5	1.574	-1.077
576	MSTRG.13593	-	Ca5	2.070	-1.075
577	MSTRG.8978	Ca_04533	Ca4	1.955	-1.074
578	MSTRG.12620	Ca_01814	Ca5	3.278	-1.073
579	MSTRG.7521	Ca_01257	Ca3	3.623	-1.068
580	MSTRG.17773	Ca_03306	Ca7	1.476	-1.068
581	MSTRG.6921	Ca_20876	Ca3	4.821	-1.068
582	MSTRG.25151	Ca_23410	scaffold775	8.882	-1.065
583	MSTRG.10215	Ca_15105	Ca4	3.523	-1.065
584	MSTRG.18612	Ca_15299	Ca7	2.907	-1.065
585	MSTRG.19472	Ca_19515	Ca7	0.633	-1.062
586	MSTRG.690	Ca_00497	Ca1	1.943	-1.061
587	MSTRG.5970	-	Ca3	0.876	-1.060
588	MSTRG.18664	-	Ca7	3.480	-1.056
589	MSTRG.18366	Ca_06668	Ca7	-0.631	-1.056
590	MSTRG.24449	Ca_26259	scaffold435	3.627	-1.055

591	MSTRG.198	Ca_00004	Ca1	2.035	-1.052
592	MSTRG.3164	Ca_12593	Ca2	0.654	-1.052
593	MSTRG.25545	Ca_24077	scaffold96	2.175	-1.051
594	MSTRG.13865	Ca_04167	Ca5	3.278	-1.051
595	MSTRG.22067	Ca_28086	scaffold10227	4.025	-1.048
596	MSTRG.2984	-	Ca1	3.363	-1.047
597	MSTRG.1724	Ca_07110	Ca1	5.671	-1.046
598	MSTRG.10735	-	Ca4	2.986	-1.046
599	MSTRG.3755	Ca_25882	Ca2	5.656	-1.045
600	MSTRG.21928	Ca_17872	Ca8	3.814	-1.038
601	MSTRG.4839	Ca_16888	Ca2	2.852	-1.037
602	MSTRG.11426	Ca_20816	Ca5	3.617	-1.037
603	MSTRG.8738	Ca_04309	Ca4	0.716	-1.034
604	MSTRG.16970	Ca_24604	Ca6	0.020	-1.034
605	MSTRG.9612	-	Ca4	2.117	-1.034
606	MSTRG.16149	Ca_24163	Ca6	3.969	-1.033
607	MSTRG.13649	Ca_03955	Ca5	3.567	-1.033
608	MSTRG.22423	-	scaffold123	2.078	-1.033
609	MSTRG.12094	Ca_16620	Ca5	4.848	-1.032
610	MSTRG.19864	-	Ca7	2.669	-1.030
611	MSTRG.9096	Ca_04642	Ca4	2.898	-1.027
612	MSTRG.18988	Ca_16058	Ca7	3.405	-1.026
613	MSTRG.17679	-	Ca7	4.410	-1.025
614	MSTRG.9132	Ca_05646	Ca4	3.784	-1.023
615	MSTRG.22565	Ca_19779	scaffold1324	1.591	-1.023
616	MSTRG.21339	Ca_10687	Ca8	3.651	-1.022
617	MSTRG.2680	-	Ca1	2.522	-1.020
618	MSTRG.2324	-	Ca1	2.678	-1.020
619	MSTRG.15836	Ca_16343	Ca6	6.676	-1.019
620	MSTRG.14693	Ca_09650	Ca6	2.795	-1.019
621	MSTRG.5861	Ca_20431	Ca3	3.283	-1.018
622	MSTRG.8208	Ca_03712	Ca4	4.266	-1.018
623	MSTRG.11032	Ca_18183	Ca5	5.653	-1.017
624	MSTRG.4290	-	Ca2	0.605	-1.016
625	MSTRG.21303	-	Ca8	1.033	-1.013
626	MSTRG.17466	Ca_13650	Ca6	4.238	-1.012
627	MSTRG.1928	Ca_06901	Ca1	0.699	-1.010

628	MSTRG.2473	Ca_21867	Ca1	6.550	-1.009
629	MSTRG.9677	Ca_19077	Ca4	3.083	-1.009
630	MSTRG.10290	Ca_13092	Ca4	5.577	-1.008
631	MSTRG.9541	Ca_14006	Ca4	4.011	-1.008
632	MSTRG.19903	Ca_10011	Ca7	3.835	-1.008
633	MSTRG.24842	-	scaffold584	0.413	-1.007
634	MSTRG.8688	Ca_08492	Ca4	6.248	-1.004
635	MSTRG.9703	Ca_20135	Ca4	2.497	-1.003
636	MSTRG.12872	Ca_01553	Ca5	4.502	-1.003
637	MSTRG.5886	Ca_06274	Ca3	2.493	-1.003
638	MSTRG.17665	Ca_03405	Ca7	0.899	-1.003
639	MSTRG.7781	Ca_07752	Ca4	4.441	-1.002
640	MSTRG.7041	Ca_00790	Ca3	4.298	-1.000
641	MSTRG.9129	Ca_05650	Ca4	1.544	1.001
642	MSTRG.9581	Ca_14048	Ca4	2.828	1.001
643	MSTRG.9570	-	Ca4	2.885	1.003
644	MSTRG.13830	-	Ca5	2.045	1.003
645	MSTRG.19203	Ca_15876	Ca7	2.689	1.004
646	MSTRG.4604	-	Ca2	-0.154	1.004
647	MSTRG.4380	Ca_14343	Ca2	4.173	1.005
648	MSTRG.8459	Ca_03455	Ca4	6.009	1.005
649	MSTRG.7738	Ca_07708	Ca4	5.801	1.008
650	MSTRG.310	Ca_00114	Ca1	5.656	1.009
651	MSTRG.20894	Ca_02285	Ca8	4.604	1.009
652	MSTRG.14644	Ca_16944	Ca6	3.762	1.010
653	MSTRG.19163	Ca_20560	Ca7	7.093	1.012
654	MSTRG.6507	Ca_07248	Ca3	4.112	1.012
655	MSTRG.15475	Ca_19667	Ca6	3.291	1.013
656	MSTRG.17123	Ca_19173	Ca6	2.659	1.013
657	MSTRG.3284	Ca_10542	Ca2	3.979	1.014
658	MSTRG.1933	Ca_06895	Ca1	5.650	1.014
659	MSTRG.21000	Ca_02174	Ca8	5.354	1.014
660	MSTRG.12099	Ca_16626	Ca5	5.454	1.015
661	MSTRG.4280	Ca_15651	Ca2	4.742	1.015
662	MSTRG.14275	Ca_25241	Ca6	8.530	1.015
663	MSTRG.10824	Ca_19249	Ca4	3.493	1.017
664	MSTRG.13942	Ca_04245	Ca5	2.025	1.017

665	MSTRG.16059	Ca_11101	Ca6	5.206	1.018
666	MSTRG.574	Ca_00367	Ca1	5.470	1.019
667	MSTRG.6722	Ca_12228	Ca3	3.152	1.020
668	MSTRG.9676	Ca_19075	Ca4	3.789	1.021
669	MSTRG.14493	Ca_05779	Ca6	8.234	1.022
670	MSTRG.20331	Ca_17980	Ca7	7.100	1.025
671	MSTRG.1992	Ca_14787	Ca1	2.115	1.025
672	MSTRG.4493	Ca_12500	Ca2	3.143	1.026
673	MSTRG.11129	Ca_25896	Ca5	4.124	1.026
674	MSTRG.10269	Ca_13109	Ca4	2.658	1.027
675	MSTRG.6901	Ca_23676	Ca3	4.385	1.027
676	MSTRG.10438	Ca_11006	Ca4	3.787	1.028
677	MSTRG.3155	Ca_12601	Ca2	6.617	1.028
678	MSTRG.9529	Ca_13994	Ca4	2.413	1.029
679	MSTRG.11738	Ca_17670	Ca5	2.777	1.029
680	MSTRG.9877	-	Ca4	3.549	1.031
681	MSTRG.5790	Ca_09468	Ca3	4.039	1.032
682	MSTRG.3432	Ca_14695	Ca2	1.956	1.033
683	MSTRG.20774	Ca_02410	Ca8	1.628	1.033
684	MSTRG.16551	Ca_22060	Ca6	4.568	1.035
685	MSTRG.22033	-	scaffold1006	0.789	1.038
686	MSTRG.15762	Ca_06548	Ca6	3.455	1.039
687	MSTRG.16348	Ca_17463	Ca6	8.536	1.041
688	MSTRG.18409	Ca_06632	Ca7	3.183	1.043
689	MSTRG.21494	Ca_11488	Ca8	2.800	1.043
690	MSTRG.4492	Ca_12501	Ca2	6.786	1.044
691	MSTRG.2892	-	Ca1	0.772	1.044
692	MSTRG.8272	Ca_03650	Ca4	1.615	1.045
693	MSTRG.7446	Ca_01188	Ca3	2.496	1.045
694	MSTRG.526	Ca_00323	Ca1	1.003	1.046
695	MSTRG.11201	Ca_18739	Ca5	1.170	1.046
696	MSTRG.15039	Ca_08516	Ca6	2.218	1.050
697	MSTRG.5916	Ca_06244	Ca3	2.556	1.050
698	MSTRG.8330	Ca_03589	Ca4	4.458	1.051
699	MSTRG.9604	Ca_17125	Ca4	4.882	1.052
700	MSTRG.10359	Ca_14911	Ca4	4.553	1.052
701	MSTRG.18909	Ca_09260	Ca7	2.492	1.052

702	MSTRG.15545	Ca_06334	Ca6	-0.505	1.053
703	MSTRG.13765	Ca_04068	Ca5	3.949	1.053
704	MSTRG.471	Ca_00264	Ca1	1.257	1.053
705	MSTRG.7636	Ca_01352	Ca3	1.971	1.053
706	MSTRG.7370	Ca_01107	Ca3	5.208	1.055
707	MSTRG.3726	Ca_17586	Ca2	2.970	1.055
708	MSTRG.4100	Ca_14958	Ca2	2.586	1.055
709	MSTRG.13220	Ca_07584	Ca5	1.636	1.056
710	MSTRG.16012	-	Ca6	-0.120	1.056
711	MSTRG.21791	Ca_13033	Ca8	6.003	1.056
712	MSTRG.9133	Ca_05647	Ca4	3.245	1.057
713	MSTRG.8713	Ca_04287	Ca4	2.463	1.058
714	MSTRG.15824	Ca_16354	Ca6	2.723	1.058
715	MSTRG.13532	Ca_12662	Ca5	5.169	1.058
716	MSTRG.5550	Ca_18263	Ca3	2.331	1.060
717	MSTRG.18061	Ca_03042	Ca7	4.873	1.061
718	MSTRG.19854	Ca_10054	Ca7	9.317	1.061
719	MSTRG.3840	Ca_11683	Ca2	2.071	1.062
720	MSTRG.19228	Ca_15852	Ca7	1.189	1.063
721	MSTRG.9450	Ca_18623	Ca4	5.504	1.063
722	MSTRG.22038	-	scaffold1006	1.808	1.063
723	MSTRG.14063	Ca_13322	Ca6	3.721	1.064
724	MSTRG.21508	Ca_11503	Ca8	3.446	1.066
725	MSTRG.4367	Ca_14360	Ca2	7.057	1.067
726	MSTRG.11578	Ca_22825	Ca5	6.906	1.067
727	MSTRG.17065	Ca_13472	Ca6	5.860	1.069
728	MSTRG.21845	Ca_12991	Ca8	4.611	1.069
729	MSTRG.20599	-	Ca8	-0.461	1.070
730	MSTRG.22515	-	scaffold1301_1	0.777	1.070
731	MSTRG.12105	Ca_16629	Ca5	7.721	1.070
732	MSTRG.9344	-	Ca4	2.440	1.070
733	MSTRG.15440	-	Ca6	1.456	1.073
734	MSTRG.2121	Ca_17336	Ca1	4.036	1.073
735	MSTRG.768	Ca_00584	Ca1	2.881	1.074
736	MSTRG.20941	Ca_02236	Ca8	2.824	1.074
737	MSTRG.7342	Ca_01083	Ca3	3.779	1.074
738	MSTRG.11936	Ca_08918	Ca5	5.590	1.074

739	MSTRG.16986	-	Ca6	1.720	1.075
740	MSTRG.2992	Ca_12908	Ca1	4.693	1.076
741	MSTRG.19466	Ca_19517	Ca7	1.458	1.077
742	MSTRG.4674	Ca_10242	Ca2	6.212	1.078
743	MSTRG.15344	Ca_05236	Ca6	6.252	1.078
744	MSTRG.15322	Ca_05206	Ca6	4.172	1.080
745	MSTRG.17978	Ca_03124	Ca7	2.267	1.080
746	MSTRG.11475	Ca_17926	Ca5	-0.724	1.080
747	MSTRG.1671	Ca_14129	Ca1	7.259	1.082
748	MSTRG.6807	Ca_11974	Ca3	6.416	1.082
749	MSTRG.14643	Ca_16943	Ca6	2.888	1.083
750	MSTRG.20626	Ca_11863	Ca8	4.093	1.084
751	MSTRG.9727	Ca_14470	Ca4	5.267	1.085
752	MSTRG.14021	Ca_13282	Ca6	9.708	1.085
753	MSTRG.23789	Ca_20593	scaffold284	3.105	1.086
754	MSTRG.9320	Ca_05462	Ca4	4.622	1.087
755	MSTRG.3201	Ca_12557	Ca2	5.555	1.087
756	MSTRG.12548	Ca_01894	Ca5	0.566	1.088
757	MSTRG.22505	-	scaffold1301_1	3.347	1.088
758	MSTRG.13580	Ca_03888	Ca5	1.609	1.089
759	MSTRG.3929	Ca_24652	Ca2	3.767	1.090
760	MSTRG.3272	Ca_10552	Ca2	4.023	1.092
761	MSTRG.15146	Ca_05042	Ca6	0.838	1.092
762	MSTRG.8030	Ca_12163	Ca4	2.115	1.094
763	MSTRG.8167	Ca_03752	Ca4	6.212	1.094
764	MSTRG.5659	-	Ca3	4.427	1.096
765	MSTRG.12524	Ca_01915	Ca5	2.342	1.097
766	MSTRG.9393	Ca_05388	Ca4	2.529	1.097
767	MSTRG.7259	Ca_01007	Ca3	3.508	1.097
768	MSTRG.3515	Ca_20938	Ca2	3.510	1.097
769	MSTRG.4885	Ca_09692	Ca2	5.095	1.098
770	MSTRG.5884	Ca_06277	Ca3	5.166	1.098
771	MSTRG.13877	Ca_04177	Ca5	4.392	1.100
772	MSTRG.18518	Ca_13184	Ca7	3.410	1.101
773	MSTRG.15559	Ca_06348	Ca6	1.982	1.102
774	MSTRG.3280	-	Ca2	4.302	1.102
775	MSTRG.12344	-	Ca5	1.160	1.103

776	MSTRG.1218	Ca_02830	Ca1	2.957	1.103
777	MSTRG.423	-	Ca1	6.077	1.104
778	MSTRG.17465	Ca_13651	Ca6	8.821	1.104
779	MSTRG.7654	Ca_01371	Ca3	1.518	1.105
780	MSTRG.1820	Ca_07013	Ca1	3.477	1.106
781	MSTRG.7655	Ca_01372	Ca3	5.611	1.106
782	MSTRG.13721	Ca_04026	Ca5	3.068	1.107
783	MSTRG.24546	-	scaffold477	1.247	1.108
784	MSTRG.3738	Ca_17574	Ca2	5.459	1.108
785	MSTRG.587	Ca_00376	Ca1	4.815	1.111
786	MSTRG.4780	Ca_15245	Ca2	2.606	1.111
787	MSTRG.10121	Ca_14846	Ca4	4.565	1.111
788	MSTRG.17289	Ca_21216	Ca6	4.678	1.111
789	MSTRG.16255	Ca_14598	Ca6	2.276	1.112
790	MSTRG.6300	Ca_08192	Ca3	1.987	1.112
791	MSTRG.4388	Ca_14336	Ca2	2.571	1.112
792	MSTRG.7042	Ca_00791	Ca3	4.185	1.113
793	MSTRG.2966	Ca_12936	Ca1	4.006	1.114
794	MSTRG.7955	Ca_12094	Ca4	4.528	1.115
795	MSTRG.8786	Ca_04353	Ca4	4.290	1.115
796	MSTRG.18094	Ca_03009	Ca7	4.728	1.116
797	MSTRG.12265	Ca_04782	Ca5	3.461	1.117
798	MSTRG.19658	Ca_11775	Ca7	2.990	1.117
799	MSTRG.8191	-	Ca4	0.456	1.117
800	MSTRG.15554	Ca_06342	Ca6	7.595	1.118
801	MSTRG.4840	Ca_16887	Ca2	4.074	1.118
802	MSTRG.9384	Ca_05398	Ca4	4.111	1.119
803	MSTRG.13202	Ca_07563	Ca5	2.919	1.120
804	MSTRG.16798	Ca_23246	Ca6	0.084	1.122
805	MSTRG.15693	Ca_06479	Ca6	4.672	1.122
806	MSTRG.2950	Ca_12950	Ca1	4.318	1.122
807	MSTRG.21181	Ca_02000	Ca8	6.299	1.123
808	MSTRG.8686	Ca_08491	Ca4	7.852	1.125
809	MSTRG.8076	Ca_03840	Ca4	0.079	1.125
810	MSTRG.2740	-	Ca1	-0.797	1.126
811	MSTRG.7401	Ca_01144	Ca3	2.479	1.127
812	MSTRG.12761	Ca_01661	Ca5	5.156	1.128

813	MSTRG.24781	-	scaffold553	2.166	1.128
814	MSTRG.6537	Ca_07277	Ca3	7.047	1.129
815	MSTRG.24689	Ca_22388	scaffold531	5.739	1.133
816	MSTRG.907	Ca_07899	Ca1	3.951	1.134
817	MSTRG.6671	Ca_07401	Ca3	4.566	1.135
818	MSTRG.21056	Ca_02128	Ca8	5.279	1.135
819	MSTRG.15920	Ca_11268	Ca6	2.419	1.136
820	MSTRG.12238	Ca_04759	Ca5	9.521	1.138
821	MSTRG.8444	Ca_03471	Ca4	7.966	1.139
822	MSTRG.24678	Ca_24531	scaffold528	2.904	1.141
823	MSTRG.2	-	C11044824	1.436	1.142
824	MSTRG.20140	Ca_13745	Ca7	4.878	1.142
825	MSTRG.17682	Ca_03389	Ca7	3.014	1.142
826	MSTRG.13311	-	Ca5	0.664	1.143
827	MSTRG.21067	Ca_02115	Ca8	1.629	1.143
828	MSTRG.1111	Ca_02935	Ca1	5.053	1.144
829	MSTRG.1934	Ca_06894	Ca1	6.061	1.145
830	MSTRG.4535	Ca_12456	Ca2	1.942	1.146
831	MSTRG.4223	Ca_14311	Ca2	4.285	1.147
832	MSTRG.17017	Ca_13516	Ca6	3.878	1.147
833	MSTRG.1872	Ca_06955	Ca1	3.664	1.148
834	MSTRG.13394	Ca_11353	Ca5	3.246	1.150
835	MSTRG.7816	Ca_07784	Ca4	5.958	1.150
836	MSTRG.21354	-	Ca8	2.266	1.150
837	MSTRG.6005	Ca_06152	Ca3	4.851	1.152
838	MSTRG.21455	-	Ca8	2.638	1.154
839	MSTRG.344	Ca_00142	Ca1	3.586	1.155
840	MSTRG.21917	Ca_17884	Ca8	4.928	1.156
841	MSTRG.15689	Ca_06474	Ca6	3.870	1.159
842	MSTRG.18509	Ca_13195	Ca7	1.897	1.159
843	MSTRG.15101	-	Ca6	1.510	1.160
844	MSTRG.586	Ca_00378	Ca1	3.557	1.162
845	MSTRG.15818	Ca_16360	Ca6	4.338	1.164
846	MSTRG.9001	Ca_04556	Ca4	3.651	1.165
847	MSTRG.23005	Ca_26647	scaffold1664	6.308	1.167
848	MSTRG.23927	-	scaffold308_2	-0.348	1.169
849	MSTRG.6531	Ca_07270	Ca3	2.991	1.169

850	MSTRG.7192	Ca_00946	Ca3	4.970	1.171
851	MSTRG.11714	-	Ca5	3.430	1.171
852	MSTRG.7426	Ca_01170	Ca3	-0.707	1.172
853	MSTRG.15849	Ca_16332	Ca6	1.176	1.172
854	MSTRG.17277	Ca_21196	Ca6	7.477	1.173
855	MSTRG.5127	-	Ca3	1.708	1.175
856	MSTRG.22232	-	scaffold109_1	3.628	1.175
857	MSTRG.7193	-	Ca3	2.294	1.175
858	MSTRG.18827	Ca_09343	Ca7	4.688	1.175
859	MSTRG.4557	Ca_12430	Ca2	5.336	1.177
860	MSTRG.17391	Ca_17440	Ca6	4.506	1.177
861	MSTRG.12500	Ca_05014	Ca5	2.996	1.178
862	MSTRG.9242	Ca_05547	Ca4	2.428	1.182
863	MSTRG.14448	Ca_05820	Ca6	7.722	1.184
864	MSTRG.3093	Ca_20670	Ca2	4.836	1.186
865	MSTRG.8273	Ca_03649	Ca4	2.254	1.187
866	MSTRG.18069	Ca_03036	Ca7	3.321	1.187
867	MSTRG.15282	Ca_05172	Ca6	1.941	1.189
868	MSTRG.12273	Ca_04789	Ca5	6.738	1.190
869	MSTRG.243	Ca_00047	Ca1	6.902	1.192
870	MSTRG.17780	Ca_03301	Ca7	3.277	1.193
871	MSTRG.16035	Ca_11123	Ca6	4.153	1.194
872	MSTRG.18585	Ca_15333	Ca7	7.533	1.196
873	MSTRG.21149	Ca_02031	Ca8	3.626	1.197
874	MSTRG.12423	Ca_04930	Ca5	2.471	1.197
875	MSTRG.406	Ca_00201	Ca1	5.665	1.198
876	MSTRG.17244	Ca_16263	Ca6	3.579	1.200
877	MSTRG.25410	-	scaffold895	4.352	1.201
878	MSTRG.22878	-	scaffold1506	0.589	1.201
879	MSTRG.2790	-	Ca1	-0.934	1.202
880	MSTRG.5433	Ca_21021	Ca3	1.554	1.205
881	MSTRG.17442	Ca_13674	Ca6	4.056	1.205
882	MSTRG.738	Ca_00547	Ca1	5.731	1.205
883	MSTRG.8443	Ca_03472	Ca4	3.662	1.213
884	MSTRG.9059	Ca_04611	Ca4	3.427	1.216
885	MSTRG.9128	Ca_05651	Ca4	3.489	1.217
886	MSTRG.21258	Ca_01930	Ca8	6.560	1.217

887	MSTRG.16321	Ca_17490	Ca6	5.501	1.219
888	MSTRG.17339	Ca_17390	Ca6	4.692	1.220
889	MSTRG.7537	Ca_01272	Ca3	2.981	1.222
890	MSTRG.1006	Ca_07994	Ca1	4.406	1.226
891	MSTRG.16423	Ca_16480	Ca6	4.675	1.229
892	MSTRG.5987	Ca_06170	Ca3	5.292	1.229
893	MSTRG.6874	Ca_12036	Ca3	6.507	1.231
894	MSTRG.22943	-	scaffold1580	0.808	1.232
895	MSTRG.7877	Ca_07845	Ca4	2.052	1.232
896	MSTRG.16540	Ca_22072	Ca6	4.372	1.233
897	MSTRG.16290	Ca_14569	Ca6	1.156	1.234
898	MSTRG.8457	-	Ca4	1.758	1.235
899	MSTRG.8337	Ca_03584	Ca4	5.007	1.238
900	MSTRG.2514	Ca_25476	Ca1	5.516	1.238
901	MSTRG.22493	-	scaffold1301_1	4.306	1.239
902	MSTRG.16663	Ca_19793	Ca6	6.283	1.239
903	MSTRG.836	Ca_00655	Ca1	5.340	1.240
904	MSTRG.24555	Ca_26711	scaffold4777	4.083	1.241
905	MSTRG.17513	-	Ca6	3.084	1.242
906	MSTRG.15918	Ca_11271	Ca6	0.936	1.244
907	MSTRG.8525	-	Ca4	0.729	1.245
908	MSTRG.3931	Ca_22030	Ca2	2.337	1.246
909	MSTRG.20998	Ca_02176	Ca8	0.698	1.246
910	MSTRG.6861	Ca_12021	Ca3	3.609	1.246
911	MSTRG.4607	Ca_17818	Ca2	1.744	1.247
912	MSTRG.12047	Ca_13368	Ca5	1.573	1.247
913	MSTRG.21869	-	Ca8	0.495	1.247
914	MSTRG.7200	Ca_00952	Ca3	3.723	1.248
915	MSTRG.16786	Ca_21944	Ca6	11.051	1.248
916	MSTRG.8641	Ca_08446	Ca4	5.763	1.252
917	MSTRG.22061	Ca_27594	scaffold1013	1.395	1.254
918	MSTRG.4540	Ca_12449	Ca2	6.296	1.254
919	MSTRG.13944	Ca_04246	Ca5	5.037	1.256
920	MSTRG.17619	Ca_20244	Ca7	2.183	1.257
921	MSTRG.12061	Ca_13358	Ca5	0.164	1.260
922	MSTRG.3814	Ca_18075	Ca2	2.856	1.261
923	MSTRG.20031	Ca_17612	Ca7	0.731	1.261

924	MSTRG.17488	Ca_13632	Ca6	6.002	1.262
925	MSTRG.10651	Ca_09138	Ca4	2.053	1.263
926	MSTRG.766	Ca_00580	Ca1	7.452	1.266
927	MSTRG.17382	Ca_17429	Ca6	4.226	1.266
928	MSTRG.21008	Ca_02170	Ca8	4.854	1.267
929	MSTRG.514	Ca_00311	Ca1	5.132	1.268
930	MSTRG.10788	-	Ca4	3.015	1.269
931	MSTRG.15070	Ca_20483	Ca6	4.836	1.270
932	MSTRG.13708	Ca_04013	Ca5	3.343	1.270
933	MSTRG.15787	Ca_06573	Ca6	5.515	1.270
934	MSTRG.13109	Ca_07471	Ca5	1.598	1.270
935	MSTRG.9048	Ca_04603	Ca4	1.998	1.271
936	MSTRG.16852	Ca_13821	Ca6	3.564	1.271
937	MSTRG.6586	Ca_07322	Ca3	2.079	1.273
938	MSTRG.6176	Ca_23888	Ca3	5.067	1.274
939	MSTRG.3077	Ca_16998	Ca2	4.844	1.274
940	MSTRG.22424	Ca_24703	scaffold123	3.544	1.274
941	MSTRG.23096	Ca_21708	scaffold174	3.236	1.276
942	MSTRG.21885	Ca_12955	Ca8	7.144	1.278
943	MSTRG.22934	Ca_21087	scaffold157	6.551	1.278
944	MSTRG.18791	Ca_09379	Ca7	4.016	1.283
945	MSTRG.14517	Ca_05752	Ca6	2.990	1.283
946	MSTRG.25507	-	scaffold93	6.456	1.286
947	MSTRG.2288	Ca_18578	Ca1	4.850	1.287
948	MSTRG.12128	Ca_16657	Ca5	7.404	1.287
949	MSTRG.20407	Ca_21371	Ca7	3.737	1.287
950	MSTRG.6516	Ca_07255	Ca3	10.927	1.289
951	MSTRG.7373	Ca_01108	Ca3	1.730	1.289
952	MSTRG.13556	-	Ca5	0.409	1.290
953	MSTRG.6123	Ca_06014	Ca3	3.538	1.291
954	MSTRG.4973	Ca_09781	Ca2	2.725	1.292
955	MSTRG.19021	Ca_23045	Ca7	6.012	1.293
956	MSTRG.17870	-	Ca7	3.695	1.298
957	MSTRG.24355	Ca_27487	scaffold4057	1.693	1.300
958	MSTRG.17156	Ca_17525	Ca6	1.991	1.302
959	MSTRG.12019	-	Ca5	2.114	1.304
960	MSTRG.14850	Ca_16752	Ca6	1.126	1.305

961	MSTRG.2246	Ca_19281	Ca1	3.007	1.308
962	MSTRG.16588	Ca_15803	Ca6	1.317	1.308
963	MSTRG.17788	-	Ca7	1.078	1.311
964	MSTRG.18532	Ca_13170	Ca7	2.766	1.314
965	MSTRG.4038	Ca_23775	Ca2	1.725	1.314
966	MSTRG.12011	Ca_13408	Ca5	1.886	1.315
967	MSTRG.11402	-	Ca5	1.817	1.320
968	MSTRG.5633	Ca_19621	Ca3	2.756	1.320
969	MSTRG.19856	Ca_10057	Ca7	10.443	1.322
970	MSTRG.17066	-	Ca6	-0.017	1.324
971	MSTRG.12345	-	Ca5	-0.014	1.327
972	MSTRG.13536	Ca_12653	Ca5	7.742	1.328
973	MSTRG.2691	Ca_18464	Ca1	6.613	1.328
974	MSTRG.15024	Ca_08532	Ca6	3.825	1.329
975	MSTRG.367	Ca_00160	Ca1	2.525	1.330
976	MSTRG.4754	Ca_10155	Ca2	2.404	1.332
977	MSTRG.11205	-	Ca5	3.401	1.332
978	MSTRG.20450	Ca_15741	Ca7	8.494	1.333
979	MSTRG.6342	Ca_08149	Ca3	1.316	1.333
980	MSTRG.6635	-	Ca3	1.463	1.335
981	MSTRG.15178	-	Ca6	0.584	1.335
982	MSTRG.7461	Ca_01207	Ca3	3.845	1.337
983	MSTRG.18067	Ca_03040	Ca7	-0.230	1.339
984	MSTRG.9664	Ca_19059	Ca4	1.693	1.340
985	MSTRG.2822	-	Ca1	1.694	1.340
986	MSTRG.8741	Ca_04312	Ca4	3.699	1.342
987	MSTRG.5362	Ca_18798	Ca3	6.720	1.343
988	MSTRG.25016	Ca_20165	scaffold674	4.303	1.347
989	MSTRG.13417	Ca_11331	Ca5	2.137	1.348
990	MSTRG.18590	-	Ca7	2.455	1.351
991	MSTRG.17283	Ca_21208	Ca6	2.571	1.352
992	MSTRG.6232	Ca_08259	Ca3	5.447	1.353
993	MSTRG.1581	Ca_02457	Ca1	3.155	1.353
994	MSTRG.3800	Ca_18060	Ca2	4.454	1.355
995	MSTRG.7528	Ca_01260	Ca3	4.260	1.355
996	MSTRG.4292	Ca_15666	Ca2	0.337	1.357
997	MSTRG.19244	Ca_15838	Ca7	4.085	1.358

998	MSTRG.20612	Ca_11875	Ca8	2.380	1.359
999	MSTRG.21439	Ca_11432	Ca8	0.167	1.361
1000	MSTRG.12050	Ca_13369	Ca5	1.895	1.362
1001	MSTRG.8411	Ca_03506	Ca4	1.417	1.363
1002	MSTRG.7034	Ca_00785	Ca3	1.350	1.363
1003	MSTRG.4170	Ca_14252	Ca2	1.496	1.364
1004	MSTRG.7559	Ca_01287	Ca3	-0.235	1.364
1005	MSTRG.9239	-	Ca4	2.935	1.364
1006	MSTRG.1267	Ca_02780	Ca1	0.622	1.364
1007	MSTRG.23575	-	scaffold2373	5.581	1.366
1008	MSTRG.11720	Ca_17689	Ca5	-0.545	1.367
1009	MSTRG.5382	Ca_18820	Ca3	6.540	1.367
1010	MSTRG.15403	Ca_05303	Ca6	2.285	1.369
1011	MSTRG.4220	Ca_14307	Ca2	2.909	1.374
1012	MSTRG.8368	Ca_03552	Ca4	4.342	1.379
1013	MSTRG.16234	-	Ca6	3.679	1.381
1014	MSTRG.25267	-	scaffold848	0.358	1.383
1015	MSTRG.20592	-	Ca8	2.009	1.384
1016	MSTRG.14898	Ca_08667	Ca6	3.286	1.389
1017	MSTRG.8356	Ca_03565	Ca4	6.144	1.393
1018	MSTRG.785	Ca_00597	Ca1	4.288	1.394
1019	MSTRG.8894	Ca_04453	Ca4	1.353	1.394
1020	MSTRG.20970	Ca_02207	Ca8	3.820	1.394
1021	MSTRG.15734	Ca_06517	Ca6	1.656	1.395
1022	MSTRG.6940	Ca_00703	Ca3	4.749	1.396
1023	MSTRG.13933	Ca_04239	Ca5	1.791	1.397
1024	MSTRG.13618	Ca_03919	Ca5	-0.380	1.399
1025	MSTRG.6837	Ca_11998	Ca3	2.963	1.399
1026	MSTRG.13162	Ca_07522	Ca5	7.651	1.400
1027	MSTRG.21065	Ca_02117	Ca8	3.844	1.402
1028	MSTRG.10025	Ca_15494	Ca4	6.006	1.403
1029	MSTRG.1601	Ca_14067	Ca1	-0.152	1.403
1030	MSTRG.14098	Ca_10297	Ca6	0.561	1.404
1031	MSTRG.3295	Ca_10527	Ca2	4.403	1.406
1032	MSTRG.21168	Ca_02012	Ca8	4.134	1.407
1033	MSTRG.24505	Ca_21726	scaffold453	4.198	1.407
1034	MSTRG.3583	Ca_18126	Ca2	2.151	1.408

1035	MSTRG.10703	-	Ca4	-0.544	1.408
1036	MSTRG.2643	Ca_13930	Ca1	1.799	1.412
1037	MSTRG.18566	Ca_15354	Ca7	2.314	1.412
1038	MSTRG.14700	Ca_09644	Ca6	0.628	1.414
1039	MSTRG.14250	Ca_10440	Ca6	4.787	1.416
1040	MSTRG.2662	Ca_18440	Ca1	1.966	1.418
1041	MSTRG.10753	Ca_18377	Ca4	5.359	1.418
1042	MSTRG.11853	Ca_09010	Ca5	3.790	1.421
1043	MSTRG.3831	Ca_18094	Ca2	1.185	1.424
1044	MSTRG.16207	Ca_16714	Ca6	0.565	1.428
1045	MSTRG.21608	Ca_18433	Ca8	5.451	1.428
1046	MSTRG.17881	Ca_03217	Ca7	2.604	1.429
1047	MSTRG.23645	-	scaffold2560	3.986	1.429
1048	MSTRG.25496	Ca_25673	scaffold924	1.227	1.430
1049	MSTRG.17519	Ca_15385	Ca6	-0.009	1.431
1050	MSTRG.13381	-	Ca5	1.357	1.437
1051	MSTRG.19377	-	Ca7	0.327	1.439
1052	MSTRG.22667	-	scaffold1348_1	1.976	1.441
1053	MSTRG.1678	Ca_14141	Ca1	2.066	1.441
1054	MSTRG.20004	Ca_20989	Ca7	4.625	1.445
1055	MSTRG.20975	Ca_02196	Ca8	4.077	1.447
1056	MSTRG.10230	Ca_15084	Ca4	7.900	1.447
1057	MSTRG.19604	Ca_18940	Ca7	1.954	1.449
1058	MSTRG.21590	Ca_18417	Ca8	1.937	1.449
1059	MSTRG.24131	-	scaffold346_1	2.408	1.450
1060	MSTRG.746	Ca_00559	Ca1	4.591	1.452
1061	MSTRG.5736	Ca_09416	Ca3	1.741	1.452
1062	MSTRG.22578	-	scaffold134	1.256	1.455
1063	MSTRG.9229	Ca_05557	Ca4	3.959	1.459
1064	MSTRG.19857	-	Ca7	2.498	1.462
1065	MSTRG.2678	Ca_18449	Ca1	1.131	1.462
1066	MSTRG.6732	Ca_12239	Ca3	3.202	1.465
1067	MSTRG.1184	Ca_02863	Ca1	3.679	1.466
1068	MSTRG.22389	Ca_22970	scaffold12	1.522	1.467
1069	MSTRG.25383	-	scaffold887_1	3.229	1.469
1070	MSTRG.10685	Ca_09167	Ca4	0.377	1.470
1071	MSTRG.17789	Ca_03294	Ca7	6.291	1.475

1072	MSTRG.9444	-	Ca4	1.365	1.476
1073	MSTRG.6895	Ca_12057	Ca3	4.673	1.477
1074	MSTRG.19275	Ca_12304	Ca7	5.514	1.480
1075	MSTRG.22706	-	scaffold1348_1	0.431	1.481
1076	MSTRG.19314	Ca_12345	Ca7	3.791	1.483
1077	MSTRG.3590	Ca_18136	Ca2	1.292	1.484
1078	MSTRG.6315	Ca_08178	Ca3	7.142	1.484
1079	MSTRG.10085	Ca_20019	Ca4	7.332	1.486
1080	MSTRG.8929	Ca_04485	Ca4	1.647	1.486
1081	MSTRG.20079	-	Ca7	0.833	1.486
1082	MSTRG.24850	-	scaffold590	0.689	1.489
1083	MSTRG.22695	-	scaffold1348_1	5.603	1.491
1084	MSTRG.21222	Ca_01963	Ca8	3.587	1.492
1085	MSTRG.25085	Ca_25050	scaffold724	-0.153	1.493
1086	MSTRG.15803	Ca_16377	Ca6	3.743	1.493
1087	MSTRG.5270	Ca_16533	Ca3	4.579	1.496
1088	MSTRG.1426	Ca_02620	Ca1	3.670	1.497
1089	MSTRG.21617	Ca_19724	Ca8	2.317	1.499
1090	MSTRG.412	Ca_00207	Ca1	2.749	1.500
1091	MSTRG.25254	Ca_22428	scaffold845	2.612	1.500
1092	MSTRG.1231	Ca_02818	Ca1	3.436	1.500
1093	MSTRG.480	Ca_00277	Ca1	4.587	1.500
1094	MSTRG.6223	Ca_08266	Ca3	1.677	1.500
1095	MSTRG.6906	-	Ca3	0.406	1.501
1096	MSTRG.1401	Ca_02638	Ca1	2.561	1.501
1097	MSTRG.12912	-	Ca5	0.603	1.502
1098	MSTRG.15848	-	Ca6	1.833	1.503
1099	MSTRG.8068	-	Ca4	2.665	1.509
1100	MSTRG.10396	Ca_14874	Ca4	3.070	1.511
1101	MSTRG.20369	-	Ca7	1.642	1.512
1102	MSTRG.6782	Ca_12291	Ca3	2.218	1.513
1103	MSTRG.12096	Ca_16624	Ca5	6.040	1.519
1104	MSTRG.21643	Ca_19746	Ca8	4.605	1.523
1105	MSTRG.14726	Ca_09623	Ca6	0.822	1.524
1106	MSTRG.21718	-	Ca8	2.860	1.525
1107	MSTRG.17128	Ca_19171	Ca6	5.624	1.527
1108	MSTRG.19247	Ca_15833	Ca7	1.605	1.527

1109	MSTRG.5988	Ca_06168	Ca3	0.364	1.528
1110	MSTRG.12471	-	Ca5	4.244	1.528
1111	MSTRG.24723	Ca_23286	scaffold537	5.549	1.529
1112	MSTRG.18007	Ca_03099	Ca7	1.455	1.532
1113	MSTRG.17632	Ca_20231	Ca7	0.397	1.536
1114	MSTRG.18838	Ca_09327	Ca7	0.988	1.537
1115	MSTRG.6957	Ca_00719	Ca3	3.493	1.537
1116	MSTRG.10094	Ca_22435	Ca4	0.760	1.538
1117	MSTRG.1949	Ca_06883	Ca1	0.928	1.539
1118	MSTRG.24959	Ca_25150	scaffold645	4.454	1.540
1119	MSTRG.4208	Ca_14290	Ca2	9.243	1.545
1120	MSTRG.21276	Ca_23582	Ca8	1.680	1.546
1121	MSTRG.24136	-	scaffold346_1	3.265	1.548
1122	MSTRG.13061	Ca_07421	Ca5	5.795	1.548
1123	MSTRG.21368	-	Ca8	2.057	1.552
1124	MSTRG.20502	-	Ca7	3.580	1.553
1125	MSTRG.21221	Ca_01964	Ca8	6.324	1.553
1126	MSTRG.10104	Ca_14861	Ca4	2.331	1.554
1127	MSTRG.18763	Ca_12825	Ca7	5.066	1.557
1128	MSTRG.2609	Ca_23538	Ca1	1.295	1.558
1129	MSTRG.16025	Ca_11131	Ca6	8.237	1.563
1130	MSTRG.1461	-	Ca1	2.143	1.563
1131	MSTRG.12908	Ca_01515	Ca5	7.142	1.564
1132	MSTRG.1516	Ca_02523	Ca1	5.781	1.566
1133	MSTRG.22638	-	scaffold1348_1	1.948	1.574
1134	MSTRG.15097	-	Ca6	0.511	1.574
1135	MSTRG.9373	Ca_05412	Ca4	5.332	1.576
1136	MSTRG.1625	Ca_14088	Ca1	6.122	1.577
1137	MSTRG.12064	Ca_13354	Ca5	5.503	1.577
1138	MSTRG.1008	Ca_07996	Ca1	7.677	1.580
1139	MSTRG.9342	Ca_05441	Ca4	6.697	1.584
1140	MSTRG.17819	Ca_03269	Ca7	4.842	1.585
1141	MSTRG.15822	Ca_16357	Ca6	3.347	1.586
1142	MSTRG.6568	Ca_07306	Ca3	1.860	1.589
1143	MSTRG.24127	-	scaffold346_1	4.014	1.589
1144	MSTRG.1637	Ca_14105	Ca1	1.552	1.592
1145	MSTRG.1830	Ca_07000	Ca1	1.361	1.595

1146	MSTRG.200	-	Ca1	0.328	1.596
1147	MSTRG.17013	Ca_13521	Ca6	1.196	1.596
1148	MSTRG.8112	Ca_03805	Ca4	1.287	1.596
1149	MSTRG.22455	Ca_21437	scaffold128	3.811	1.597
1150	MSTRG.13398	Ca_11349	Ca5	2.702	1.598
1151	MSTRG.4858	Ca_16870	Ca2	3.513	1.598
1152	MSTRG.17202	Ca_22925	Ca6	2.292	1.601
1153	MSTRG.17389	-	Ca6	2.041	1.601
1154	MSTRG.18458	Ca_06589	Ca7	4.349	1.602
1155	MSTRG.11873	Ca_08988	Ca5	2.961	1.606
1156	MSTRG.16833	-	Ca6	2.824	1.609
1157	MSTRG.2626	Ca_13966	Ca1	3.484	1.611
1158	MSTRG.2227	-	Ca1	-0.314	1.612
1159	MSTRG.535	Ca_00331	Ca1	3.244	1.614
1160	MSTRG.24507	Ca_21732	scaffold453	1.616	1.618
1161	MSTRG.5945	Ca_06208	Ca3	0.894	1.620
1162	MSTRG.7578	Ca_01307	Ca3	-0.629	1.624
1163	MSTRG.23600	Ca_25869	scaffold2415	5.217	1.624
1164	MSTRG.2429	-	Ca1	-2.402	1.625
1165	MSTRG.18616	Ca_15295	Ca7	1.915	1.627
1166	MSTRG.14508	Ca_05762	Ca6	0.398	1.627
1167	MSTRG.18589	Ca_15322	Ca7	6.497	1.628
1168	MSTRG.23025	-	scaffold167	2.629	1.631
1169	MSTRG.3496	-	Ca2	1.348	1.632
1170	MSTRG.3251	-	Ca2	2.624	1.632
1171	MSTRG.7806	Ca_07771	Ca4	0.844	1.634
1172	MSTRG.12022	-	Ca5	0.639	1.634
1173	MSTRG.22295	Ca_26846	scaffold1135	3.503	1.634
1174	MSTRG.14564	Ca_05699	Ca6	5.723	1.636
1175	MSTRG.5330	Ca_20955	Ca3	0.354	1.637
1176	MSTRG.18066	Ca_03041	Ca7	2.987	1.637
1177	MSTRG.13671	Ca_03977	Ca5	3.392	1.638
1178	MSTRG.22812	-	scaffold1419	0.900	1.639
1179	MSTRG.1623	Ca_14087	Ca1	6.142	1.639
1180	MSTRG.14449	Ca_05819	Ca6	0.705	1.639
1181	MSTRG.19808	Ca_10100	Ca7	2.824	1.651
1182	MSTRG.19933	Ca_16156	Ca7	2.759	1.653

1183	MSTRG.18619	Ca_15296	Ca7	4.564	1.654
1184	MSTRG.15323	Ca_05208	Ca6	4.788	1.654
1185	MSTRG.81	Ca_27676	C11115550	0.661	1.655
1186	MSTRG.16195	Ca_16706	Ca6	2.676	1.661
1187	MSTRG.15810	-	Ca6	0.849	1.662
1188	MSTRG.4261	Ca_17277	Ca2	0.565	1.664
1189	MSTRG.10925	Ca_10769	Ca4	5.602	1.664
1190	MSTRG.617	Ca_00412	Ca1	5.697	1.670
1191	MSTRG.4140	-	Ca2	1.470	1.671
1192	MSTRG.17765	-	Ca7	5.801	1.672
1193	MSTRG.4427	Ca_16127	Ca2	4.003	1.678
1194	MSTRG.6952	Ca_00712	Ca3	0.189	1.680
1195	MSTRG.6301	Ca_08194	Ca3	1.723	1.681
1196	MSTRG.821	Ca_00633	Ca1	1.651	1.681
1197	MSTRG.12372	Ca_04881	Ca5	4.716	1.683
1198	MSTRG.15995	-	Ca6	0.569	1.683
1199	MSTRG.24159	Ca_26736	scaffold350	3.880	1.684
1200	MSTRG.17305	Ca_19018	Ca6	0.003	1.684
1201	MSTRG.15490	Ca_06282	Ca6	3.171	1.688
1202	MSTRG.23573	Ca_27075	scaffold2373	-1.049	1.689
1203	MSTRG.4567	Ca_12419	Ca2	5.448	1.691
1204	MSTRG.7561	Ca_01291	Ca3	5.711	1.694
1205	MSTRG.12297	Ca_04814	Ca5	2.271	1.695
1206	MSTRG.13750	Ca_04055	Ca5	4.288	1.695
1207	MSTRG.5947	Ca_06207	Ca3	1.504	1.697
1208	MSTRG.487	Ca_00282	Ca1	0.519	1.697
1209	MSTRG.24039	Ca_25706	scaffold3321	1.148	1.698
1210	MSTRG.22668	-	scaffold1348_1	0.867	1.698
1211	MSTRG.22390	Ca_22967	scaffold12	1.901	1.698
1212	MSTRG.7950	Ca_12091	Ca4	5.754	1.701
1213	MSTRG.15075	Ca_20489	Ca6	2.301	1.714
1214	MSTRG.21552	Ca_11547	Ca8	0.122	1.714
1215	MSTRG.2194	Ca_20618	Ca1	1.423	1.714
1216	MSTRG.10629	Ca_09111	Ca4	-0.288	1.717
1217	MSTRG.25571	-	scaffold98	-0.593	1.718
1218	MSTRG.13700	Ca_04005	Ca5	3.626	1.730
1219	MSTRG.325	-	Ca1	0.471	1.731

1220	MSTRG.947	Ca_07943	Ca1	6.705	1.733
1221	MSTRG.3621	Ca_21470	Ca2	3.407	1.735
1222	MSTRG.3870	-	Ca2	0.097	1.740
1223	MSTRG.24820	Ca_27413	scaffold5687	3.215	1.742
1224	MSTRG.2359	Ca_26748	Ca1	0.104	1.742
1225	MSTRG.1603	Ca_14072	Ca1	3.187	1.748
1226	MSTRG.14513	Ca_05754	Ca6	4.134	1.749
1227	MSTRG.11666	Ca_20083	Ca5	3.433	1.751
1228	MSTRG.9123	Ca_05657	Ca4	1.334	1.751
1229	MSTRG.550	-	Ca1	-0.069	1.756
1230	MSTRG.13892	Ca_04193	Ca5	4.159	1.758
1231	MSTRG.1784	Ca_07051	Ca1	0.177	1.760
1232	MSTRG.12347	Ca_04858	Ca5	6.310	1.762
1233	MSTRG.14576	-	Ca6	-0.231	1.762
1234	MSTRG.9401	-	Ca4	-0.636	1.763
1235	MSTRG.18704	Ca_12765	Ca7	-0.103	1.763
1236	MSTRG.23354	-	scaffold2018	-1.087	1.767
1237	MSTRG.6280	Ca_08212	Ca3	8.325	1.767
1238	MSTRG.17073	Ca_13462	Ca6	4.438	1.767
1239	MSTRG.19319	Ca_12340	Ca7	2.058	1.770
1240	MSTRG.9149	Ca_05633	Ca4	1.626	1.773
1241	MSTRG.20936	Ca_02241	Ca8	0.600	1.774
1242	MSTRG.23311	Ca_20921	scaffold198	0.937	1.774
1243	MSTRG.21012	Ca_02167	Ca8	3.975	1.776
1244	MSTRG.9031	Ca_04586	Ca4	1.626	1.779
1245	MSTRG.4215	Ca_14303	Ca2	-0.187	1.780
1246	MSTRG.10197	Ca_15126	Ca4	4.022	1.781
1247	MSTRG.15665	Ca_06452	Ca6	9.299	1.785
1248	MSTRG.23792	Ca_20600	scaffold284	7.728	1.785
1249	MSTRG.2233	Ca_19292	Ca1	4.247	1.798
1250	MSTRG.16302	Ca_26118	Ca6	5.111	1.802
1251	MSTRG.16974	Ca_24607	Ca6	4.037	1.802
1252	MSTRG.2129	-	Ca1	0.608	1.803
1253	MSTRG.11920	Ca_08932	Ca5	-1.084	1.803
1254	MSTRG.8885	Ca_04443	Ca4	3.551	1.807
1255	MSTRG.19237	Ca_15844	Ca7	5.407	1.809
1256	MSTRG.1990	Ca_14789	Ca1	5.418	1.814

1257	MSTRG.11388	Ca_17116	Ca5	0.904	1.817
1258	MSTRG.9078	Ca_04628	Ca4	3.428	1.819
1259	MSTRG.22421	Ca_27098	scaffold1219	0.194	1.824
1260	MSTRG.25418	-	scaffold895	2.171	1.831
1261	MSTRG.7488	Ca_01230	Ca3	6.081	1.834
1262	MSTRG.5653	Ca_19640	Ca3	3.610	1.834
1263	MSTRG.4235	Ca_17248	Ca2	7.959	1.834
1264	MSTRG.25104	Ca_23809	scaffold731	1.523	1.837
1265	MSTRG.24182	Ca_25858	scaffold36	4.409	1.839
1266	MSTRG.13809	Ca_04111	Ca5	1.164	1.841
1267	MSTRG.2637	Ca_13958	Ca1	3.181	1.841
1268	MSTRG.25595	-	scaffold983	-0.576	1.842
1269	MSTRG.17858	Ca_03237	Ca7	4.519	1.842
1270	MSTRG.17815	-	Ca7	2.726	1.845
1271	MSTRG.25036	Ca_23185	scaffold682	2.911	1.845
1272	MSTRG.11338	Ca_21231	Ca5	3.956	1.851
1273	MSTRG.14961	Ca_08595	Ca6	-0.412	1.854
1274	MSTRG.5160	Ca_22377	Ca3	5.115	1.856
1275	MSTRG.6513	Ca_07254	Ca3	2.505	1.856
1276	MSTRG.24772	Ca_19924	scaffold553	0.799	1.862
1277	MSTRG.14743	Ca_09603	Ca6	3.182	1.862
1278	MSTRG.12900	Ca_01525	Ca5	1.062	1.863
1279	MSTRG.1578	Ca_02469	Ca1	4.008	1.863
1280	MSTRG.2941	-	Ca1	4.958	1.870
1281	MSTRG.9994	-	Ca4	0.269	1.874
1282	MSTRG.6556	Ca_07296	Ca3	2.976	1.875
1283	MSTRG.22437	-	scaffold1259	0.951	1.876
1284	MSTRG.18230	-	Ca7	-0.091	1.880
1285	MSTRG.15788	Ca_06574	Ca6	1.877	1.881
1286	MSTRG.18374	Ca_06660	Ca7	2.197	1.882
1287	MSTRG.24628	Ca_25364	scaffold498	4.113	1.884
1288	MSTRG.9804	Ca_16561	Ca4	1.739	1.886
1289	MSTRG.7191	Ca_00945	Ca3	0.744	1.887
1290	MSTRG.14282	-	Ca6	4.575	1.887
1291	MSTRG.22552	-	scaffold1324	-0.069	1.899
1292	MSTRG.7857	Ca_07825	Ca4	1.060	1.900
1293	MSTRG.4468	Ca_12525	Ca2	1.741	1.900

1294	MSTRG.4113	Ca_14942	Ca2	1.280	1.900
1295	MSTRG.21141	Ca_02041	Ca8	2.505	1.905
1296	MSTRG.10318	Ca_13067	Ca4	4.073	1.906
1297	MSTRG.7270	Ca_01017	Ca3	5.753	1.907
1298	MSTRG.4941	Ca_09747	Ca2	5.236	1.909
1299	MSTRG.17756	Ca_03319	Ca7	-0.037	1.911
1300	MSTRG.21159	Ca_02019	Ca8	6.975	1.918
1301	MSTRG.4016	-	Ca2	-0.352	1.919
1302	MSTRG.4429	Ca_16126	Ca2	4.576	1.919
1303	MSTRG.20845	Ca_02336	Ca8	2.276	1.925
1304	MSTRG.20986	-	Ca8	-0.765	1.929
1305	MSTRG.5238	Ca_25770	Ca3	5.598	1.931
1306	MSTRG.4461	Ca_16084	Ca2	0.313	1.931
1307	MSTRG.8269	-	Ca4	2.237	1.932
1308	MSTRG.16777	Ca_23160	Ca6	1.731	1.940
1309	MSTRG.16938	-	Ca6	-0.337	1.941
1310	MSTRG.18944	Ca_16018	Ca7	7.360	1.941
1311	MSTRG.20594	Ca_11888	Ca8	0.047	1.942
1312	MSTRG.15784	-	Ca6	-1.553	1.947
1313	MSTRG.2679	Ca_18450	Ca1	2.789	1.948
1314	MSTRG.13552	Ca_12639	Ca5	6.280	1.948
1315	MSTRG.8754	Ca_04324	Ca4	5.632	1.950
1316	MSTRG.4624	Ca_10291	Ca2	3.545	1.953
1317	MSTRG.1494	-	Ca1	-0.748	1.954
1318	MSTRG.3869	Ca_11644	Ca2	2.012	1.956
1319	MSTRG.2701	Ca_18472	Ca1	2.175	1.959
1320	MSTRG.1410	Ca_02630	Ca1	3.104	1.962
1321	MSTRG.7114	Ca_00867	Ca3	2.338	1.962
1322	MSTRG.2092	Ca_17365	Ca1	6.378	1.963
1323	MSTRG.20294	Ca_20250	Ca7	2.613	1.967
1324	MSTRG.24469	Ca_26058	scaffold4452	2.926	1.967
1325	MSTRG.9513	-	Ca4	1.031	1.969
1326	MSTRG.12042	Ca_13375	Ca5	3.405	1.976
1327	MSTRG.25140	-	scaffold766	-1.786	1.979
1328	MSTRG.13018	Ca_01402	Ca5	4.003	1.980
1329	MSTRG.23063	Ca_25721	scaffold1710	1.313	1.985
1330	MSTRG.2192	Ca_20624	Ca1	3.370	1.987

1331	MSTRG.18220	Ca_06793	Ca7	1.659	1.993
1332	MSTRG.13195	Ca_07557	Ca5	0.703	2.001
1333	MSTRG.20049	Ca_17633	Ca7	1.646	2.003
1334	MSTRG.11691	Ca_21970	Ca5	1.151	2.005
1335	MSTRG.17286	Ca_21212	Ca6	3.963	2.009
1336	MSTRG.22691	-	scaffold1348_1	4.451	2.022
1337	MSTRG.20738	Ca_02445	Ca8	2.622	2.023
1338	MSTRG.23404	-	scaffold206	-1.367	2.026
1339	MSTRG.3866	Ca_11648	Ca2	-1.068	2.029
1340	MSTRG.17509	-	Ca6	6.185	2.030
1341	MSTRG.25253	Ca_22426	scaffold845	1.622	2.030
1342	MSTRG.1214	Ca_02835	Ca1	1.472	2.032
1343	MSTRG.12428	Ca_04936	Ca5	2.348	2.032
1344	MSTRG.21754	Ca_22732	Ca8	2.778	2.033
1345	MSTRG.20740	-	Ca8	-0.168	2.035
1346	MSTRG.22234	-	scaffold109_1	2.362	2.035
1347	MSTRG.6872	Ca_12034	Ca3	5.844	2.036
1348	MSTRG.13357	Ca_11390	Ca5	0.051	2.041
1349	MSTRG.6594	Ca_07330	Ca3	-0.347	2.041
1350	MSTRG.2608	-	Ca1	-0.575	2.047
1351	MSTRG.7832	Ca_07799	Ca4	2.662	2.048
1352	MSTRG.12898	Ca_01527	Ca5	1.808	2.049
1353	MSTRG.10351	Ca_14921	Ca4	4.652	2.052
1354	MSTRG.539	Ca_00335	Ca1	0.264	2.052
1355	MSTRG.15460	-	Ca6	0.449	2.058
1356	MSTRG.9833	Ca_16612	Ca4	6.554	2.060
1357	MSTRG.20971	Ca_02206	Ca8	3.480	2.067
1358	MSTRG.18926	Ca_09240	Ca7	7.123	2.069
1359	MSTRG.16235	-	Ca6	0.536	2.071
1360	MSTRG.1680	Ca_14144	Ca1	4.985	2.072
1361	MSTRG.1904	Ca_06917	Ca1	6.451	2.085
1362	MSTRG.17144	-	Ca6	-1.617	2.087
1363	MSTRG.7580	Ca_01312	Ca3	3.900	2.090
1364	MSTRG.12931	Ca_01491	Ca5	3.215	2.091
1365	MSTRG.5709	Ca_09381	Ca3	4.840	2.091
1366	MSTRG.2677	Ca_18448	Ca1	-0.289	2.093
1367	MSTRG.18868	Ca_09299	Ca7	4.390	2.095

1368	MSTRG.12678	Ca_01742	Ca5	0.024	2.097
1369	MSTRG.19076	Ca_09947	Ca7	2.739	2.097
1370	MSTRG.20438	-	Ca7	-1.414	2.100
1371	MSTRG.17232	Ca_18910	Ca6	1.351	2.108
1372	MSTRG.23596	-	scaffold240	-0.431	2.109
1373	MSTRG.25252	Ca_22425	scaffold845	1.952	2.110
1374	MSTRG.8350	Ca_03572	Ca4	4.672	2.123
1375	MSTRG.4254	Ca_17270	Ca2	0.892	2.128
1376	MSTRG.22068	-	scaffold10260	-0.451	2.129
1377	MSTRG.11332	Ca_21238	Ca5	2.954	2.131
1378	MSTRG.20010	Ca_20981	Ca7	-0.284	2.136
1379	MSTRG.21343	Ca_10684	Ca8	1.825	2.136
1380	MSTRG.21423	Ca_10608	Ca8	1.860	2.138
1381	MSTRG.12971	Ca_01449	Ca5	5.157	2.143
1382	MSTRG.20841	Ca_02339	Ca8	2.709	2.146
1383	MSTRG.15596	Ca_06386	Ca6	2.374	2.146
1384	MSTRG.16477	Ca_15192	Ca6	2.215	2.163
1385	MSTRG.11608	Ca_18223	Ca5	-0.257	2.168
1386	MSTRG.6888	Ca_12049	Ca3	1.000	2.168
1387	MSTRG.7949	Ca_12090	Ca4	6.210	2.173
1388	MSTRG.13378	Ca_11364	Ca5	-0.588	2.186
1389	MSTRG.20103	Ca_17794	Ca7	-0.361	2.187
1390	MSTRG.5376	-	Ca3	0.506	2.188
1391	MSTRG.7284	-	Ca3	-0.455	2.190
1392	MSTRG.8455	Ca_03462	Ca4	0.657	2.190
1393	MSTRG.16186	Ca_16693	Ca6	3.396	2.192
1394	MSTRG.21183	Ca_01998	Ca8	1.810	2.193
1395	MSTRG.2834	Ca_13562	Ca1	5.237	2.198
1396	MSTRG.18641	Ca_17318	Ca7	0.790	2.199
1397	MSTRG.532	Ca_00328	Ca1	2.885	2.200
1398	MSTRG.18243	Ca_06773	Ca7	0.813	2.204
1399	MSTRG.9349	Ca_05434	Ca4	4.773	2.212
1400	MSTRG.16331	-	Ca6	0.733	2.219
1401	MSTRG.5203	Ca_20661	Ca3	4.325	2.222
1402	MSTRG.1589	Ca_02451	Ca1	5.862	2.226
1403	MSTRG.13770	Ca_04075	Ca5	2.267	2.236
1404	MSTRG.5125	-	Ca3	1.106	2.240

1405	MSTRG.14886	-	Ca6	-0.096	2.246
1406	MSTRG.4988	Ca_09800	Ca2	6.730	2.247
1407	MSTRG.20743	-	Ca8	2.078	2.253
1408	MSTRG.23186	-	scaffold1844	4.651	2.255
1409	MSTRG.3948	-	Ca2	2.586	2.259
1410	MSTRG.24633	Ca_25368	scaffold498	3.083	2.260
1411	MSTRG.7166	Ca_00922	Ca3	-0.053	2.263
1412	MSTRG.17813	Ca_03276	Ca7	1.850	2.267
1413	MSTRG.14182	Ca_10368	Ca6	0.673	2.268
1414	MSTRG.24236	Ca_23621	scaffold38	4.159	2.269
1415	MSTRG.8772	Ca_04343	Ca4	4.838	2.270
1416	MSTRG.13693	Ca_03998	Ca5	2.630	2.272
1417	MSTRG.18219	Ca_06794	Ca7	3.428	2.278
1418	MSTRG.960	Ca_07955	Ca1	2.753	2.283
1419	MSTRG.11776	-	Ca5	0.413	2.285
1420	MSTRG.18923	Ca_09243	Ca7	6.086	2.292
1421	MSTRG.14489	-	Ca6	2.642	2.292
1422	MSTRG.13271	Ca_07638	Ca5	1.374	2.293
1423	MSTRG.16281	Ca_14577	Ca6	0.526	2.294
1424	MSTRG.4237	Ca_17249	Ca2	7.013	2.299
1425	MSTRG.20914	Ca_02264	Ca8	2.792	2.301
1426	MSTRG.4475	-	Ca2	3.361	2.307
1427	MSTRG.4378	Ca_14344	Ca2	2.778	2.309
1428	MSTRG.13037	Ca_01382	Ca5	-0.666	2.325
1429	MSTRG.3338	Ca_10489	Ca2	0.008	2.327
1430	MSTRG.18614	Ca_15298	Ca7	-1.168	2.338
1431	MSTRG.20501	-	Ca7	0.073	2.341
1432	MSTRG.577	-	Ca1	-0.867	2.346
1433	MSTRG.11831	Ca_09038	Ca5	3.697	2.354
1434	MSTRG.10275	Ca_13105	Ca4	1.743	2.359
1435	MSTRG.7278	Ca_01026	Ca3	2.230	2.360
1436	MSTRG.13623	Ca_03929	Ca5	1.137	2.366
1437	MSTRG.21251	Ca_01935	Ca8	3.612	2.368
1438	MSTRG.14004	Ca_13265	Ca6	2.504	2.372
1439	MSTRG.7142	Ca_00898	Ca3	0.642	2.381
1440	MSTRG.23901	Ca_26659	scaffold303	5.033	2.385
1441	MSTRG.15624	-	Ca6	4.822	2.402

1442	MSTRG.13130	-	Ca5	-0.142	2.407
1443	MSTRG.9569	Ca_14034	Ca4	1.407	2.410
1444	MSTRG.22227	-	scaffold109_1	1.160	2.438
1445	MSTRG.16148	Ca_24166	Ca6	1.173	2.442
1446	MSTRG.8188	-	Ca4	-1.948	2.447
1447	MSTRG.22243	-	scaffold109_1	1.619	2.462
1448	MSTRG.5095	-	Ca3	-1.220	2.470
1449	MSTRG.19276	Ca_12305	Ca7	-0.491	2.471
1450	MSTRG.12976	Ca_01445	Ca5	4.133	2.474
1451	MSTRG.19586	Ca_26609	Ca7	1.699	2.476
1452	MSTRG.10309	-	Ca4	-2.515	2.477
1453	MSTRG.7747	Ca_07719	Ca4	0.396	2.490
1454	MSTRG.23411	Ca_21894	scaffold210	1.286	2.491
1455	MSTRG.15997	Ca_11189	Ca6	2.198	2.492
1456	MSTRG.6919	-	Ca3	4.081	2.492
1457	MSTRG.9054	-	Ca4	-0.631	2.492
1458	MSTRG.14748	-	Ca6	-0.418	2.510
1459	MSTRG.6589	Ca_07325	Ca3	3.058	2.515
1460	MSTRG.16502	Ca_15222	Ca6	4.060	2.530
1461	MSTRG.12536	Ca_01903	Ca5	4.071	2.546
1462	MSTRG.10311	-	Ca4	-0.176	2.547
1463	MSTRG.21383	Ca_10655	Ca8	-1.442	2.551
1464	MSTRG.11817	-	Ca5	-0.955	2.553
1465	MSTRG.592	Ca_00387	Ca1	-0.450	2.554
1466	MSTRG.11917	-	Ca5	1.309	2.556
1467	MSTRG.15008	Ca_08546	Ca6	7.575	2.558
1468	MSTRG.10225	Ca_15089	Ca4	1.961	2.573
1469	MSTRG.8333	Ca_03587	Ca4	0.982	2.583
1470	MSTRG.8469	Ca_03440	Ca4	-1.159	2.587
1471	MSTRG.3149	-	Ca2	3.282	2.588
1472	MSTRG.24883	-	scaffold599	-1.611	2.591
1473	MSTRG.21244	Ca_01941	Ca8	1.239	2.595
1474	MSTRG.9735	Ca_14462	Ca4	0.567	2.597
1475	MSTRG.7326	-	Ca3	5.271	2.605
1476	MSTRG.20915	Ca_02263	Ca8	3.827	2.606
1477	MSTRG.24852	-	scaffold590	-1.441	2.612
1478	MSTRG.20931	-	Ca8	-0.076	2.615

1479	MSTRG.25349	Ca_22181	scaffold88	0.930	2.616
1480	MSTRG.1906	Ca_06919	Ca1	-0.835	2.617
1481	MSTRG.11016	Ca_18168	Ca5	-1.302	2.628
1482	MSTRG.19781	Ca_10128	Ca7	0.398	2.635
1483	MSTRG.15026	Ca_08531	Ca6	6.201	2.635
1484	MSTRG.12245	-	Ca5	-0.605	2.657
1485	MSTRG.20452	Ca_15742	Ca7	8.086	2.670
1486	MSTRG.17246	Ca_16265	Ca6	1.563	2.673
1487	MSTRG.410	Ca_00205	Ca1	1.282	2.687
1488	MSTRG.6656	Ca_07391	Ca3	0.550	2.687
1489	MSTRG.2394	Ca_18504	Ca1	5.545	2.693
1490	MSTRG.25345	Ca_22178	scaffold88	4.758	2.697
1491	MSTRG.20766	Ca_02422	Ca8	1.450	2.706
1492	MSTRG.20184	Ca_22799	Ca7	1.304	2.706
1493	MSTRG.3005	Ca_12890	Ca1	2.438	2.712
1494	MSTRG.8293	Ca_03626	Ca4	1.998	2.714
1495	MSTRG.17900	Ca_03201	Ca7	2.526	2.732
1496	MSTRG.2818	Ca_13575	Ca1	0.997	2.735
1497	MSTRG.17944	Ca_03158	Ca7	1.290	2.736
1498	MSTRG.11033	Ca_18188	Ca5	0.848	2.751
1499	MSTRG.2980	-	Ca1	0.100	2.757
1500	MSTRG.3597	Ca_18141	Ca2	3.510	2.765
1501	MSTRG.21116	Ca_02070	Ca8	2.978	2.794
1502	MSTRG.20002	Ca_20992	Ca7	6.333	2.817
1503	MSTRG.5878	Ca_20406	Ca3	1.623	2.826
1504	MSTRG.4608	Ca_17816	Ca2	1.256	2.826
1505	MSTRG.3433	Ca_14693	Ca2	5.480	2.840
1506	MSTRG.22904	Ca_23862	scaffold1545	3.254	2.840
1507	MSTRG.9044	-	Ca4	-0.407	2.859
1508	MSTRG.305	Ca_00107	Ca1	-0.347	2.870
1509	MSTRG.17518	Ca_15382	Ca6	-2.522	2.876
1510	MSTRG.16209	Ca_16717	Ca6	3.993	2.880
1511	MSTRG.7369	Ca_01119	Ca3	0.576	2.882
1512	MSTRG.13063	Ca_07423	Ca5	3.068	2.884
1513	MSTRG.20566	Ca_11914	Ca8	-0.386	2.911
1514	MSTRG.8853	-	Ca4	6.479	2.915
1515	MSTRG.7177	Ca_00933	Ca3	-0.989	2.920

1516	MSTRG.10093	-	Ca4	0.942	2.923
1517	MSTRG.18769	Ca_12830	Ca7	5.046	2.930
1518	MSTRG.8018	Ca_12153	Ca4	0.011	2.936
1519	MSTRG.17688	-	Ca7	3.624	2.950
1520	MSTRG.2720	Ca_23106	Ca1	5.362	2.965
1521	MSTRG.11819	-	Ca5	-0.804	2.970
1522	MSTRG.17571	Ca_18876	Ca6	-0.005	2.971
1523	MSTRG.11083	-	Ca5	-0.585	2.971
1524	MSTRG.25068	Ca_24965	scaffold716	0.374	2.981
1525	MSTRG.19607	Ca_18941	Ca7	1.407	2.995
1526	MSTRG.24770	Ca_21501	scaffold548	3.629	2.995
1527	MSTRG.23545	-	scaffold2356	-0.959	3.022
1528	MSTRG.21363	-	Ca8	0.200	3.027
1529	MSTRG.21301	Ca_10730	Ca8	1.774	3.041
1530	MSTRG.1548	Ca_02491	Ca1	3.682	3.052
1531	MSTRG.8069	Ca_03847	Ca4	3.431	3.058
1532	MSTRG.8620	Ca_08429	Ca4	2.239	3.065
1533	MSTRG.7890	-	Ca4	0.579	3.084
1534	MSTRG.15721	-	Ca6	0.747	3.088
1535	MSTRG.8941	Ca_04499	Ca4	0.371	3.090
1536	MSTRG.9528	Ca_13997	Ca4	-1.725	3.115
1537	MSTRG.21399	-	Ca8	-1.135	3.133
1538	MSTRG.17832	Ca_03257	Ca7	-1.316	3.139
1539	MSTRG.3032	Ca_12865	Ca1	3.091	3.140
1540	MSTRG.8903	Ca_04466	Ca4	2.753	3.144
1541	MSTRG.14570	Ca_05688	Ca6	0.637	3.185
1542	MSTRG.16910	-	Ca6	-0.910	3.202
1543	MSTRG.2119	Ca_17339	Ca1	4.374	3.224
1544	MSTRG.61	-	C11096254	-0.047	3.227
1545	MSTRG.24825	-	scaffold5739	-0.358	3.227
1546	MSTRG.1546	Ca_02493	Ca1	3.124	3.245
1547	MSTRG.16766	Ca_23152	Ca6	5.713	3.247
1548	MSTRG.24304	Ca_22300	scaffold398	-1.287	3.259
1549	MSTRG.5654	Ca_19641	Ca3	2.317	3.271
1550	MSTRG.14761	Ca_09586	Ca6	0.904	3.281
1551	MSTRG.3208	Ca_12535	Ca2	-0.467	3.283
1552	MSTRG.21832	Ca_12999	Ca8	0.180	3.292

1553	MSTRG.16253	Ca_14604	Ca6	2.615	3.298
1554	MSTRG.10760	Ca_18369	Ca4	4.745	3.310
1555	MSTRG.19954	Ca_16176	Ca7	-0.901	3.343
1556	MSTRG.16937	-	Ca6	-0.190	3.352
1557	MSTRG.5638	Ca_19627	Ca3	0.639	3.358
1558	MSTRG.16472	Ca_15189	Ca6	-0.708	3.368
1559	MSTRG.8168	-	Ca4	0.389	3.372
1560	MSTRG.777	-	Ca1	2.814	3.377
1561	MSTRG.8718	-	Ca4	0.248	3.379
1562	MSTRG.4926	Ca_09731	Ca2	0.555	3.380
1563	MSTRG.16424	Ca_16482	Ca6	-0.449	3.387
1564	MSTRG.2825	Ca_13567	Ca1	3.102	3.405
1565	MSTRG.22927	Ca_21077	scaffold157	-0.744	3.417
1566	MSTRG.10357	Ca_14913	Ca4	-1.090	3.431
1567	MSTRG.13994	-	Ca6	0.119	3.481
1568	MSTRG.17605	Ca_18846	Ca6	2.402	3.484
1569	MSTRG.10705	-	Ca4	-1.555	3.527
1570	MSTRG.17581	-	Ca6	-2.074	3.571
1571	MSTRG.20901	Ca_02279	Ca8	3.812	3.608
1572	MSTRG.2909	-	Ca1	-1.674	3.620
1573	MSTRG.14999	Ca_08560	Ca6	2.099	3.631
1574	MSTRG.2627	-	Ca1	-0.385	3.662
1575	MSTRG.22301	Ca_22323	scaffold1151	-1.092	3.664
1576	MSTRG.10233	-	Ca4	1.891	3.671
1577	MSTRG.13733	Ca_04038	Ca5	0.543	3.681
1578	MSTRG.24626	Ca_25362	scaffold498	1.039	3.696
1579	MSTRG.14866	Ca_16738	Ca6	6.726	3.697
1580	MSTRG.20595	-	Ca8	-1.055	3.702
1581	MSTRG.17269	Ca_16286	Ca6	1.823	3.709
1582	MSTRG.12270	-	Ca5	1.809	3.711
1583	MSTRG.5281	Ca_16514	Ca3	3.081	3.719
1584	MSTRG.7773	Ca_07743	Ca4	1.179	3.722
1585	MSTRG.22258	-	scaffold1107	-1.277	3.759
1586	MSTRG.14491	Ca_05777	Ca6	1.198	3.823
1587	MSTRG.2551	Ca_26100	Ca1	-2.300	3.832
1588	MSTRG.12272	Ca_04788	Ca5	9.065	3.860
1589	MSTRG.2460	-	Ca1	0.727	3.863

1590	MSTRG.11718	-	Ca5	-1.387	3.881
1591	MSTRG.22980	-	scaffold1633	-2.573	3.908
1592	MSTRG.24620	Ca_26761	scaffold495	0.994	3.935
1593	MSTRG.17669	Ca_03399	Ca7	3.161	3.940
1594	MSTRG.1025	Ca_08014	Ca1	-0.150	3.963
1595	MSTRG.24386	-	scaffold419	-2.998	3.967
1596	MSTRG.8847	Ca_04402	Ca4	-0.416	3.969
1597	MSTRG.16533	Ca_24447	Ca6	2.601	3.984
1598	MSTRG.6448	-	Ca3	-0.293	3.998
1599	MSTRG.24901	-	scaffold6181	-2.246	4.042
1600	MSTRG.1888	Ca_06938	Ca1	-1.487	4.078
1601	MSTRG.22984	-	scaffold1633	-3.470	4.108
1602	MSTRG.6691	Ca_12198	Ca3	2.728	4.125
1603	MSTRG.7563	Ca_01292	Ca3	3.693	4.166
1604	MSTRG.19078	Ca_09943	Ca7	3.623	4.169
1605	MSTRG.21361	-	Ca8	0.657	4.196
1606	MSTRG.12271	-	Ca5	5.779	4.202
1607	MSTRG.15124	-	Ca6	0.232	4.257
1608	MSTRG.2552	-	Ca1	1.654	4.302
1609	MSTRG.2100	-	Ca1	-2.457	4.316
1610	MSTRG.23180	Ca_26998	scaffold1825	-2.149	4.321
1611	MSTRG.10284	-	Ca4	3.264	4.321
1612	MSTRG.24088	-	scaffold3397	-0.231	4.323
1613	MSTRG.7348	Ca_01090	Ca3	-1.041	4.343
1614	MSTRG.17009	-	Ca6	-3.411	4.356
1615	MSTRG.17974	Ca_03127	Ca7	-0.579	4.358
1616	MSTRG.17109	Ca_19194	Ca6	-1.586	4.363
1617	MSTRG.13742	Ca_04048	Ca5	-0.666	4.417
1618	MSTRG.13197	Ca_07560	Ca5	1.958	4.446
1619	MSTRG.17975	Ca_03126	Ca7	0.930	4.488
1620	MSTRG.23578	-	scaffold2373	0.218	4.499
1621	MSTRG.6610	Ca_07345	Ca3	-0.744	4.514
1622	MSTRG.19329	-	Ca7	1.255	4.530
1623	MSTRG.22053	-	scaffold1010	-1.617	4.553
1624	MSTRG.24255	Ca_27532	scaffold3934	-3.016	4.570
1625	MSTRG.8193	Ca_03727	Ca4	-1.707	4.587
1626	MSTRG.1344	Ca_02690	Ca1	-0.527	4.615

1627	MSTRG.15847	-	Ca6	-2.932	4.732
1628	MSTRG.4694	Ca_10219	Ca2	-0.149	4.742
1629	MSTRG.19739	Ca_11696	Ca7	0.172	4.748
1630	MSTRG.13602	-	Ca5	-1.272	4.801
1631	MSTRG.21448	-	Ca8	-3.008	4.860
1632	MSTRG.18702	-	Ca7	-2.974	4.862
1633	MSTRG.24479	-	scaffold450	-2.924	4.886
1634	MSTRG.10538	-	Ca4	-1.280	4.906
1635	MSTRG.9479	-	Ca4	-2.043	4.950
1636	MSTRG.9066	-	Ca4	-2.144	4.996
1637	MSTRG.2485	-	Ca1	-2.876	5.023
1638	MSTRG.24023	-	scaffold3254_2	-0.468	5.029
1639	MSTRG.2183	Ca_20633	Ca1	-0.466	5.038
1640	MSTRG.1907	-	Ca1	-0.993	5.089
1641	MSTRG.21094	Ca_02088	Ca8	2.659	5.094
1642	MSTRG.17854	-	Ca7	-0.997	5.111
1643	MSTRG.12874	Ca_01550	Ca5	-1.406	5.113
1644	MSTRG.4574	-	Ca2	-2.872	5.147
1645	MSTRG.564	-	Ca1	-2.635	5.155
1646	MSTRG.23483	-	scaffold223	-2.811	5.183
1647	MSTRG.4476	Ca_12515	Ca2	3.352	5.190
1648	MSTRG.23367	-	scaffold2033	-2.455	5.213
1649	MSTRG.3467	Ca_14653	Ca2	1.392	5.238
1650	MSTRG.7951	Ca_12092	Ca4	3.127	5.253
1651	MSTRG.4211	-	Ca2	-2.250	5.264
1652	MSTRG.2122	Ca_08869	Ca1	1.001	5.284
1653	MSTRG.21147	-	Ca8	-1.393	5.296
1654	MSTRG.19750	-	Ca7	-1.352	5.307
1655	MSTRG.2908	-	Ca1	-2.458	5.315
1656	MSTRG.7695	-	Ca4	-2.415	5.331
1657	MSTRG.8047	Ca_03865	Ca4	1.042	5.362
1658	MSTRG.5730	-	Ca3	-3.213	5.363
1659	MSTRG.13740	-	Ca5	-3.220	5.458
1660	MSTRG.25440	-	scaffold913	-2.429	5.464
1661	MSTRG.23735	-	scaffold2734	-0.114	5.475
1662	MSTRG.17231	Ca_18908	Ca6	-0.392	5.517
1663	MSTRG.3018	-	Ca1	-2.967	5.522

1664	MSTRG.15996	-	Ca6	-3.576	5.522
1665	MSTRG.11295	-	Ca5	0.096	5.525
1666	MSTRG.12131	-	Ca5	-2.057	5.529
1667	MSTRG.5358	-	Ca3	-2.760	5.558
1668	MSTRG.24158	-	scaffold350	-1.103	5.586
1669	MSTRG.9714	-	Ca4	-1.958	5.593
1670	MSTRG.19120	Ca_09889	Ca7	-1.141	5.615
1671	MSTRG.16624	-	Ca6	-2.901	5.650
1672	MSTRG.25441	-	scaffold913	-2.971	5.650
1673	MSTRG.9086	-	Ca4	-3.206	5.697
1674	MSTRG.20825	Ca_02358	Ca8	4.397	5.706
1675	MSTRG.2541	-	Ca1	-4.199	5.739
1676	MSTRG.24087	-	scaffold3397	-2.545	5.744
1677	MSTRG.24369	-	scaffold411	-3.934	5.749
1678	MSTRG.10547	-	Ca4	-3.638	5.764
1679	MSTRG.3936	Ca_22037	Ca2	-1.285	5.779
1680	MSTRG.6955	-	Ca3	-1.509	5.794
1681	MSTRG.8523	Ca_08338	Ca4	-1.649	5.821
1682	MSTRG.9330	-	Ca4	-2.726	5.897
1683	MSTRG.23319	-	scaffold1981	-2.664	5.916
1684	MSTRG.4373	-	Ca2	-1.856	5.929
1685	MSTRG.16467	Ca_15179	Ca6	-1.265	5.945
1686	MSTRG.23576	-	scaffold2378	-3.138	6.013
1687	MSTRG.7468	-	Ca3	-3.156	6.023
1688	MSTRG.13905	Ca_04210	Ca5	-1.682	6.030
1689	MSTRG.24549	-	scaffold4773	-4.454	6.051
1690	MSTRG.18234	-	Ca7	-0.559	6.062
1691	MSTRG.2549	Ca_26097	Ca1	-1.698	6.080
1692	MSTRG.24276	-	scaffold396	-1.729	6.149
1693	MSTRG.3434	Ca_14692	Ca2	-0.581	6.152
1694	MSTRG.24450	Ca_26260	scaffold435	-0.963	6.186
1695	MSTRG.24098	-	scaffold340	-2.511	6.214
1696	MSTRG.23048	-	scaffold1703	-2.563	6.232
1697	MSTRG.19824	-	Ca7	-4.370	6.242
1698	MSTRG.11546	-	Ca5	-3.773	6.258
1699	MSTRG.13692	Ca_03999	Ca5	-3.439	6.353
1700	MSTRG.3082	-	Ca2	-1.029	6.440

1701	MSTRG.9392	-	Ca4	0.221	6.453
1702	MSTRG.2487	-	Ca1	-2.920	6.500
1703	MSTRG.11482	Ca_17927	Ca5	-2.388	6.531
1704	MSTRG.22769	-	scaffold1382	-2.645	6.552
1705	MSTRG.8082	-	Ca4	-2.888	6.554
1706	MSTRG.15796	-	Ca6	-2.318	6.557
1707	MSTRG.17720	Ca_03349	Ca7	-1.665	6.563
1708	MSTRG.2970	-	Ca1	-2.402	6.575
1709	MSTRG.2506	Ca_25472	Ca1	-3.311	6.580
1710	MSTRG.16230	-	Ca6	-3.598	6.627
1711	MSTRG.2364	Ca_25066	Ca1	-0.152	6.640
1712	MSTRG.8813	Ca_04377	Ca4	-3.979	6.649
1713	MSTRG.20779	-	Ca8	-2.954	6.667
1714	MSTRG.24433	-	scaffold421_1	-1.749	6.669
1715	MSTRG.13818	-	Ca5	-0.640	6.692
1716	MSTRG.17532	-	Ca6	-4.324	6.720
1717	MSTRG.10167	-	Ca4	-0.639	6.777
1718	MSTRG.3779	Ca_18775	Ca2	-3.173	6.781
1719	MSTRG.25333	-	scaffold876	-1.722	6.816
1720	MSTRG.289	-	Ca1	-3.966	6.826
1721	MSTRG.17489	-	Ca6	-0.544	6.859
1722	MSTRG.17008	-	Ca6	-4.380	6.896
1723	MSTRG.3856	-	Ca2	-1.972	6.905
1724	MSTRG.24881	-	scaffold599	-1.660	6.944
1725	MSTRG.5708	Ca_19354	Ca3	1.482	6.953
1726	MSTRG.9333	Ca_05449	Ca4	-0.316	6.958
1727	MSTRG.6652	-	Ca3	-4.357	6.965
1728	MSTRG.2489	-	Ca1	-3.315	7.003
1729	MSTRG.5432	-	Ca3	-4.057	7.007
1730	MSTRG.15938	Ca_11245	Ca6	-2.182	7.010
1731	MSTRG.8561	-	Ca4	-0.032	7.023
1732	MSTRG.18685	-	Ca7	-2.921	7.027
1733	MSTRG.19482	Ca_19504	Ca7	-1.558	7.033
1734	MSTRG.24141	-	scaffold346_1	-3.002	7.034
1735	MSTRG.16665	-	Ca6	-3.918	7.071
1736	MSTRG.24654	-	scaffold513	-4.154	7.147
1737	MSTRG.17517	Ca_15380	Ca6	-3.162	7.203

1738	MSTRG.22272	-	scaffold1116	-3.444	7.243
1739	MSTRG.17373	Ca_17424	Ca6	0.947	7.321
1740	MSTRG.25077	-	scaffold720	-3.810	7.348
1741	MSTRG.15894	Ca_19857	Ca6	-2.475	7.348
1742	MSTRG.24045	Ca_28178	scaffold3337	-3.264	7.363
1743	MSTRG.7013	-	Ca3	-4.043	7.389
1744	MSTRG.6482	-	Ca3	-3.545	7.399
1745	MSTRG.6184	-	Ca3	-0.696	7.408
1746	MSTRG.21358	-	Ca8	-2.457	7.441
1747	MSTRG.3772	-	Ca2	-3.078	7.483
1748	MSTRG.22425	-	scaffold1231	-2.993	7.521
1749	MSTRG.23053	Ca_27772	scaffold1706	0.599	7.595
1750	MSTRG.19865	-	Ca7	-1.311	7.603
1751	MSTRG.19650	-	Ca7	-4.129	7.607
1752	MSTRG.15556	-	Ca6	0.867	7.651
1753	MSTRG.23793	-	scaffold284	-3.570	7.701
1754	MSTRG.23643	Ca_26665	scaffold2557	-2.981	7.762
1755	MSTRG.24044	-	scaffold3337	-4.268	7.813
1756	MSTRG.7635	-	Ca3	-2.319	7.828
1757	MSTRG.5298	-	Ca3	-3.846	7.839
1758	MSTRG.19215	-	Ca7	-0.816	7.851
1759	MSTRG.2368	-	Ca1	-1.286	7.862
1760	MSTRG.16268	-	Ca6	-1.542	7.867
1761	MSTRG.24885	Ca_25342	scaffold599	-1.254	7.905
1762	MSTRG.21452	-	Ca8	-2.585	7.982
1763	MSTRG.2476	Ca_21868	Ca1	0.680	8.088
1764	MSTRG.24462	Ca_25414	scaffold44	-3.495	8.115
1765	MSTRG.25191	Ca_27768	scaffold799	-3.437	8.187
1766	MSTRG.21450	-	Ca8	-2.860	8.252
1767	MSTRG.16572	-	Ca6	-3.198	8.252
1768	MSTRG.23300	-	scaffold198	-2.946	8.271
1769	MSTRG.15833	-	Ca6	-2.574	8.280
1770	MSTRG.2488	-	Ca1	-3.961	8.348
1771	MSTRG.24244	-	scaffold3817	-3.827	8.616
1772	MSTRG.25338	Ca_28083	scaffold877	0.516	8.647
1773	MSTRG.21451	-	Ca8	-3.559	8.686
1774	MSTRG.16979	-	Ca6	-3.588	8.755

1775	MSTRG.2434	Ca_24388	Ca1	-3.566	8.949
1776	MSTRG.4757	-	Ca2	-3.046	8.987
1777	MSTRG.2710	-	Ca1	-3.638	9.028
1778	MSTRG.21449	-	Ca8	-3.531	9.440
1779	MSTRG.1583	-	Ca1	0.637	10.953

Supplementary Table 10: PRR resistance genes in moderately PRR resistant genotype Yorker (Yor-C) differently expressed under control condition compared to PRR suceptible genotype Rupali

Serial Number	gene id_working	Reference gene_id	Chromosome	Average Expression	log2(fold_change)
1	MSTRG.1583	-	Ca1	-11.154	0.637
2	MSTRG.16458	Ca_15171	Ca6	-10.228	-3.339
3	MSTRG.16749	-	Ca6	-9.833	-5.005
4	MSTRG.6227	Ca_08265	Ca3	-9.479	-2.994
5	MSTRG.17326	-	Ca6	-9.431	-2.871
6	MSTRG.23053	Ca_27772	scaffold1706	-9.368	0.599
7	MSTRG.21788	-	Ca8	-9.178	-3.361
8	MSTRG.19215	-	Ca7	-9.127	-0.816
9	MSTRG.2368	-	Ca1	-8.530	-1.286
10	MSTRG.19962	-	Ca7	-8.505	-4.072
11	MSTRG.24276	-	scaffold396	-8.485	-1.729
12	MSTRG.24885	Ca_25342	scaffold599	-8.483	-1.254
13	MSTRG.8561	-	Ca4	-8.333	-0.032
14	MSTRG.9811	Ca_16572	Ca4	-8.156	-4.403
15	MSTRG.78	Ca_27990	C11107558	-8.141	-4.665
16	MSTRG.24368	-	scaffold411	-8.031	-3.194
17	MSTRG.2476	Ca_21868	Ca1	-8.003	0.680
18	MSTRG.25338	Ca_28083	scaffold877	-7.932	0.516
19	MSTRG.15556	-	Ca6	-7.867	0.867
20	MSTRG.20530	-	Ca7	-7.826	-3.661
21	MSTRG.17373	Ca_17424	Ca6	-7.787	0.947
22	MSTRG.24280	-	scaffold396	-7.633	-4.098
23	MSTRG.3082	-	Ca2	-7.617	-1.029
24	MSTRG.22514	-	scaffold1301_1	-7.501	-4.213
25	MSTRG.19865	-	Ca7	-7.486	-1.311
26	MSTRG.10167	-	Ca4	-7.412	-0.639
27	MSTRG.23835	-	scaffold290	-7.331	-1.481
28	MSTRG.16268	-	Ca6	-7.295	-1.542
29	MSTRG.3856	-	Ca2	-7.252	-1.972
30	MSTRG.22463	-	scaffold128	-7.237	-4.293
31	MSTRG.16134	Ca_11027	Ca6	-7.129	-2.471
32	MSTRG.14997	Ca_08561	Ca6	-7.026	-4.149
33	MSTRG.9560	-	Ca4	-7.016	-4.258
34	MSTRG.24201	-	scaffold3654	-6.959	-4.030
35	MSTRG.156	-	C11165890	-6.950	-2.650

36	MSTRG.1062	-	Ca1	-6.905	-4.378
37	MSTRG.14933	Ca_08624	Ca6	-6.892	4.107
38	MSTRG.1518	Ca_02522	Ca1	-6.787	3.990
39	MSTRG.4373	-	Ca2	-6.755	-1.856
40	MSTRG.24098	-	scaffold340	-6.731	-2.511
41	MSTRG.24281	-	scaffold396	-6.689	-4.288
42	MSTRG.22464	-	scaffold128	-6.650	-3.632
43	MSTRG.11482	Ca_17927	Ca5	-6.645	-2.388
44	MSTRG.7695	-	Ca4	-6.587	-2.415
45	MSTRG.6184	-	Ca3	-6.577	-0.696
46	MSTRG.627	Ca_00424	Ca1	-6.465	3.485
47	MSTRG.13905	Ca_04210	Ca5	-6.443	-1.682
48	MSTRG.24830	-	scaffold575	-6.428	-4.061
49	MSTRG.564	-	Ca1	-6.282	-2.635
50	MSTRG.24251	Ca_27766	scaffold387	-6.259	-2.473
51	MSTRG.19827	-	Ca7	-6.257	0.125
52	MSTRG.9714	-	Ca4	-6.180	-1.958
53	MSTRG.2936	Ca_21552	Ca1	-6.172	-1.451
54	MSTRG.22051	-	scaffold1010	-6.076	-3.633
55	MSTRG.5773	Ca_09449	Ca3	-5.759	-1.503
56	MSTRG.11295	-	Ca5	-5.743	0.096
57	MSTRG.19120	Ca_09889	Ca7	-5.731	-1.141
58	MSTRG.5151	-	Ca3	-5.722	-3.521
59	MSTRG.23262	-	scaffold193	-5.669	-2.188
60	MSTRG.8047	Ca_03865	Ca4	-5.646	1.042
61	MSTRG.19750	-	Ca7	-5.594	-1.352
62	MSTRG.24158	-	scaffold350	-5.587	-1.103
63	MSTRG.19482	Ca_19504	Ca7	-5.510	-1.558
64	MSTRG.14951	Ca_08607	Ca6	-5.475	2.233
65	MSTRG.18234	-	Ca7	-5.454	-0.559
66	MSTRG.19329	-	Ca7	-5.415	1.255
67	MSTRG.19828	Ca_10080	Ca7	-5.398	-1.065
68	MSTRG.3434	Ca_14692	Ca2	-5.396	-0.581
69	MSTRG.4476	Ca_12515	Ca2	-5.347	3.352
70	MSTRG.5099	-	Ca3	-5.332	-1.999
71	MSTRG.22425	-	scaffold1231	-5.331	-2.993
72	MSTRG.9167	-	Ca4	-5.263	-1.511

73	MSTRG.22450	-	scaffold128	-5.247	-3.572
74	MSTRG.3412	-	Ca2	-5.234	-2.924
75	MSTRG.17086	Ca_13450	Ca6	-5.135	-1.496
76	MSTRG.20501	-	Ca7	-5.116	0.073
77	MSTRG.16272	Ca_14582	Ca6	-5.097	2.129
78	MSTRG.24069	Ca_21291	scaffold336	-5.085	1.218
79	MSTRG.25031	-	scaffold682	-5.059	-3.410
80	MSTRG.5460	Ca_22692	Ca3	-4.983	-0.708
81	MSTRG.19453	-	Ca7	-4.918	-1.782
82	MSTRG.13992	Ca_13254	Ca6	-4.897	0.207
83	MSTRG.25424	-	scaffold9	-4.863	-0.960
84	MSTRG.6963	-	Ca3	-4.812	-1.764
85	MSTRG.8930	Ca_04486	Ca4	-4.715	1.244
86	MSTRG.14999	Ca_08560	Ca6	-4.706	2.099
87	MSTRG.13197	Ca_07560	Ca5	-4.675	1.958
88	MSTRG.21832	Ca_12999	Ca8	-4.605	0.180
89	MSTRG.24450	Ca_26260	scaffold435	-4.479	-0.963
90	MSTRG.17085	Ca_13451	Ca6	-4.470	-0.272
91	MSTRG.14491	Ca_05777	Ca6	-4.316	1.198
92	MSTRG.24087	-	scaffold3397	-4.299	-2.545
93	MSTRG.20875	Ca_02306	Ca8	-4.292	0.993
94	MSTRG.24403	-	scaffold420	-4.259	-3.412
95	MSTRG.14873	Ca_16734	Ca6	-4.253	0.657
96	MSTRG.24622	-	scaffold4978	-4.207	-1.076
97	MSTRG.2627	-	Ca1	-4.202	-0.385
98	MSTRG.12271	-	Ca5	-4.167	5.779
99	MSTRG.12874	Ca_01550	Ca5	-4.126	-1.406
100	MSTRG.23754	-	scaffold2763	-4.089	0.877
101	MSTRG.12885	-	Ca5	-4.037	0.929
102	MSTRG.3032	Ca_12865	Ca1	-4.005	3.091
103	MSTRG.16424	Ca_16482	Ca6	-3.996	-0.449
104	MSTRG.16397	Ca_16454	Ca6	-3.995	-1.388
105	MSTRG.11070	-	Ca5	-3.933	-2.213
106	MSTRG.12272	Ca_04788	Ca5	-3.898	9.065
107	MSTRG.7714	Ca_07686	Ca4	-3.891	1.129
108	MSTRG.7951	Ca_12092	Ca4	-3.881	3.127
109	MSTRG.18796	Ca_09372	Ca7	-3.879	0.827

110	MSTRG.6615	-	Ca3	-3.865	0.754
111	MSTRG.1888	Ca_06938	Ca1	-3.848	-1.487
112	MSTRG.23879	-	scaffold298	-3.820	-0.872
113	MSTRG.22871	Ca_24096	scaffold1504	-3.797	-1.792
114	MSTRG.22268	Ca_27287	scaffold1114	-3.792	-1.656
115	MSTRG.6962	-	Ca3	-3.790	0.016
116	MSTRG.8168	-	Ca4	-3.781	0.389
117	MSTRG.7369	Ca_01119	Ca3	-3.772	0.576
118	MSTRG.2495	Ca_19441	Ca1	-3.753	1.593
119	MSTRG.16533	Ca_24447	Ca6	-3.731	2.601
120	MSTRG.22449	-	scaffold128	-3.691	-0.862
121	MSTRG.14866	Ca_16738	Ca6	-3.633	6.726
122	MSTRG.2581	Ca_21824	Ca1	-3.618	1.566
123	MSTRG.23390	Ca_25493	scaffold205	-3.584	-0.461
124	MSTRG.19586	Ca_26609	Ca7	-3.562	1.699
125	MSTRG.25345	Ca_22178	scaffold88	-3.529	4.758
126	MSTRG.2935	-	Ca1	-3.499	1.559
127	MSTRG.20817	Ca_02363	Ca8	-3.488	-0.076
128	MSTRG.7773	Ca_07743	Ca4	-3.486	1.179
129	MSTRG.15374	Ca_05267	Ca6	-3.457	1.225
130	MSTRG.7177	Ca_00933	Ca3	-3.442	-0.989
131	MSTRG.12270	-	Ca5	-3.435	1.809
132	MSTRG.7832	Ca_07799	Ca4	-3.404	2.662
133	MSTRG.10760	Ca_18369	Ca4	-3.361	4.745
134	MSTRG.10284	-	Ca4	-3.350	3.264
135	MSTRG.18484	Ca_13222	Ca7	-3.341	1.887
136	MSTRG.9044	-	Ca4	-3.312	-0.407
137	MSTRG.13018	Ca_01402	Ca5	-3.283	4.003
138	MSTRG.5376	-	Ca3	-3.263	0.506
139	MSTRG.24620	Ca_26761	scaffold495	-3.239	0.994
140	MSTRG.23578	-	scaffold2373	-3.196	0.218
141	MSTRG.19218	Ca_15861	Ca7	-3.161	4.348
142	MSTRG.442	Ca_00235	Ca1	-3.147	-0.508
143	MSTRG.1002	Ca_07992	Ca1	-3.145	-0.233
144	MSTRG.23901	Ca_26659	scaffold303	-3.137	5.033
145	MSTRG.4395	Ca_14332	Ca2	-3.136	0.604
146	MSTRG.11819	-	Ca5	-3.121	-0.804

147	MSTRG.7904	Ca_07872	Ca4	-3.120	-1.608
148	MSTRG.20002	Ca_20992	Ca7	-3.066	6.333
149	MSTRG.20566	Ca_11914	Ca8	-3.019	-0.386
150	MSTRG.22390	Ca_22967	scaffold12	-3.000	1.901
151	MSTRG.2504	-	Ca1	-2.998	-2.240
152	MSTRG.13954	Ca_04257	Ca5	-2.990	0.026
153	MSTRG.1025	Ca_08014	Ca1	-2.982	-0.150
154	MSTRG.24267	Ca_24514	scaffold395	-2.981	-2.945
155	MSTRG.11817	-	Ca5	-2.973	-0.955
156	MSTRG.5881	Ca_06279	Ca3	-2.972	4.397
157	MSTRG.24088	-	scaffold3397	-2.971	-0.231
158	MSTRG.10093	-	Ca4	-2.969	0.942
159	MSTRG.1540	-	Ca1	-2.955	2.723
160	MSTRG.19607	Ca_18941	Ca7	-2.908	1.407
161	MSTRG.24038	Ca_25759	scaffold332	-2.897	0.557
162	MSTRG.8979	Ca_04534	Ca4	-2.871	3.500
163	MSTRG.3737	Ca_17575	Ca2	-2.868	2.637
164	MSTRG.22582	Ca_22584	scaffold134	-2.867	3.530
165	MSTRG.4471	-	Ca2	-2.863	-1.110
166	MSTRG.8914	Ca_04473	Ca4	-2.861	2.570
167	MSTRG.11563	-	Ca5	-2.850	0.301
168	MSTRG.22560	Ca_19775	scaffold1324	-2.828	0.884
169	MSTRG.14961	Ca_08595	Ca6	-2.819	-0.412
170	MSTRG.16455	Ca_15167	Ca6	-2.810	4.873
171	MSTRG.10197	Ca_15126	Ca4	-2.809	4.022
172	MSTRG.8903	Ca_04466	Ca4	-2.803	2.753
173	MSTRG.7726	Ca_07697	Ca4	-2.801	5.158
174	MSTRG.24282	Ca_23555	scaffold396	-2.791	2.151
175	MSTRG.21090	Ca_02094	Ca8	-2.786	-0.898
176	MSTRG.12022	-	Ca5	-2.765	0.639
177	MSTRG.3305	Ca_10519	Ca2	-2.748	0.269
178	MSTRG.15229	-	Ca6	-2.661	-0.765
179	MSTRG.7284	-	Ca3	-2.660	-0.455
180	MSTRG.19390	Ca_14490	Ca7	-2.644	3.462
181	MSTRG.5878	Ca_20406	Ca3	-2.642	1.623
182	MSTRG.10685	Ca_09167	Ca4	-2.618	0.377
183	MSTRG.10239	Ca_13140	Ca4	-2.617	-0.911

184	MSTRG.9664	Ca_19059	Ca4	-2.603	1.693
185	MSTRG.17331	Ca_19039	Ca6	-2.593	-0.743
186	MSTRG.11562	-	Ca5	-2.592	0.100
187	MSTRG.8293	Ca_03626	Ca4	-2.579	1.998
188	MSTRG.14004	Ca_13265	Ca6	-2.574	2.504
189	MSTRG.13037	Ca_01382	Ca5	-2.562	-0.666
190	MSTRG.23572	Ca_27073	scaffold2373	-2.555	3.577
191	MSTRG.14734	Ca_09610	Ca6	-2.553	2.804
192	MSTRG.2559	Ca_21686	Ca1	-2.550	1.140
193	MSTRG.8553	-	Ca4	-2.536	-0.202
194	MSTRG.19276	Ca_12305	Ca7	-2.534	-0.491
195	MSTRG.18374	Ca_06660	Ca7	-2.533	2.197
196	MSTRG.19076	Ca_09947	Ca7	-2.532	2.739
197	MSTRG.10351	Ca_14921	Ca4	-2.530	4.652
198	MSTRG.13063	Ca_07423	Ca5	-2.523	3.068
199	MSTRG.22312	Ca_22343	scaffold1151	-2.519	-0.221
200	MSTRG.11584	-	Ca5	-2.519	3.122
201	MSTRG.22493	-	scaffold1301_1	-2.518	4.306
202	MSTRG.2720	Ca_23106	Ca1	-2.506	5.362
203	MSTRG.21787	Ca_13034	Ca8	-2.499	2.521
204	MSTRG.6331	Ca_08157	Ca3	-2.499	-0.603
205	MSTRG.16281	Ca_14577	Ca6	-2.495	0.526
206	MSTRG.20915	Ca_02263	Ca8	-2.487	3.827
207	MSTRG.3337	Ca_10490	Ca2	-2.475	0.496
208	MSTRG.7747	Ca_07719	Ca4	-2.472	0.396
209	MSTRG.21157	Ca_02024	Ca8	-2.469	1.614
210	MSTRG.20452	Ca_15742	Ca7	-2.456	8.086
211	MSTRG.18387	Ca_06650	Ca7	-2.449	0.002
212	MSTRG.6568	Ca_07306	Ca3	-2.445	1.860
213	MSTRG.6678	Ca_12188	Ca3	-2.436	0.848
214	MSTRG.4947	Ca_09753	Ca2	-2.430	1.819
215	MSTRG.2702	-	Ca1	-2.416	0.599
216	MSTRG.21244	Ca_01941	Ca8	-2.416	1.239
217	MSTRG.5317	Ca_25280	Ca3	-2.396	1.306
218	MSTRG.8547	Ca_08357	Ca4	-2.391	0.346
219	MSTRG.20010	Ca_20981	Ca7	-2.380	-0.284
220	MSTRG.15026	Ca_08531	Ca6	-2.379	6.201

221	MSTRG.23261	-	scaffold193	-2.373	-1.602
222	MSTRG.11501	Ca_17948	Ca5	-2.372	4.634
223	MSTRG.11583	-	Ca5	-2.369	1.874
224	MSTRG.11831	Ca_09038	Ca5	-2.363	3.697
225	MSTRG.9383	Ca_05399	Ca4	-2.363	1.595
226	MSTRG.6945	Ca_00707	Ca3	-2.347	5.429
227	MSTRG.15228	Ca_05124	Ca6	-2.344	-0.161
228	MSTRG.7697	Ca_07667	Ca4	-2.340	0.260
229	MSTRG.5203	Ca_20661	Ca3	-2.333	4.325
230	MSTRG.3338	Ca_10489	Ca2	-2.332	0.008
231	MSTRG.2713	-	Ca1	-2.328	-1.934
232	MSTRG.18868	Ca_09299	Ca7	-2.328	4.390
233	MSTRG.15097	-	Ca6	-2.327	0.511
234	MSTRG.10111	Ca_14855	Ca4	-2.327	2.898
235	MSTRG.18944	Ca_16018	Ca7	-2.324	7.360
236	MSTRG.25312	-	scaffold873	-2.317	-0.427
237	MSTRG.24304	Ca_22300	scaffold398	-2.308	-1.287
238	MSTRG.18230	-	Ca7	-2.306	-0.091
239	MSTRG.7617	Ca_01339	Ca3	-2.304	2.918
240	MSTRG.7142	Ca_00898	Ca3	-2.300	0.642
241	MSTRG.17813	Ca_03276	Ca7	-2.296	1.850
242	MSTRG.14170	Ca_10359	Ca6	-2.292	2.559
243	MSTRG.5913	Ca_06245	Ca3	-2.289	3.914
244	MSTRG.1937	Ca_06892	Ca1	-2.285	5.754
245	MSTRG.16948	Ca_17712	Ca6	-2.281	1.937
246	MSTRG.23831	-	scaffold287	-2.280	-1.647
247	MSTRG.12900	Ca_01525	Ca5	-2.279	1.062
248	MSTRG.5709	Ca_09381	Ca3	-2.260	4.840
249	MSTRG.7580	Ca_01312	Ca3	-2.257	3.900
250	MSTRG.14761	Ca_09586	Ca6	-2.255	0.904
251	MSTRG.15517	Ca_06307	Ca6	-2.244	-0.688
252	MSTRG.20743	-	Ca8	-2.232	2.078
253	MSTRG.16597	Ca_15786	Ca6	-2.220	-0.552
254	MSTRG.5638	Ca_19627	Ca3	-2.220	0.639
255	MSTRG.22295	Ca_26846	scaffold1135	-2.212	3.503
256	MSTRG.16373	-	Ca6	-2.212	4.851
257	MSTRG.25016	Ca_20165	scaffold674	-2.212	4.303

258	MSTRG.11181	Ca_21565	Ca5	-2.209	6.429
259	MSTRG.532	Ca_00328	Ca1	-2.197	2.885
260	MSTRG.9856	Ca_20443	Ca4	-2.193	4.838
261	MSTRG.20407	Ca_21371	Ca7	-2.192	3.737
262	MSTRG.22383	-	scaffold1197	-2.185	0.015
263	MSTRG.947	Ca_07943	Ca1	-2.177	6.705
264	MSTRG.18637	Ca_17322	Ca7	-2.174	0.805
265	MSTRG.4475	-	Ca2	-2.172	3.361
266	MSTRG.17900	Ca_03201	Ca7	-2.170	2.526
267	MSTRG.6232	Ca_08259	Ca3	-2.166	5.447
268	MSTRG.1990	Ca_14789	Ca1	-2.151	5.418
269	MSTRG.17372	-	Ca6	-2.144	0.827
270	MSTRG.21916	Ca_17883	Ca8	-2.136	1.166
271	MSTRG.7278	Ca_01026	Ca3	-2.131	2.230
272	MSTRG.406	Ca_00201	Ca1	-2.129	5.665
273	MSTRG.22667	-	scaffold1348_1	-2.126	1.976
274	MSTRG.18243	Ca_06773	Ca7	-2.125	0.813
275	MSTRG.12971	Ca_01449	Ca5	-2.124	5.157
276	MSTRG.8940	Ca_04497	Ca4	-2.121	1.573
277	MSTRG.10225	Ca_15089	Ca4	-2.116	1.961
278	MSTRG.15475	Ca_19667	Ca6	-2.111	3.291
279	MSTRG.10347	Ca_14927	Ca4	-2.094	4.519
280	MSTRG.20368	Ca_20205	Ca7	-2.094	0.069
281	MSTRG.6589	Ca_07325	Ca3	-2.093	3.058
282	MSTRG.13860	Ca_04164	Ca5	-2.091	5.019
283	MSTRG.10959	-	Ca4	-2.086	5.386
284	MSTRG.17126	Ca_19170	Ca6	-2.081	-0.644
285	MSTRG.13892	Ca_04193	Ca5	-2.079	4.159
286	MSTRG.12678	Ca_01742	Ca5	-2.077	0.024
287	MSTRG.9078	Ca_04628	Ca4	-2.073	3.428
288	MSTRG.23186	-	scaffold1844	-2.070	4.651
289	MSTRG.22845	Ca_26807	scaffold1467	-2.061	3.095
290	MSTRG.4941	Ca_09747	Ca2	-2.060	5.236
291	MSTRG.5291	-	Ca3	-2.060	-0.780
292	MSTRG.6919	-	Ca3	-2.053	4.081
293	MSTRG.19314	Ca_12345	Ca7	-2.052	3.791
294	MSTRG.25496	Ca_25673	scaffold924	-2.043	1.227

295	MSTRG.1214	Ca_02835	Ca1	-2.042	1.472
296	MSTRG.22691	-	scaffold1348_1	-2.038	4.451
297	MSTRG.9363	Ca_05419	Ca4	-2.035	4.604
298	MSTRG.1872	Ca_06955	Ca1	-2.030	3.664
299	MSTRG.3005	Ca_12890	Ca1	-2.028	2.438
300	MSTRG.8948	Ca_04504	Ca4	-2.019	-0.427
301	MSTRG.15312	Ca_05200	Ca6	-2.015	1.267
302	MSTRG.6556	Ca_07296	Ca3	-2.015	2.976
303	MSTRG.24633	Ca_25368	scaffold498	-2.007	3.083
304	MSTRG.4557	Ca_12430	Ca2	-2.003	5.336
305	MSTRG.18220	Ca_06793	Ca7	-1.988	1.659
306	MSTRG.17128	Ca_19171	Ca6	-1.984	5.624
307	MSTRG.3067	Ca_16983	Ca2	-1.982	3.024
308	MSTRG.11714	-	Ca5	-1.962	3.430
309	MSTRG.13700	Ca_04005	Ca5	-1.960	3.626
310	MSTRG.22706	-	scaffold1348_1	-1.958	0.431
311	MSTRG.21270	Ca_23578	Ca8	-1.957	4.818
312	MSTRG.15490	Ca_06282	Ca6	-1.957	3.171
313	MSTRG.487	Ca_00282	Ca1	-1.956	0.519
314	MSTRG.22904	Ca_23862	scaffold1545	-1.953	3.254
315	MSTRG.17564	Ca_15425	Ca6	-1.952	6.726
316	MSTRG.10650	Ca_09136	Ca4	-1.950	3.397
317	MSTRG.18219	Ca_06794	Ca7	-1.946	3.428
318	MSTRG.7561	Ca_01291	Ca3	-1.944	5.711
319	MSTRG.12398	Ca_04904	Ca5	-1.942	-0.317
320	MSTRG.10674	Ca_09155	Ca4	-1.937	2.649
321	MSTRG.5653	Ca_19640	Ca3	-1.937	3.610
322	MSTRG.4931	Ca_09738	Ca2	-1.936	0.309
323	MSTRG.11919	-	Ca5	-1.931	1.322
324	MSTRG.21643	Ca_19746	Ca8	-1.927	4.605
325	MSTRG.12898	Ca_01527	Ca5	-1.924	1.808
326	MSTRG.18641	Ca_17318	Ca7	-1.918	0.790
327	MSTRG.3948	-	Ca2	-1.917	2.586
328	MSTRG.4499	Ca_12491	Ca2	-1.916	0.927
329	MSTRG.325	-	Ca1	-1.903	0.471
330	MSTRG.9213	Ca_05575	Ca4	-1.900	2.124
331	MSTRG.2122	Ca_08869	Ca1	-1.899	1.001

332	MSTRG.15557	Ca_06344	Ca6	-1.895	5.786
333	MSTRG.12579	Ca_01862	Ca5	-1.892	2.369
334	MSTRG.19980	-	Ca7	-1.891	-1.764
335	MSTRG.17280	Ca_21198	Ca6	-1.890	0.953
336	MSTRG.19037	-	Ca7	-1.890	-0.061
337	MSTRG.11607	-	Ca5	-1.886	-2.040
338	MSTRG.24628	Ca_25364	scaffold498	-1.881	4.113
339	MSTRG.960	Ca_07955	Ca1	-1.881	2.753
340	MSTRG.25253	Ca_22426	scaffold845	-1.878	1.622
341	MSTRG.16302	Ca_26118	Ca6	-1.875	5.111
342	MSTRG.4215	Ca_14303	Ca2	-1.855	-0.187
343	MSTRG.7193	-	Ca3	-1.854	2.294
344	MSTRG.13697	Ca_04002	Ca5	-1.846	2.843
345	MSTRG.17765	-	Ca7	-1.844	5.801
346	MSTRG.6656	Ca_07391	Ca3	-1.843	0.550
347	MSTRG.16588	Ca_15803	Ca6	-1.842	1.317
348	MSTRG.22243	-	scaffold109_1	-1.842	1.619
349	MSTRG.16663	Ca_19793	Ca6	-1.834	6.283
350	MSTRG.10396	Ca_14874	Ca4	-1.834	3.070
351	MSTRG.24355	Ca_27487	scaffold4057	-1.832	1.693
352	MSTRG.18011	Ca_03094	Ca7	-1.828	5.328
353	MSTRG.1670	Ca_14134	Ca1	-1.826	6.633
354	MSTRG.16961	Ca_23446	Ca6	-1.825	6.104
355	MSTRG.5231	-	Ca3	-1.823	1.135
356	MSTRG.3874	-	Ca2	-1.815	2.179
357	MSTRG.19377	-	Ca7	-1.814	0.327
358	MSTRG.9384	Ca_05398	Ca4	-1.811	4.111
359	MSTRG.346	Ca_00144	Ca1	-1.810	2.336
360	MSTRG.25418	-	scaffold895	-1.809	2.171
361	MSTRG.21773	-	Ca8	-1.806	-0.993
362	MSTRG.14700	Ca_09644	Ca6	-1.805	0.628
363	MSTRG.22578	-	scaffold134	-1.804	1.256
364	MSTRG.24469	Ca_26058	scaffold4452	-1.803	2.926
365	MSTRG.12761	Ca_01661	Ca5	-1.802	5.156
366	MSTRG.18240	Ca_06777	Ca7	-1.801	1.531
367	MSTRG.22668	-	scaffold1348_1	-1.801	0.867
368	MSTRG.22068	-	scaffold10260	-1.789	-0.451

369	MSTRG.22455	Ca_21437	scaffold128	-1.786	3.811
370	MSTRG.6872	Ca_12034	Ca3	-1.785	5.844
371	MSTRG.21791	Ca_13033	Ca8	-1.780	6.003
372	MSTRG.24182	Ca_25858	scaffold36	-1.776	4.409
373	MSTRG.13693	Ca_03998	Ca5	-1.776	2.630
374	MSTRG.6280	Ca_08212	Ca3	-1.775	8.325
375	MSTRG.16803	Ca_23252	Ca6	-1.773	3.349
376	MSTRG.23063	Ca_25721	scaffold1710	-1.773	1.313
377	MSTRG.15008	Ca_08546	Ca6	-1.771	7.575
378	MSTRG.11033	Ca_18188	Ca5	-1.769	0.848
379	MSTRG.13708	Ca_04013	Ca5	-1.766	3.343
380	MSTRG.13357	Ca_11390	Ca5	-1.762	0.051
381	MSTRG.10191	Ca_15134	Ca4	-1.753	-0.696
382	MSTRG.8929	Ca_04485	Ca4	-1.749	1.647
383	MSTRG.14576	-	Ca6	-1.747	-0.231
384	MSTRG.1578	Ca_02469	Ca1	-1.745	4.008
385	MSTRG.6957	Ca_00719	Ca3	-1.745	3.493
386	MSTRG.25103	-	scaffold731	-1.743	-0.610
387	MSTRG.16174	Ca_16682	Ca6	-1.741	4.622
388	MSTRG.16133	Ca_11028	Ca6	-1.736	0.161
389	MSTRG.22195	-	scaffold1067	-1.733	-0.275
390	MSTRG.4031	Ca_23768	Ca2	-1.732	0.490
391	MSTRG.1985	-	Ca1	-1.727	-0.019
392	MSTRG.10811	Ca_19262	Ca4	-1.709	1.006
393	MSTRG.9149	Ca_05633	Ca4	-1.708	1.626
394	MSTRG.9836	Ca_25308	Ca4	-1.707	2.668
395	MSTRG.17156	Ca_17525	Ca6	-1.701	1.991
396	MSTRG.2092	Ca_17365	Ca1	-1.701	6.378
397	MSTRG.8963	Ca_04518	Ca4	-1.698	2.476
398	MSTRG.909	Ca_07904	Ca1	-1.693	6.331
399	MSTRG.25252	Ca_22425	scaffold845	-1.692	1.952
400	MSTRG.4461	Ca_16084	Ca2	-1.685	0.313
401	MSTRG.1658	Ca_14123	Ca1	-1.685	5.124
402	MSTRG.4261	Ca_17277	Ca2	-1.676	0.565
403	MSTRG.2966	Ca_12936	Ca1	-1.674	4.006
404	MSTRG.12806	Ca_01616	Ca5	-1.673	6.773
405	MSTRG.1516	Ca_02523	Ca1	-1.671	5.781

406	MSTRG.17998	Ca_03107	Ca7	-1.670	4.357
407	MSTRG.12730	Ca_01693	Ca5	-1.667	2.606
408	MSTRG.9529	Ca_13994	Ca4	-1.667	2.413
409	MSTRG.18249	Ca_06767	Ca7	-1.666	0.451
410	MSTRG.6176	Ca_23888	Ca3	-1.666	5.067
411	MSTRG.2454	-	Ca1	-1.664	1.995
412	MSTRG.11866	Ca_08997	Ca5	-1.662	6.650
413	MSTRG.3590	Ca_18136	Ca2	-1.658	1.292
414	MSTRG.6021	Ca_06128	Ca3	-1.652	6.509
415	MSTRG.12042	Ca_13375	Ca5	-1.649	3.405
416	MSTRG.19392	Ca_14493	Ca7	-1.646	6.143
417	MSTRG.14858	Ca_16748	Ca6	-1.638	1.659
418	MSTRG.2677	Ca_18448	Ca1	-1.637	-0.289
419	MSTRG.25244	Ca_22412	scaffold845	-1.633	0.835
420	MSTRG.22550	Ca_19763	scaffold1324	-1.628	4.009
421	MSTRG.9128	Ca_05651	Ca4	-1.628	3.489
422	MSTRG.9242	Ca_05547	Ca4	-1.627	2.428
423	MSTRG.3583	Ca_18126	Ca2	-1.620	2.151
424	MSTRG.19779	Ca_10131	Ca7	-1.608	6.201
425	MSTRG.24723	Ca_23286	scaffold537	-1.608	5.549
426	MSTRG.18066	Ca_03041	Ca7	-1.606	2.987
427	MSTRG.575	Ca_00369	Ca1	-1.605	4.997
428	MSTRG.23096	Ca_21708	scaffold174	-1.602	3.236
429	MSTRG.18069	Ca_03036	Ca7	-1.601	3.321
430	MSTRG.4608	Ca_17816	Ca2	-1.600	1.256
431	MSTRG.4797	Ca_15263	Ca2	-1.597	2.447
432	MSTRG.14941	Ca_08618	Ca6	-1.596	0.632
433	MSTRG.14564	Ca_05699	Ca6	-1.594	5.723
434	MSTRG.15849	Ca_16332	Ca6	-1.594	1.176
435	MSTRG.1108	Ca_02939	Ca1	-1.592	3.550
436	MSTRG.6283	Ca_08210	Ca3	-1.590	3.369
437	MSTRG.13202	Ca_07563	Ca5	-1.590	2.919
438	MSTRG.1949	Ca_06883	Ca1	-1.585	0.928
439	MSTRG.23876	Ca_20553	scaffold296	-1.584	3.497
440	MSTRG.17492	Ca_13630	Ca6	-1.584	7.719
441	MSTRG.13842	Ca_04144	Ca5	-1.583	0.336
442	MSTRG.17496	-	Ca6	-1.583	8.959

443	MSTRG.11460	Ca_26864	Ca5	-1.582	2.901
444	MSTRG.7563	Ca_01292	Ca3	-1.580	3.693
445	MSTRG.19274	Ca_12303	Ca7	-1.577	4.074
446	MSTRG.3570	Ca_18112	Ca2	-1.577	5.567
447	MSTRG.13220	Ca_07584	Ca5	-1.576	1.636
448	MSTRG.19243	Ca_15837	Ca7	-1.573	0.660
449	MSTRG.19043	Ca_09975	Ca7	-1.569	2.733
450	MSTRG.15017	Ca_08538	Ca6	-1.569	4.459
451	MSTRG.14843	Ca_16761	Ca6	-1.568	3.688
452	MSTRG.5785	Ca_09462	Ca3	-1.567	7.880
453	MSTRG.20461	Ca_15745	Ca7	-1.566	6.045
454	MSTRG.14581	Ca_05678	Ca6	-1.565	3.370
455	MSTRG.9778	Ca_14408	Ca4	-1.563	0.868
456	MSTRG.3402	Ca_21097	Ca2	-1.563	4.299
457	MSTRG.6913	Ca_20870	Ca3	-1.561	3.061
458	MSTRG.8350	Ca_03572	Ca4	-1.558	4.672
459	MSTRG.1006	Ca_07994	Ca1	-1.555	4.406
460	MSTRG.2755	-	Ca1	-1.549	2.820
461	MSTRG.21830	Ca_13001	Ca8	-1.543	4.071
462	MSTRG.7257	Ca_01005	Ca3	-1.541	5.832
463	MSTRG.10925	Ca_10769	Ca4	-1.540	5.602
464	MSTRG.18973	Ca_16048	Ca7	-1.538	3.626
465	MSTRG.2394	Ca_18504	Ca1	-1.537	5.545
466	MSTRG.16354	Ca_17460	Ca6	-1.535	1.959
467	MSTRG.7828	-	Ca4	-1.534	0.529
468	MSTRG.8761	Ca_04334	Ca4	-1.533	3.363
469	MSTRG.21221	Ca_01964	Ca8	-1.532	6.324
470	MSTRG.617	Ca_00412	Ca1	-1.530	5.697
471	MSTRG.22583	-	scaffold134	-1.526	0.376
472	MSTRG.7816	Ca_07784	Ca4	-1.525	5.958
473	MSTRG.1267	Ca_02780	Ca1	-1.521	0.622
474	MSTRG.18838	Ca_09327	Ca7	-1.521	0.988
475	MSTRG.23575	-	scaffold2373	-1.520	5.581
476	MSTRG.11960	Ca_08894	Ca5	-1.513	3.956
477	MSTRG.1075	Ca_08071	Ca1	-1.513	2.526
478	MSTRG.6691	Ca_12198	Ca3	-1.511	2.728
479	MSTRG.15001	Ca_08555	Ca6	-1.508	0.893

480	MSTRG.12434	Ca_04942	Ca5	-1.506	8.186
481	MSTRG.6874	Ca_12036	Ca3	-1.505	6.507
482	MSTRG.9928	Ca_14166	Ca4	-1.504	5.493
483	MSTRG.5550	Ca_18263	Ca3	-1.504	2.331
484	MSTRG.24546	-	scaffold477	-1.504	1.247
485	MSTRG.13436	Ca_11312	Ca5	-1.503	3.752
486	MSTRG.9511	Ca_21607	Ca4	-1.501	3.053
487	MSTRG.15292	-	Ca6	-1.501	-0.386
488	MSTRG.4235	Ca_17248	Ca2	-1.500	7.959
489	MSTRG.1994	Ca_14786	Ca1	-1.497	4.141
490	MSTRG.19598	Ca_18931	Ca7	-1.497	2.456
491	MSTRG.7326	-	Ca3	-1.496	5.271
492	MSTRG.21251	Ca_01935	Ca8	-1.492	3.612
493	MSTRG.20608	Ca_11877	Ca8	-1.489	6.511
494	MSTRG.7839	Ca_07807	Ca4	-1.486	4.523
495	MSTRG.4220	Ca_14307	Ca2	-1.485	2.909
496	MSTRG.15344	Ca_05236	Ca6	-1.484	6.252
497	MSTRG.18141	Ca_02961	Ca7	-1.484	0.958
498	MSTRG.9031	Ca_04586	Ca4	-1.483	1.626
499	MSTRG.18531	Ca_13173	Ca7	-1.481	3.967
500	MSTRG.16817	Ca_24868	Ca6	-1.479	5.535
501	MSTRG.18351	Ca_06683	Ca7	-1.478	3.601
502	MSTRG.17389	-	Ca6	-1.478	2.041
503	MSTRG.4952	-	Ca2	-1.476	1.041
504	MSTRG.10104	Ca_14861	Ca4	-1.475	2.331
505	MSTRG.253	Ca_00056	Ca1	-1.475	5.307
506	MSTRG.9214	Ca_05574	Ca4	-1.474	5.819
507	MSTRG.6703	-	Ca3	-1.468	-0.239
508	MSTRG.19244	Ca_15838	Ca7	-1.465	4.085
509	MSTRG.22652	-	scaffold1348_1	-1.465	5.388
510	MSTRG.1589	Ca_02451	Ca1	-1.464	5.862
511	MSTRG.17382	Ca_17429	Ca6	-1.464	4.226
512	MSTRG.5238	Ca_25770	Ca3	-1.462	5.598
513	MSTRG.6861	Ca_12021	Ca3	-1.461	3.609
514	MSTRG.22919	Ca_21064	scaffold157	-1.455	6.635
515	MSTRG.20845	Ca_02336	Ca8	-1.453	2.276
516	MSTRG.24192	Ca_24991	scaffold362	-1.448	2.927

517	MSTRG.22959	Ca_20809	scaffold1580	-1.447	1.754
518	MSTRG.12673	Ca_01749	Ca5	-1.446	5.024
519	MSTRG.16911	Ca_17751	Ca6	-1.445	-1.442
520	MSTRG.10363	Ca_14909	Ca4	-1.445	2.426
521	MSTRG.14683	-	Ca6	-1.444	0.290
522	MSTRG.18265	Ca_06752	Ca7	-1.442	0.656
523	MSTRG.22515	-	scaffold1301_1	-1.437	0.777
524	MSTRG.7949	Ca_12090	Ca4	-1.435	6.210
525	MSTRG.14850	Ca_16752	Ca6	-1.433	1.126
526	MSTRG.13239	Ca_07604	Ca5	-1.432	3.583
527	MSTRG.6104	Ca_06034	Ca3	-1.432	5.391
528	MSTRG.21426	Ca_10604	Ca8	-1.431	4.067
529	MSTRG.10286	Ca_13097	Ca4	-1.431	1.275
530	MSTRG.3869	Ca_11644	Ca2	-1.430	2.012
531	MSTRG.16257	Ca_14594	Ca6	-1.430	0.213
532	MSTRG.1231	Ca_02818	Ca1	-1.424	3.436
533	MSTRG.20561	Ca_11917	Ca8	-1.423	6.157
534	MSTRG.12273	Ca_04789	Ca5	-1.422	6.738
535	MSTRG.4624	Ca_10291	Ca2	-1.421	3.545
536	MSTRG.15686	Ca_06470	Ca6	-1.421	0.897
537	MSTRG.21141	Ca_02041	Ca8	-1.419	2.505
538	MSTRG.14071	Ca_13329	Ca6	-1.418	2.757
539	MSTRG.16348	Ca_17463	Ca6	-1.416	8.536
540	MSTRG.13944	Ca_04246	Ca5	-1.416	5.037
541	MSTRG.19658	Ca_11775	Ca7	-1.414	2.990
542	MSTRG.5736	Ca_09416	Ca3	-1.413	1.741
543	MSTRG.25251	Ca_22420	scaffold845	-1.413	1.098
544	MSTRG.1239	-	Ca1	-1.412	1.388
545	MSTRG.18763	Ca_12825	Ca7	-1.412	5.066
546	MSTRG.15920	Ca_11268	Ca6	-1.411	2.419
547	MSTRG.24886	-	scaffold599	-1.411	-0.570
548	MSTRG.3394	Ca_21102	Ca2	-1.407	4.391
549	MSTRG.19545	Ca_23639	Ca7	-1.404	-0.030
550	MSTRG.13153	Ca_07514	Ca5	-1.402	0.304
551	MSTRG.15031	Ca_08525	Ca6	-1.400	7.408
552	MSTRG.6538	-	Ca3	-1.398	0.089
553	MSTRG.12095	-	Ca5	-1.388	1.045

554	MSTRG.12827	Ca_01600	Ca5	-1.386	1.350
555	MSTRG.517	Ca_00313	Ca1	-1.386	3.635
556	MSTRG.6352	-	Ca3	-1.378	-0.647
557	MSTRG.13669	Ca_03975	Ca5	-1.377	3.343
558	MSTRG.19999	Ca_20995	Ca7	-1.377	2.940
559	MSTRG.14282	-	Ca6	-1.376	4.575
560	MSTRG.8422	Ca_03495	Ca4	-1.376	0.745
561	MSTRG.2609	Ca_23538	Ca1	-1.376	1.295
562	MSTRG.23428	Ca_24892	scaffold212	-1.372	2.709
563	MSTRG.3403	-	Ca2	-1.371	2.411
564	MSTRG.9393	Ca_05388	Ca4	-1.371	2.529
565	MSTRG.23739	-	scaffold2738	-1.370	1.642
566	MSTRG.22790	-	scaffold1417	-1.370	0.462
567	MSTRG.5621	Ca_21139	Ca3	-1.368	4.733
568	MSTRG.11239	Ca_20333	Ca5	-1.366	2.590
569	MSTRG.1426	Ca_02620	Ca1	-1.366	3.670
570	MSTRG.6223	Ca_08266	Ca3	-1.366	1.677
571	MSTRG.89	Ca_27884	C11124530	-1.364	2.244
572	MSTRG.8167	Ca_03752	Ca4	-1.363	6.212
573	MSTRG.4399	-	Ca2	-1.358	1.444
574	MSTRG.23519	Ca_25418	scaffold2330	-1.358	4.472
575	MSTRG.22535	Ca_26611	scaffold1315	-1.356	1.280
576	MSTRG.14250	Ca_10440	Ca6	-1.356	4.787
577	MSTRG.20031	Ca_17612	Ca7	-1.355	0.731
578	MSTRG.12260	Ca_04778	Ca5	-1.353	1.926
579	MSTRG.17939	-	Ca7	-1.350	2.841
580	MSTRG.24507	Ca_21732	scaffold453	-1.350	1.616
581	MSTRG.12128	Ca_16657	Ca5	-1.348	7.404
582	MSTRG.8564	Ca_08365	Ca4	-1.347	3.020
583	MSTRG.11949	Ca_08904	Ca5	-1.346	1.749
584	MSTRG.20450	Ca_15741	Ca7	-1.345	8.494
585	MSTRG.8409	Ca_03508	Ca4	-1.342	1.705
586	MSTRG.14898	Ca_08667	Ca6	-1.342	3.286
587	MSTRG.15559	Ca_06348	Ca6	-1.340	1.982
588	MSTRG.7891	Ca_07859	Ca4	-1.338	3.543
589	MSTRG.6005	Ca_06152	Ca3	-1.336	4.851
590	MSTRG.18044	Ca_03065	Ca7	-1.336	1.335

591	MSTRG.6982	Ca_00738	Ca3	-1.333	1.924
592	MSTRG.23359	Ca_26286	scaffold2027	-1.329	3.169
593	MSTRG.17292	Ca_21219	Ca6	-1.328	1.721
594	MSTRG.8878	Ca_04438	Ca4	-1.328	2.910
595	MSTRG.13809	Ca_04111	Ca5	-1.326	1.164
596	MSTRG.9189	Ca_05594	Ca4	-1.326	0.992
597	MSTRG.2365	-	Ca1	-1.322	-1.528
598	MSTRG.596	Ca_00391	Ca1	-1.320	2.262
599	MSTRG.19208	-	Ca7	-1.318	0.464
600	MSTRG.11205	-	Ca5	-1.318	3.401
601	MSTRG.4207	Ca_14289	Ca2	-1.316	2.498
602	MSTRG.1401	Ca_02638	Ca1	-1.316	2.561
603	MSTRG.22525	Ca_25873	scaffold1313	-1.315	2.398
604	MSTRG.3181	Ca_12574	Ca2	-1.314	5.670
605	MSTRG.12051	-	Ca5	-1.312	0.151
606	MSTRG.5609	Ca_21122	Ca3	-1.312	7.854
607	MSTRG.16799	-	Ca6	-1.311	-0.505
608	MSTRG.24863	-	scaffold593	-1.308	-0.221
609	MSTRG.15	-	C11053314	-1.306	0.768
610	MSTRG.18616	Ca_15295	Ca7	-1.305	1.915
611	MSTRG.23944	Ca_21798	scaffold314	-1.305	2.034
612	MSTRG.6570	Ca_07309	Ca3	-1.304	4.154
613	MSTRG.21421	Ca_10605	Ca8	-1.304	2.690
614	MSTRG.11318	-	Ca5	-1.302	5.289
615	MSTRG.12209	Ca_04731	Ca5	-1.301	-0.924
616	MSTRG.17963	Ca_03140	Ca7	-1.299	1.371
617	MSTRG.18750	-	Ca7	-1.296	-0.647
618	MSTRG.22725	-	scaffold1348_1	-1.296	2.353
619	MSTRG.1750	Ca_07081	Ca1	-1.292	3.171
620	MSTRG.18458	Ca_06589	Ca7	-1.292	4.349
621	MSTRG.14546	Ca_05719	Ca6	-1.289	5.732
622	MSTRG.23789	Ca_20593	scaffold284	-1.288	3.105
623	MSTRG.14643	Ca_16943	Ca6	-1.280	2.888
624	MSTRG.13061	Ca_07421	Ca5	-1.279	5.795
625	MSTRG.16502	Ca_15222	Ca6	-1.279	4.060
626	MSTRG.17589	Ca_18860	Ca6	-1.277	5.196
627	MSTRG.14891	Ca_08672	Ca6	-1.273	3.679

628	MSTRG.18542	Ca_13162	Ca7	-1.272	6.141
629	MSTRG.13670	Ca_03976	Ca5	-1.272	6.026
630	MSTRG.8068	-	Ca4	-1.271	2.665
631	MSTRG.6782	Ca_12291	Ca3	-1.271	2.218
632	MSTRG.3238	Ca_10584	Ca2	-1.270	4.483
633	MSTRG.14953	Ca_08603	Ca6	-1.269	1.375
634	MSTRG.19933	Ca_16156	Ca7	-1.268	2.759
635	MSTRG.11853	Ca_09010	Ca5	-1.268	3.790
636	MSTRG.21845	Ca_12991	Ca8	-1.267	4.611
637	MSTRG.18061	Ca_03042	Ca7	-1.266	4.873
638	MSTRG.2422	Ca_22558	Ca1	-1.262	1.972
639	MSTRG.14701	Ca_09643	Ca6	-1.262	2.413
640	MSTRG.4781	-	Ca2	-1.262	1.791
641	MSTRG.7636	Ca_01352	Ca3	-1.260	1.971
642	MSTRG.24590	Ca_25565	scaffold485	-1.258	2.126
643	MSTRG.18791	Ca_09379	Ca7	-1.258	4.016
644	MSTRG.16168	Ca_16676	Ca6	-1.258	1.637
645	MSTRG.18546	Ca_13159	Ca7	-1.257	1.204
646	MSTRG.243	Ca_00047	Ca1	-1.257	6.902
647	MSTRG.3219	-	Ca2	-1.257	0.614
648	MSTRG.23387	Ca_26621	scaffold2040	-1.254	3.624
649	MSTRG.14513	Ca_05754	Ca6	-1.253	4.134
650	MSTRG.12500	Ca_05014	Ca5	-1.253	2.996
651	MSTRG.16186	Ca_16693	Ca6	-1.253	3.396
652	MSTRG.21789	-	Ca8	-1.249	1.864
653	MSTRG.12047	Ca_13368	Ca5	-1.247	1.573
654	MSTRG.3613	Ca_21476	Ca2	-1.247	3.556
655	MSTRG.16833	-	Ca6	-1.246	2.824
656	MSTRG.16477	Ca_15192	Ca6	-1.240	2.215
657	MSTRG.11961	Ca_08893	Ca5	-1.239	3.912
658	MSTRG.7950	Ca_12091	Ca4	-1.236	5.754
659	MSTRG.20331	Ca_17980	Ca7	-1.234	7.100
660	MSTRG.6254	-	Ca3	-1.233	2.118
661	MSTRG.17858	Ca_03237	Ca7	-1.233	4.519
662	MSTRG.20049	Ca_17633	Ca7	-1.228	1.646
663	MSTRG.12054	Ca_13365	Ca5	-1.228	1.786
664	MSTRG.14743	Ca_09603	Ca6	-1.224	3.182

665	MSTRG.17087	Ca_13449	Ca6	-1.223	3.443
666	MSTRG.10797	Ca_19272	Ca4	-1.222	3.720
667	MSTRG.536	Ca_00332	Ca1	-1.217	2.183
668	MSTRG.271	Ca_00077	Ca1	-1.215	1.177
669	MSTRG.14466	Ca_05799	Ca6	-1.215	0.326
670	MSTRG.5160	Ca_22377	Ca3	-1.215	5.115
671	MSTRG.14862	Ca_16743	Ca6	-1.215	6.418
672	MSTRG.6558	Ca_07298	Ca3	-1.214	2.079
673	MSTRG.16878	Ca_13848	Ca6	-1.214	1.833
674	MSTRG.9590	Ca_14059	Ca4	-1.213	3.263
675	MSTRG.20400	-	Ca7	-1.212	-1.139
676	MSTRG.13735	Ca_04041	Ca5	-1.212	3.282
677	MSTRG.21422	-	Ca8	-1.211	-1.683
678	MSTRG.15492	Ca_06285	Ca6	-1.210	3.946
679	MSTRG.21192	-	Ca8	-1.209	-1.440
680	MSTRG.4038	Ca_23775	Ca2	-1.208	1.725
681	MSTRG.14448	Ca_05820	Ca6	-1.208	7.722
682	MSTRG.10629	Ca_09111	Ca4	-1.207	-0.288
683	MSTRG.11578	Ca_22825	Ca5	-1.206	6.906
684	MSTRG.20903	Ca_02276	Ca8	-1.205	4.780
685	MSTRG.1933	Ca_06895	Ca1	-1.205	5.650
686	MSTRG.10023	Ca_15488	Ca4	-1.204	5.021
687	MSTRG.25209	-	scaffold811	-1.202	-0.500
688	MSTRG.20534	Ca_26358	Ca7	-1.199	5.138
689	MSTRG.8978	Ca_04533	Ca4	-1.197	1.955
690	MSTRG.24505	Ca_21726	scaffold453	-1.196	4.198
691	MSTRG.3512	Ca_20936	Ca2	-1.196	6.644
692	MSTRG.14717	Ca_09628	Ca6	-1.196	1.352
693	MSTRG.23099	Ca_21713	scaffold174	-1.195	1.573
694	MSTRG.11885	Ca_08971	Ca5	-1.193	6.025
695	MSTRG.9239	-	Ca4	-1.193	2.935
696	MSTRG.13377	Ca_11365	Ca5	-1.193	3.526
697	MSTRG.16902	Ca_13878	Ca6	-1.192	4.692
698	MSTRG.15010	Ca_08544	Ca6	-1.192	1.507
699	MSTRG.20294	Ca_20250	Ca7	-1.191	2.613
700	MSTRG.9216	Ca_05572	Ca4	-1.190	2.692
701	MSTRG.2861	Ca_13532	Ca1	-1.189	2.948

702	MSTRG.25371	-	scaffold882	-1.188	1.513
703	MSTRG.4194	Ca_14278	Ca2	-1.188	2.505
704	MSTRG.23025	-	scaffold167	-1.188	2.629
705	MSTRG.16209	Ca_16717	Ca6	-1.187	3.993
706	MSTRG.18067	Ca_03040	Ca7	-1.187	-0.230
707	MSTRG.7342	Ca_01083	Ca3	-1.187	3.779
708	MSTRG.14167	-	Ca6	-1.186	1.219
709	MSTRG.1992	Ca_14787	Ca1	-1.185	2.115
710	MSTRG.1573	Ca_02465	Ca1	-1.185	6.983
711	MSTRG.19254	Ca_22133	Ca7	-1.184	2.531
712	MSTRG.19748	Ca_23327	Ca7	-1.183	1.358
713	MSTRG.9215	Ca_05573	Ca4	-1.183	0.450
714	MSTRG.22638	-	scaffold1348_1	-1.182	1.948
715	MSTRG.17214	Ca_18891	Ca6	-1.180	2.591
716	MSTRG.24678	Ca_24531	scaffold528	-1.179	2.904
717	MSTRG.19906	Ca_10009	Ca7	-1.177	8.245
718	MSTRG.17480	Ca_13639	Ca6	-1.176	1.454
719	MSTRG.9291	Ca_05491	Ca4	-1.173	5.417
720	MSTRG.13394	Ca_11353	Ca5	-1.173	3.246
721	MSTRG.17682	Ca_03389	Ca7	-1.173	3.014
722	MSTRG.21455	-	Ca8	-1.171	2.638
723	MSTRG.6545	Ca_07286	Ca3	-1.168	2.740
724	MSTRG.11435	Ca_20827	Ca5	-1.167	4.961
725	MSTRG.1917	-	Ca1	-1.166	3.102
726	MSTRG.6531	Ca_07270	Ca3	-1.165	2.991
727	MSTRG.425	Ca_00217	Ca1	-1.165	2.504
728	MSTRG.13087	Ca_07447	Ca5	-1.164	6.597
729	MSTRG.10691	Ca_09174	Ca4	-1.163	2.622
730	MSTRG.1934	Ca_06894	Ca1	-1.163	6.061
731	MSTRG.15588	Ca_06378	Ca6	-1.163	2.493
732	MSTRG.12416	Ca_04924	Ca5	-1.161	1.751
733	MSTRG.18094	Ca_03009	Ca7	-1.160	4.728
734	MSTRG.3222	Ca_12547	Ca2	-1.159	2.913
735	MSTRG.10910	Ca_10785	Ca4	-1.158	4.691
736	MSTRG.21582	Ca_18412	Ca8	-1.158	7.757
737	MSTRG.15024	Ca_08532	Ca6	-1.158	3.825
738	MSTRG.20962	-	Ca8	-1.158	3.301

739	MSTRG.7446	Ca_01188	Ca3	-1.158	2.496
740	MSTRG.12818	Ca_01606	Ca5	-1.156	1.358
741	MSTRG.742	Ca_00553	Ca1	-1.155	0.770
742	MSTRG.19913	Ca_10002	Ca7	-1.155	1.312
743	MSTRG.7862	Ca_07828	Ca4	-1.154	4.974
744	MSTRG.25125	-	scaffold7355	-1.153	6.106
745	MSTRG.21330	Ca_10697	Ca8	-1.153	4.222
746	MSTRG.4140	-	Ca2	-1.152	1.470
747	MSTRG.3885	Ca_11627	Ca2	-1.152	2.402
748	MSTRG.14304	Ca_05954	Ca6	-1.152	2.179
749	MSTRG.1857	Ca_06970	Ca1	-1.150	4.815
750	MSTRG.16605	Ca_15778	Ca6	-1.148	2.830
751	MSTRG.4858	Ca_16870	Ca2	-1.148	3.513
752	MSTRG.14063	Ca_13322	Ca6	-1.146	3.721
753	MSTRG.18784	-	Ca7	-1.145	-0.094
754	MSTRG.7200	Ca_00952	Ca3	-1.141	3.723
755	MSTRG.829	Ca_00647	Ca1	-1.140	2.031
756	MSTRG.3814	Ca_18075	Ca2	-1.139	2.856
757	MSTRG.17498	Ca_13623	Ca6	-1.139	4.924
758	MSTRG.13631	Ca_03940	Ca5	-1.138	1.984
759	MSTRG.7192	Ca_00946	Ca3	-1.138	4.970
760	MSTRG.10230	Ca_15084	Ca4	-1.138	7.900
761	MSTRG.345	Ca_00143	Ca1	-1.136	5.096
762	MSTRG.4677	Ca_10238	Ca2	-1.136	5.002
763	MSTRG.15529	Ca_06315	Ca6	-1.136	6.885
764	MSTRG.25410	-	scaffold895	-1.136	4.352
765	MSTRG.2974	Ca_12925	Ca1	-1.134	2.806
766	MSTRG.13162	Ca_07522	Ca5	-1.133	7.651
767	MSTRG.9466	Ca_18637	Ca4	-1.132	7.569
768	MSTRG.4468	Ca_12525	Ca2	-1.131	1.741
769	MSTRG.18841	Ca_09325	Ca7	-1.130	7.436
770	MSTRG.19951	Ca_16173	Ca7	-1.126	2.084
771	MSTRG.22022	-	scaffold1006	-1.125	6.862
772	MSTRG.24149	Ca_24496	scaffold349	-1.123	3.478
773	MSTRG.1413	Ca_02628	Ca1	-1.121	3.547
774	MSTRG.13403	Ca_11343	Ca5	-1.121	3.138
775	MSTRG.12417	Ca_04926	Ca5	-1.121	1.730

776	MSTRG.21125	Ca_02060	Ca8	-1.120	1.848
777	MSTRG.15865	-	Ca6	-1.120	2.185
778	MSTRG.10121	Ca_14846	Ca4	-1.119	4.565
779	MSTRG.688	Ca_00495	Ca1	-1.119	1.665
780	MSTRG.19275	Ca_12304	Ca7	-1.118	5.514
781	MSTRG.9855	Ca_20441	Ca4	-1.117	3.876
782	MSTRG.9439	Ca_05350	Ca4	-1.117	3.603
783	MSTRG.16217	Ca_16725	Ca6	-1.116	2.331
784	MSTRG.19818	Ca_10090	Ca7	-1.116	7.361
785	MSTRG.19003	Ca_16073	Ca7	-1.116	1.037
786	MSTRG.2801	Ca_13602	Ca1	-1.115	2.562
787	MSTRG.2279	Ca_18301	Ca1	-1.114	2.661
788	MSTRG.25544	-	scaffold96	-1.113	-1.156
789	MSTRG.5313	-	Ca3	-1.113	-1.236
790	MSTRG.21885	Ca_12955	Ca8	-1.113	7.144
791	MSTRG.21025	Ca_02153	Ca8	-1.112	6.018
792	MSTRG.4864	Ca_16864	Ca2	-1.111	4.159
793	MSTRG.14455	Ca_05814	Ca6	-1.110	3.780
794	MSTRG.3846	Ca_11680	Ca2	-1.109	3.648
795	MSTRG.10069	Ca_19997	Ca4	-1.107	5.496
796	MSTRG.4628	Ca_10285	Ca2	-1.107	5.022
797	MSTRG.6586	Ca_07322	Ca3	-1.107	2.079
798	MSTRG.10009	-	Ca4	-1.105	-0.307
799	MSTRG.13571	Ca_03879	Ca5	-1.104	6.384
800	MSTRG.18532	Ca_13170	Ca7	-1.103	2.766
801	MSTRG.2562	Ca_21688	Ca1	-1.103	4.998
802	MSTRG.17364	Ca_17413	Ca6	-1.102	1.385
803	MSTRG.5558	Ca_18277	Ca3	-1.101	4.328
804	MSTRG.14032	Ca_13294	Ca6	-1.100	4.265
805	MSTRG.20914	Ca_02264	Ca8	-1.097	2.792
806	MSTRG.8356	Ca_03565	Ca4	-1.097	6.144
807	MSTRG.22232	-	scaffold109_1	-1.096	3.628
808	MSTRG.2419	Ca_22565	Ca1	-1.096	3.241
809	MSTRG.15718	Ca_06502	Ca6	-1.095	2.744
810	MSTRG.21956	-	Ca8	-1.095	-0.235
811	MSTRG.14372	Ca_05889	Ca6	-1.095	0.776
812	MSTRG.2025	Ca_14758	Ca1	-1.094	5.657

813	MSTRG.14302	Ca_05956	Ca6	-1.094	5.517
814	MSTRG.14824	Ca_16780	Ca6	-1.093	3.839
815	MSTRG.18846	Ca_09321	Ca7	-1.092	4.034
816	MSTRG.13575	Ca_03882	Ca5	-1.091	3.981
817	MSTRG.12293	Ca_04810	Ca5	-1.089	2.898
818	MSTRG.12877	Ca_01546	Ca5	-1.087	3.601
819	MSTRG.14139	Ca_10324	Ca6	-1.087	2.829
820	MSTRG.17716	-	Ca7	-1.087	3.382
821	MSTRG.1189	Ca_02857	Ca1	-1.085	4.532
822	MSTRG.21272	Ca_23579	Ca8	-1.084	2.098
823	MSTRG.2893	Ca_25715	Ca1	-1.084	7.440
824	MSTRG.2987	Ca_12914	Ca1	-1.082	6.806
825	MSTRG.3240	Ca_10579	Ca2	-1.081	5.252
826	MSTRG.18748	Ca_12811	Ca7	-1.080	4.967
827	MSTRG.949	Ca_07945	Ca1	-1.079	1.216
828	MSTRG.22801	-	scaffold1417	-1.077	1.532
829	MSTRG.11873	Ca_08988	Ca5	-1.077	2.961
830	MSTRG.9676	Ca_19075	Ca4	-1.077	3.789
831	MSTRG.4754	Ca_10155	Ca2	-1.076	2.404
832	MSTRG.10961	Ca_23011	Ca4	-1.076	2.815
833	MSTRG.12096	Ca_16624	Ca5	-1.075	6.040
834	MSTRG.2002	Ca_14781	Ca1	-1.075	4.126
835	MSTRG.13469	Ca_12727	Ca5	-1.072	4.107
836	MSTRG.14438	Ca_05828	Ca6	-1.072	4.245
837	MSTRG.21705	Ca_16791	Ca8	-1.071	3.771
838	MSTRG.6035	Ca_06114	Ca3	-1.071	4.528
839	MSTRG.12524	Ca_01915	Ca5	-1.071	2.342
840	MSTRG.6149	Ca_05989	Ca3	-1.069	2.060
841	MSTRG.3497	-	Ca2	-1.069	0.590
842	MSTRG.20440	-	Ca7	-1.068	1.168
843	MSTRG.6655	Ca_07390	Ca3	-1.068	1.756
844	MSTRG.17391	Ca_17440	Ca6	-1.067	4.506
845	MSTRG.2847	Ca_13545	Ca1	-1.067	1.616
846	MSTRG.8163	Ca_03754	Ca4	-1.065	2.982
847	MSTRG.10180	Ca_15149	Ca4	-1.064	1.422
848	MSTRG.6870	Ca_12032	Ca3	-1.064	2.150
849	MSTRG.18550	Ca_13155	Ca7	-1.063	5.855

850	MSTRG.22969	Ca_27087	scaffold1607	-1.062	5.403
851	MSTRG.9455	Ca_18625	Ca4	-1.060	3.447
852	MSTRG.15000	Ca_08557	Ca6	-1.059	2.071
853	MSTRG.24300	Ca_22295	scaffold398	-1.059	3.576
854	MSTRG.6667	-	Ca3	-1.058	4.498
855	MSTRG.4847	Ca_16882	Ca2	-1.057	2.178
856	MSTRG.21234	Ca_01955	Ca8	-1.055	3.741
857	MSTRG.18998	Ca_16066	Ca7	-1.055	4.521
858	MSTRG.23477	-	scaffold222	-1.054	0.011
859	MSTRG.15370	Ca_05262	Ca6	-1.053	6.021
860	MSTRG.16737	Ca_15949	Ca6	-1.053	2.812
861	MSTRG.22044	-	scaffold1006	-1.053	2.333
862	MSTRG.11504	Ca_17953	Ca5	-1.052	3.188
863	MSTRG.367	Ca_00160	Ca1	-1.052	2.525
864	MSTRG.23287	-	scaffold1962	-1.051	2.752
865	MSTRG.4442	Ca_16103	Ca2	-1.051	3.507
866	MSTRG.20605	Ca_11881	Ca8	-1.050	3.184
867	MSTRG.9227	Ca_05559	Ca4	-1.049	3.979
868	MSTRG.23656	Ca_22991	scaffold2575	-1.049	3.497
869	MSTRG.9212	Ca_05576	Ca4	-1.046	4.700
870	MSTRG.13750	Ca_04055	Ca5	-1.045	4.288
871	MSTRG.19613	Ca_18947	Ca7	-1.045	4.400
872	MSTRG.19394	Ca_14497	Ca7	-1.043	1.604
873	MSTRG.5980	Ca_06175	Ca3	-1.043	5.078
874	MSTRG.15907	Ca_11281	Ca6	-1.042	0.320
875	MSTRG.13755	Ca_04060	Ca5	-1.041	7.318
876	MSTRG.12265	Ca_04782	Ca5	-1.041	3.461
877	MSTRG.858	Ca_00679	Ca1	-1.041	4.002
878	MSTRG.6518	Ca_07258	Ca3	-1.039	2.142
879	MSTRG.825	Ca_00641	Ca1	-1.039	2.018
880	MSTRG.12672	Ca_01751	Ca5	-1.037	5.504
881	MSTRG.2809	-	Ca1	-1.034	0.715
882	MSTRG.9441	Ca_05348	Ca4	-1.033	3.259
883	MSTRG.14517	Ca_05752	Ca6	-1.033	2.990
884	MSTRG.878	Ca_00694	Ca1	-1.033	10.132
885	MSTRG.7226	Ca_00974	Ca3	-1.032	0.856
886	MSTRG.7140	Ca_00896	Ca3	-1.032	5.240

887	MSTRG.95	Ca_28135	C11132160	-1.031	0.898
888	MSTRG.10215	Ca_15105	Ca4	-1.030	3.523
889	MSTRG.309	Ca_00113	Ca1	-1.030	4.423
890	MSTRG.4607	Ca_17818	Ca2	-1.029	1.744
891	MSTRG.8008	Ca_12143	Ca4	-1.029	5.350
892	MSTRG.3214	Ca_12553	Ca2	-1.029	7.160
893	MSTRG.23710	Ca_25333	scaffold271	-1.025	2.235
894	MSTRG.25520	-	scaffold93	-1.025	0.270
895	MSTRG.5553	Ca_18271	Ca3	-1.025	6.659
896	MSTRG.4540	Ca_12449	Ca2	-1.024	6.296
897	MSTRG.334	-	Ca1	-1.023	3.748
898	MSTRG.6072	Ca_06076	Ca3	-1.023	3.519
899	MSTRG.19610	Ca_18948	Ca7	-1.019	2.178
900	MSTRG.11206	Ca_18723	Ca5	-1.017	2.620
901	MSTRG.14242	Ca_10434	Ca6	-1.017	0.749
902	MSTRG.3929	Ca_24652	Ca2	-1.017	3.767
903	MSTRG.18619	Ca_15296	Ca7	-1.017	4.564
904	MSTRG.4625	Ca_10290	Ca2	-1.017	3.687
905	MSTRG.19088	Ca_09932	Ca7	-1.017	3.597
906	MSTRG.16816	-	Ca6	-1.015	3.598
907	MSTRG.8762	Ca_04335	Ca4	-1.014	3.222
908	MSTRG.1431	Ca_02615	Ca1	-1.013	5.158
909	MSTRG.4948	Ca_09755	Ca2	-1.010	1.337
910	MSTRG.14179	Ca_10365	Ca6	-1.009	4.120
911	MSTRG.17704	Ca_03370	Ca7	-1.007	0.765
912	MSTRG.9927	Ca_14170	Ca4	-1.007	2.423
913	MSTRG.11989	Ca_13430	Ca5	-1.006	5.509
914	MSTRG.14018	Ca_13279	Ca6	-1.003	2.816
915	MSTRG.5001	Ca_09809	Ca2	-1.000	7.734
916	MSTRG.460	Ca_00253	Ca1	-1.000	5.659
917	MSTRG.9642	Ca_17162	Ca4	-1.000	1.872
918	MSTRG.16840	Ca_24237	Ca6	1.000	5.467
919	MSTRG.377	-	Ca1	1.003	2.047
920	MSTRG.11962	Ca_08892	Ca5	1.004	6.530
921	MSTRG.21928	Ca_17872	Ca8	1.005	3.814
922	MSTRG.24758	Ca_23922	scaffold545	1.005	2.801
923	MSTRG.15704	Ca_06488	Ca6	1.007	5.353

924	MSTRG.16871	Ca_13840	Ca6	1.010	4.907
925	MSTRG.20014	-	Ca7	1.011	3.360
926	MSTRG.14365	Ca_05895	Ca6	1.015	0.888
927	MSTRG.7640	Ca_01359	Ca3	1.015	5.108
928	MSTRG.13205	Ca_07569	Ca5	1.016	3.096
929	MSTRG.5970	-	Ca3	1.018	0.876
930	MSTRG.1160	Ca_02885	Ca1	1.019	5.733
931	MSTRG.4552	Ca_12435	Ca2	1.026	7.363
932	MSTRG.21529	Ca_11524	Ca8	1.027	7.587
933	MSTRG.10672	Ca_09156	Ca4	1.030	3.632
934	MSTRG.13852	Ca_04158	Ca5	1.030	2.293
935	MSTRG.15601	Ca_06390	Ca6	1.030	7.414
936	MSTRG.5498	Ca_22496	Ca3	1.031	4.892
937	MSTRG.21935	Ca_17864	Ca8	1.034	4.886
938	MSTRG.19128	Ca_09876	Ca7	1.040	3.563
939	MSTRG.22297	Ca_26366	scaffold1145	1.040	4.894
940	MSTRG.16985	Ca_20707	Ca6	1.046	6.715
941	MSTRG.22211	Ca_24277	scaffold1089	1.047	5.680
942	MSTRG.748	Ca_00561	Ca1	1.048	3.218
943	MSTRG.3641	Ca_22315	Ca2	1.051	2.332
944	MSTRG.23154	Ca_23259	scaffold1777	1.052	4.751
945	MSTRG.16970	Ca_24604	Ca6	1.052	0.020
946	MSTRG.15593	Ca_06384	Ca6	1.055	3.699
947	MSTRG.17524	Ca_15390	Ca6	1.056	1.860
948	MSTRG.21144	Ca_02036	Ca8	1.059	3.840
949	MSTRG.15489	Ca_19648	Ca6	1.062	0.904
950	MSTRG.619	Ca_00414	Ca1	1.062	2.999
951	MSTRG.17660	Ca_03409	Ca7	1.062	1.244
952	MSTRG.13647	Ca_03953	Ca5	1.065	6.497
953	MSTRG.22167	Ca_21777	scaffold1060	1.067	7.400
954	MSTRG.18210	-	Ca7	1.077	3.954
955	MSTRG.15287	Ca_05177	Ca6	1.081	5.908
956	MSTRG.22889	Ca_26423	scaffold1496	1.085	7.807
957	MSTRG.13267	-	Ca5	1.086	2.645
958	MSTRG.17943	Ca_03159	Ca7	1.086	0.959
959	MSTRG.23246	Ca_24715	scaffold1918	1.087	5.054
960	MSTRG.15590	Ca_06380	Ca6	1.090	5.240

961	MSTRG.4806	Ca_15268	Ca2	1.090	5.283
962	MSTRG.1399	Ca_02648	Ca1	1.091	6.446
963	MSTRG.17240	Ca_18917	Ca6	1.091	12.049
964	MSTRG.13751	Ca_04056	Ca5	1.092	5.094
965	MSTRG.15853	Ca_16325	Ca6	1.095	4.343
966	MSTRG.10676	Ca_09157	Ca4	1.102	8.558
967	MSTRG.8969	Ca_04525	Ca4	1.103	3.405
968	MSTRG.5969	-	Ca3	1.103	3.852
969	MSTRG.1755	-	Ca1	1.108	5.201
970	MSTRG.4213	Ca_14297	Ca2	1.112	3.662
971	MSTRG.17278	Ca_21197	Ca6	1.113	7.164
972	MSTRG.834	Ca_00654	Ca1	1.121	1.465
973	MSTRG.5687	-	Ca3	1.124	3.660
974	MSTRG.6921	Ca_20876	Ca3	1.128	4.821
975	MSTRG.426	Ca_00220	Ca1	1.129	2.665
976	MSTRG.12067	Ca_13350	Ca5	1.132	2.173
977	MSTRG.4541	Ca_12448	Ca2	1.133	5.250
978	MSTRG.16034	Ca_11124	Ca6	1.134	2.374
979	MSTRG.20776	Ca_02412	Ca8	1.136	5.986
980	MSTRG.16236	Ca_14618	Ca6	1.136	7.311
981	MSTRG.17488	Ca_13632	Ca6	1.136	6.002
982	MSTRG.9703	Ca_20135	Ca4	1.138	2.497
983	MSTRG.19904	Ca_10012	Ca7	1.138	3.521
984	MSTRG.7085	Ca_00833	Ca3	1.140	1.540
985	MSTRG.815	Ca_00626	Ca1	1.142	2.022
986	MSTRG.11655	Ca_21153	Ca5	1.143	3.510
987	MSTRG.24132	-	scaffold346_1	1.143	2.190
988	MSTRG.25099	Ca_23807	scaffold731	1.143	5.592
989	MSTRG.1645	Ca_14111	Ca1	1.147	2.795
990	MSTRG.4543	Ca_12446	Ca2	1.152	3.991
991	MSTRG.9738	Ca_14458	Ca4	1.153	3.237
992	MSTRG.10421	Ca_11015	Ca4	1.153	4.887
993	MSTRG.16558	Ca_22054	Ca6	1.155	4.852
994	MSTRG.2278	Ca_18303	Ca1	1.156	1.406
995	MSTRG.4724	Ca_10191	Ca2	1.158	2.198
996	MSTRG.21505	Ca_11501	Ca8	1.163	6.563
997	MSTRG.22037	-	scaffold1006	1.168	4.774

998	MSTRG.428	Ca_00219	Ca1	1.171	5.466
999	MSTRG.23254	Ca_25164	scaffold193	1.172	3.231
1000	MSTRG.5600	Ca_23331	Ca3	1.174	3.962
1001	MSTRG.6674	Ca_12185	Ca3	1.175	5.649
1002	MSTRG.10229	-	Ca4	1.176	1.693
1003	MSTRG.20775	Ca_02413	Ca8	1.176	2.385
1004	MSTRG.22010	-	scaffold1006	1.179	5.438
1005	MSTRG.8102	Ca_03817	Ca4	1.181	1.633
1006	MSTRG.19194	Ca_15884	Ca7	1.182	2.922
1007	MSTRG.1144	Ca_02901	Ca1	1.183	3.657
1008	MSTRG.8377	Ca_03541	Ca4	1.185	2.245
1009	MSTRG.13060	Ca_07420	Ca5	1.188	2.658
1010	MSTRG.6495	Ca_07234	Ca3	1.189	5.627
1011	MSTRG.8626	Ca_08436	Ca4	1.190	5.355
1012	MSTRG.2629	Ca_13964	Ca1	1.206	4.777
1013	MSTRG.23989	Ca_24183	scaffold3170	1.208	2.853
1014	MSTRG.18428	Ca_06615	Ca7	1.211	2.804
1015	MSTRG.10834	Ca_10861	Ca4	1.211	4.099
1016	MSTRG.19979	Ca_16196	Ca7	1.212	0.713
1017	MSTRG.1138	Ca_02911	Ca1	1.214	1.793
1018	MSTRG.17441	-	Ca6	1.214	1.166
1019	MSTRG.24189	-	scaffold362	1.215	-1.115
1020	MSTRG.2172	Ca_22105	Ca1	1.216	5.531
1021	MSTRG.5585	Ca_23346	Ca3	1.219	4.058
1022	MSTRG.497	Ca_00295	Ca1	1.223	1.689
1023	MSTRG.6646	Ca_07380	Ca3	1.226	3.380
1024	MSTRG.9429	Ca_05361	Ca4	1.227	5.223
1025	MSTRG.22894	Ca_25147	scaffold1511	1.230	4.676
1026	MSTRG.24435	-	scaffold421_2	1.231	2.246
1027	MSTRG.997	Ca_07988	Ca1	1.234	5.582
1028	MSTRG.10971	Ca_23020	Ca4	1.235	2.939
1029	MSTRG.7942	Ca_12085	Ca4	1.235	5.478
1030	MSTRG.2745	-	Ca1	1.235	3.553
1031	MSTRG.890	Ca_07886	Ca1	1.238	0.817
1032	MSTRG.19671	-	Ca7	1.240	3.999
1033	MSTRG.22008	-	scaffold1006	1.242	2.304
1034	MSTRG.11903	Ca_08954	Ca5	1.244	2.409

1035	MSTRG.25164	Ca_27351	scaffold7800	1.251	2.318
1036	MSTRG.4271	-	Ca2	1.253	1.306
1037	MSTRG.9141	Ca_05640	Ca4	1.253	5.269
1038	MSTRG.25001	-	scaffold6704	1.259	-1.997
1039	MSTRG.5465	Ca_25322	Ca3	1.261	2.439
1040	MSTRG.10219	Ca_15098	Ca4	1.264	4.070
1041	MSTRG.14193	Ca_10384	Ca6	1.265	3.075
1042	MSTRG.21650	Ca_16840	Ca8	1.266	4.743
1043	MSTRG.23719	Ca_26034	scaffold2720	1.267	2.974
1044	MSTRG.5271	Ca_16532	Ca3	1.267	2.823
1045	MSTRG.21038	Ca_02141	Ca8	1.271	2.808
1046	MSTRG.15136	-	Ca6	1.271	4.113
1047	MSTRG.5631	Ca_19619	Ca3	1.271	4.895
1048	MSTRG.11821	Ca_09044	Ca5	1.276	1.837
1049	MSTRG.7025	Ca_00776	Ca3	1.279	5.371
1050	MSTRG.14075	Ca_13335	Ca6	1.281	6.426
1051	MSTRG.12073	Ca_13345	Ca5	1.287	6.252
1052	MSTRG.21311	Ca_10716	Ca8	1.287	3.216
1053	MSTRG.1598	Ca_14069	Ca1	1.287	-0.002
1054	MSTRG.13189	Ca_07550	Ca5	1.287	0.776
1055	MSTRG.15573	-	Ca6	1.290	3.251
1056	MSTRG.7302	Ca_01051	Ca3	1.292	4.373
1057	MSTRG.7304	Ca_01053	Ca3	1.294	2.222
1058	MSTRG.1391	Ca_02649	Ca1	1.298	3.755
1059	MSTRG.11403	Ca_17085	Ca5	1.298	3.460
1060	MSTRG.14339	Ca_05922	Ca6	1.304	5.256
1061	MSTRG.10028	Ca_15496	Ca4	1.305	5.305
1062	MSTRG.17978	Ca_03124	Ca7	1.308	2.267
1063	MSTRG.4151	-	Ca2	1.308	1.566
1064	MSTRG.11118	Ca_24950	Ca5	1.314	2.407
1065	MSTRG.11384	Ca_17101	Ca5	1.315	5.516
1066	MSTRG.19051	Ca_09970	Ca7	1.324	2.955
1067	MSTRG.19949	Ca_16169	Ca7	1.342	2.673
1068	MSTRG.15207	Ca_05106	Ca6	1.343	4.866
1069	MSTRG.21475	Ca_11462	Ca8	1.350	5.580
1070	MSTRG.8398	Ca_03519	Ca4	1.350	-0.171
1071	MSTRG.10346	Ca_14929	Ca4	1.350	9.595

1072	MSTRG.13764	Ca_04067	Ca5	1.351	3.466
1073	MSTRG.22133	Ca_17224	scaffold1047	1.354	2.205
1074	MSTRG.17910	Ca_03188	Ca7	1.355	4.452
1075	MSTRG.24346	Ca_24360	scaffold404	1.360	2.683
1076	MSTRG.3371	Ca_10455	Ca2	1.365	3.864
1077	MSTRG.10144	Ca_14822	Ca4	1.368	1.305
1078	MSTRG.16707	Ca_15917	Ca6	1.372	4.689
1079	MSTRG.21395	Ca_10643	Ca8	1.376	1.823
1080	MSTRG.21282	Ca_23585	Ca8	1.379	5.211
1081	MSTRG.23424	-	scaffold2103	1.385	-0.632
1082	MSTRG.23034	-	scaffold1687	1.386	0.204
1083	MSTRG.11812	Ca_15625	Ca5	1.391	3.364
1084	MSTRG.19994	Ca_21000	Ca7	1.391	0.253
1085	MSTRG.5602	Ca_21116	Ca3	1.397	4.700
1086	MSTRG.14692	Ca_09651	Ca6	1.399	2.216
1087	MSTRG.12251	Ca_04769	Ca5	1.400	4.704
1088	MSTRG.10525	Ca_10900	Ca4	1.405	0.342
1089	MSTRG.5597	Ca_23335	Ca3	1.406	0.038
1090	MSTRG.1168	Ca_02879	Ca1	1.413	4.970
1091	MSTRG.1120	Ca_02925	Ca1	1.414	2.011
1092	MSTRG.19480	Ca_19509	Ca7	1.418	3.840
1093	MSTRG.19514	Ca_19903	Ca7	1.420	3.397
1094	MSTRG.18721	Ca_12781	Ca7	1.420	0.845
1095	MSTRG.9199	Ca_05585	Ca4	1.422	1.088
1096	MSTRG.14234	Ca_10424	Ca6	1.425	-0.091
1097	MSTRG.18666	Ca_17294	Ca7	1.429	3.387
1098	MSTRG.5633	Ca_19621	Ca3	1.432	2.756
1099	MSTRG.12094	Ca_16620	Ca5	1.434	4.848
1100	MSTRG.9739	-	Ca4	1.436	2.492
1101	MSTRG.1565	-	Ca1	1.436	0.999
1102	MSTRG.16181	Ca_16684	Ca6	1.442	5.661
1103	MSTRG.19738	Ca_11697	Ca7	1.453	3.460
1104	MSTRG.2297	Ca_18585	Ca1	1.462	6.209
1105	MSTRG.15962	Ca_11225	Ca6	1.465	7.578
1106	MSTRG.20484	-	Ca7	1.475	2.138
1107	MSTRG.10030	Ca_15498	Ca4	1.476	2.360
1108	MSTRG.6602	Ca_07339	Ca3	1.477	8.507

1109	MSTRG.5859	Ca_20433	Ca3	1.477	2.173
1110	MSTRG.8742	Ca_04313	Ca4	1.483	2.893
1111	MSTRG.18815	Ca_09355	Ca7	1.492	1.964
1112	MSTRG.19845	Ca_10065	Ca7	1.496	3.327
1113	MSTRG.7156	Ca_00913	Ca3	1.500	7.486
1114	MSTRG.15164	Ca_05064	Ca6	1.501	4.777
1115	MSTRG.15570	Ca_06359	Ca6	1.501	1.503
1116	MSTRG.20953	Ca_02223	Ca8	1.501	1.400
1117	MSTRG.9593	-	Ca4	1.503	-0.620
1118	MSTRG.11415	Ca_17071	Ca5	1.504	1.883
1119	MSTRG.12460	Ca_04971	Ca5	1.506	-0.191
1120	MSTRG.20252	-	Ca7	1.507	1.672
1121	MSTRG.1776	Ca_07059	Ca1	1.509	0.368
1122	MSTRG.9444	-	Ca4	1.512	1.365
1123	MSTRG.22590	Ca_22590	scaffold134	1.513	3.541
1124	MSTRG.10339	Ca_14936	Ca4	1.515	2.646
1125	MSTRG.19236	Ca_15845	Ca7	1.530	6.483
1126	MSTRG.15341	Ca_05233	Ca6	1.534	5.680
1127	MSTRG.15213	Ca_05110	Ca6	1.536	9.202
1128	MSTRG.1117	Ca_02929	Ca1	1.538	3.826
1129	MSTRG.453	Ca_00247	Ca1	1.539	-0.092
1130	MSTRG.7551	Ca_01281	Ca3	1.540	1.275
1131	MSTRG.2339	Ca_20295	Ca1	1.541	1.993
1132	MSTRG.21862	Ca_12972	Ca8	1.543	1.003
1133	MSTRG.25151	Ca_23410	scaffold775	1.545	8.882
1134	MSTRG.1281	Ca_02766	Ca1	1.545	3.525
1135	MSTRG.3482	Ca_19687	Ca2	1.545	3.735
1136	MSTRG.19049	Ca_09969	Ca7	1.549	5.388
1137	MSTRG.20746	Ca_02438	Ca8	1.550	2.418
1138	MSTRG.14434	-	Ca6	1.553	1.906
1139	MSTRG.14747	Ca_09598	Ca6	1.559	4.458
1140	MSTRG.10341	Ca_14935	Ca4	1.561	3.394
1141	MSTRG.17870	-	Ca7	1.562	3.695
1142	MSTRG.21286	Ca_23588	Ca8	1.563	3.047
1143	MSTRG.639	Ca_00437	Ca1	1.566	3.717
1144	MSTRG.7706	Ca_07674	Ca4	1.568	1.155
1145	MSTRG.21711	Ca_23843	Ca8	1.569	1.796

1146	MSTRG.7309	Ca_01059	Ca3	1.572	5.019
1147	MSTRG.9677	Ca_19077	Ca4	1.587	3.083
1148	MSTRG.9398	-	Ca4	1.592	1.065
1149	MSTRG.12008	Ca_13410	Ca5	1.596	2.458
1150	MSTRG.3306	Ca_10518	Ca2	1.603	2.829
1151	MSTRG.7543	Ca_01273	Ca3	1.611	-2.029
1152	MSTRG.23792	Ca_20600	scaffold284	1.611	7.728
1153	MSTRG.2129	-	Ca1	1.611	0.608
1154	MSTRG.751	Ca_00568	Ca1	1.612	0.836
1155	MSTRG.10190	Ca_15136	Ca4	1.622	7.692
1156	MSTRG.15053	Ca_20467	Ca6	1.623	5.286
1157	MSTRG.13507	Ca_12684	Ca5	1.636	4.633
1158	MSTRG.2771	Ca_22680	Ca1	1.642	3.606
1159	MSTRG.17154	Ca_17522	Ca6	1.651	3.031
1160	MSTRG.20500	-	Ca7	1.660	-0.656
1161	MSTRG.25493	-	scaffold924	1.662	0.286
1162	MSTRG.11880	Ca_08977	Ca5	1.666	1.581
1163	MSTRG.21225	Ca_01961	Ca8	1.670	3.456
1164	MSTRG.4104	Ca_14956	Ca2	1.672	2.338
1165	MSTRG.5161	Ca_22375	Ca3	1.674	1.784
1166	MSTRG.7782	Ca_07754	Ca4	1.682	2.908
1167	MSTRG.5094	Ca_19393	Ca3	1.684	5.095
1168	MSTRG.17829	Ca_03258	Ca7	1.685	1.839
1169	MSTRG.10905	Ca_10798	Ca4	1.685	3.353
1170	MSTRG.13059	-	Ca5	1.689	0.918
1171	MSTRG.4413	Ca_16139	Ca2	1.699	3.968
1172	MSTRG.13091	Ca_07450	Ca5	1.709	0.197
1173	MSTRG.10677	-	Ca4	1.718	3.085
1174	MSTRG.13573	Ca_03883	Ca5	1.722	6.875
1175	MSTRG.440	Ca_00234	Ca1	1.723	3.874
1176	MSTRG.7923	Ca_12068	Ca4	1.726	6.002
1177	MSTRG.13988	Ca_13252	Ca6	1.729	0.920
1178	MSTRG.15216	-	Ca6	1.751	3.532
1179	MSTRG.16109	Ca_11054	Ca6	1.754	1.127
1180	MSTRG.19009	Ca_23032	Ca7	1.764	3.392
1181	MSTRG.16555	Ca_22055	Ca6	1.776	3.133
1182	MSTRG.13984	Ca_13249	Ca6	1.777	3.955

1183	MSTRG.23069	Ca_25726	scaffold1710	1.778	3.348
1184	MSTRG.18366	Ca_06668	Ca7	1.778	-0.631
1185	MSTRG.16596	Ca_15792	Ca6	1.789	3.444
1186	MSTRG.10344	Ca_14931	Ca4	1.791	2.923
1187	MSTRG.9323	Ca_05458	Ca4	1.796	2.043
1188	MSTRG.18224	-	Ca7	1.799	2.416
1189	MSTRG.23649	Ca_26161	scaffold2569	1.804	1.178
1190	MSTRG.13629	Ca_03936	Ca5	1.804	0.288
1191	MSTRG.6980	Ca_00737	Ca3	1.804	5.257
1192	MSTRG.3940	Ca_22040	Ca2	1.807	-0.193
1193	MSTRG.10330	Ca_13052	Ca4	1.811	4.697
1194	MSTRG.20789	Ca_02397	Ca8	1.834	5.379
1195	MSTRG.4421	Ca_16136	Ca2	1.834	3.158
1196	MSTRG.24664	-	scaffold5226	1.850	0.526
1197	MSTRG.8692	-	Ca4	1.852	2.342
1198	MSTRG.690	Ca_00497	Ca1	1.859	1.943
1199	MSTRG.8556	Ca_08363	Ca4	1.871	3.162
1200	MSTRG.25579	Ca_21391	scaffold98	1.880	5.866
1201	MSTRG.20803	Ca_02379	Ca8	1.886	-0.350
1202	MSTRG.15139	Ca_05033	Ca6	1.894	4.595
1203	MSTRG.16955	-	Ca6	1.908	-0.135
1204	MSTRG.5797	-	Ca3	1.929	-0.484
1205	MSTRG.17916	Ca_03183	Ca7	1.930	0.095
1206	MSTRG.21551	Ca_11546	Ca8	1.946	5.127
1207	MSTRG.8435	Ca_03482	Ca4	1.953	4.852
1208	MSTRG.19050	Ca_09968	Ca7	1.968	3.986
1209	MSTRG.1588	Ca_02452	Ca1	1.970	2.130
1210	MSTRG.17465	Ca_13651	Ca6	1.971	8.821
1211	MSTRG.18229	Ca_06784	Ca7	1.978	3.872
1212	MSTRG.6094	-	Ca3	1.987	-3.080
1213	MSTRG.6967	Ca_00727	Ca3	1.989	2.691
1214	MSTRG.9831	-	Ca4	1.994	3.406
1215	MSTRG.19903	Ca_10011	Ca7	1.994	3.835
1216	MSTRG.20933	Ca_02243	Ca8	1.997	2.644
1217	MSTRG.9166	Ca_05616	Ca4	2.014	4.239
1218	MSTRG.2721	-	Ca1	2.043	-1.741
1219	MSTRG.6015	Ca_06140	Ca3	2.051	-0.669

1220	MSTRG.3372	-	Ca2	2.073	3.858
1221	MSTRG.18247	Ca_06769	Ca7	2.078	7.110
1222	MSTRG.4446	Ca_16100	Ca2	2.085	1.058
1223	MSTRG.14557	-	Ca6	2.096	-0.181
1224	MSTRG.15447	Ca_22015	Ca6	2.108	2.959
1225	MSTRG.1576	Ca_02462	Ca1	2.110	1.301
1226	MSTRG.20006	Ca_20988	Ca7	2.122	1.945
1227	MSTRG.430	-	Ca1	2.126	-1.065
1228	MSTRG.3259	Ca_10561	Ca2	2.127	5.158
1229	MSTRG.16069	Ca_11087	Ca6	2.137	5.167
1230	MSTRG.16151	Ca_24160	Ca6	2.157	1.237
1231	MSTRG.11153	Ca_20731	Ca5	2.172	5.160
1232	MSTRG.21043	Ca_02137	Ca8	2.178	6.402
1233	MSTRG.9414	Ca_05372	Ca4	2.178	-0.041
1234	MSTRG.13753	Ca_04059	Ca5	2.178	2.294
1235	MSTRG.23403	-	scaffold206	2.180	2.322
1236	MSTRG.22206	Ca_24273	scaffold1089	2.202	4.630
1237	MSTRG.7691	Ca_07664	Ca4	2.211	3.548
1238	MSTRG.10809	-	Ca4	2.216	0.538
1239	MSTRG.21566	-	Ca8	2.220	-0.202
1240	MSTRG.11988	Ca_13431	Ca5	2.223	5.163
1241	MSTRG.11274	Ca_19988	Ca5	2.229	1.879
1242	MSTRG.675	Ca_00482	Ca1	2.261	4.482
1243	MSTRG.23552	-	scaffold2371	2.278	1.102
1244	MSTRG.9301	Ca_05484	Ca4	2.284	3.942
1245	MSTRG.19570	-	Ca7	2.297	-0.180
1246	MSTRG.21541	Ca_11536	Ca8	2.299	0.704
1247	MSTRG.20598	Ca_11885	Ca8	2.309	3.513
1248	MSTRG.3199	Ca_12556	Ca2	2.324	1.378
1249	MSTRG.11283	Ca_23782	Ca5	2.331	3.247
1250	MSTRG.22517	Ca_26764	scaffold1309	2.361	0.321
1251	MSTRG.21908	Ca_17891	Ca8	2.363	2.547
1252	MSTRG.20708	Ca_15039	Ca8	2.386	1.322
1253	MSTRG.17035	-	Ca6	2.397	0.914
1254	MSTRG.20410	Ca_15698	Ca7	2.405	4.453
1255	MSTRG.23035	-	scaffold1687	2.416	0.658
1256	MSTRG.15509	Ca_06299	Ca6	2.429	4.231

1257	MSTRG.19704	Ca_11733	Ca7	2.514	-0.633
1258	MSTRG.23536	Ca_26079	scaffold235	2.518	5.805
1259	MSTRG.11349	Ca_23746	Ca5	2.533	4.453
1260	MSTRG.2715	Ca_18485	Ca1	2.539	8.362
1261	MSTRG.22067	Ca_28086	scaffold10227	2.552	4.025
1262	MSTRG.10329	Ca_13053	Ca4	2.556	2.385
1263	MSTRG.19504	-	Ca7	2.590	4.212
1264	MSTRG.10123	-	Ca4	2.596	0.191
1265	MSTRG.8870	Ca_04426	Ca4	2.610	3.639
1266	MSTRG.471	Ca_00264	Ca1	2.627	1.257
1267	MSTRG.25541	Ca_26911	scaffold953	2.652	1.660
1268	MSTRG.9893	Ca_23165	Ca4	2.689	6.208
1269	MSTRG.9835	-	Ca4	2.745	-1.374
1270	MSTRG.1045	Ca_08031	Ca1	2.760	5.160
1271	MSTRG.23908	Ca_25904	scaffold305	2.768	0.496
1272	MSTRG.16892	-	Ca6	2.784	-1.938
1273	MSTRG.5705	-	Ca3	2.787	4.530
1274	MSTRG.10287	Ca_13096	Ca4	2.824	4.033
1275	MSTRG.13238	-	Ca5	2.851	2.221
1276	MSTRG.24812	Ca_23129	scaffold562	2.895	5.538
1277	MSTRG.655	Ca_00464	Ca1	2.897	-0.222
1278	MSTRG.2640	Ca_13939	Ca1	2.900	3.021
1279	MSTRG.10527	-	Ca4	2.919	-0.446
1280	MSTRG.4602	Ca_17822	Ca2	2.943	1.807
1281	MSTRG.17924	Ca_03175	Ca7	2.969	5.513
1282	MSTRG.17034	-	Ca6	2.974	0.902
1283	MSTRG.23963	-	scaffold314	2.981	0.131
1284	MSTRG.10100	Ca_22449	Ca4	3.013	-1.634
1285	MSTRG.19679	-	Ca7	3.057	-0.333
1286	MSTRG.5819	Ca_09495	Ca3	3.189	2.203
1287	MSTRG.8437	Ca_03479	Ca4	3.190	5.353
1288	MSTRG.9933	-	Ca4	3.191	2.111
1289	MSTRG.17274	Ca_16294	Ca6	3.242	0.931
1290	MSTRG.8589	Ca_08398	Ca4	3.254	3.295
1291	MSTRG.20599	-	Ca8	3.307	-0.461
1292	MSTRG.21768	Ca_13048	Ca8	3.318	3.117
1293	MSTRG.22768	Ca_24878	scaffold1382	3.322	-1.836

1294	MSTRG.8588	Ca_08397	Ca4	3.360	3.438
1295	MSTRG.16966	Ca_23440	Ca6	3.416	-0.218
1296	MSTRG.18209	-	Ca7	3.535	0.896
1297	MSTRG.10331	Ca_13051	Ca4	3.593	-0.447
1298	MSTRG.6310	-	Ca3	3.599	-0.823
1299	MSTRG.9416	-	Ca4	3.664	-1.650
1300	MSTRG.4765	-	Ca2	3.779	1.484
1301	MSTRG.2555	-	Ca1	3.796	0.600
1302	MSTRG.18981	Ca_16053	Ca7	3.890	0.409
1303	MSTRG.20171	Ca_13797	Ca7	3.927	-1.231
1304	MSTRG.12074	Ca_13344	Ca5	3.946	-0.254
1305	MSTRG.7144	Ca_00901	Ca3	3.948	-1.678
1306	MSTRG.17344	-	Ca6	4.015	-1.532
1307	MSTRG.552	-	Ca1	4.017	2.723
1308	MSTRG.1993	-	Ca1	4.018	-0.752
1309	MSTRG.466	Ca_00258	Ca1	4.150	3.954
1310	MSTRG.20707	Ca_15040	Ca8	4.164	3.252
1311	MSTRG.555	Ca_00351	Ca1	4.219	3.318
1312	MSTRG.8555	Ca_08362	Ca4	4.253	1.390
1313	MSTRG.22149	-	scaffold1052	4.266	-2.764
1314	MSTRG.470	Ca_00263	Ca1	4.274	2.194
1315	MSTRG.12177	-	Ca5	4.284	-3.398
1316	MSTRG.9480	-	Ca4	4.368	-1.004
1317	MSTRG.549	Ca_00345	Ca1	4.452	2.258
1318	MSTRG.15258	Ca_05148	Ca6	4.474	0.226
1319	MSTRG.11203	-	Ca5	4.483	0.464
1320	MSTRG.12445	Ca_04955	Ca5	4.703	1.255
1321	MSTRG.24156	-	scaffold3497	4.713	-3.054
1322	MSTRG.15963	-	Ca6	4.739	1.711
1323	MSTRG.19667	-	Ca7	4.853	-1.705
1324	MSTRG.3134	Ca_12619	Ca2	4.994	-4.201
1325	MSTRG.11421	-	Ca5	5.072	-3.376
1326	MSTRG.22571	Ca_19787	scaffold1324	5.160	4.048
1327	MSTRG.23812	Ca_25387	scaffold287	5.337	0.409
1328	MSTRG.10340	-	Ca4	5.382	0.359
1329	MSTRG.19645	Ca_11789	Ca7	5.400	2.840
1330	MSTRG.19669	-	Ca7	5.447	-0.088

1331	MSTRG.24993	-	scaffold661	5.462	-0.794
1332	MSTRG.1344	Ca_02690	Ca1	5.479	-0.527
1333	MSTRG.9415	-	Ca4	5.486	0.554
1334	MSTRG.543	Ca_00340	Ca1	5.502	2.350
1335	MSTRG.9417	-	Ca4	5.534	-1.657
1336	MSTRG.4517	-	Ca2	5.538	-0.389
1337	MSTRG.16926	-	Ca6	5.557	-2.107
1338	MSTRG.71	-	C11103858	5.670	-0.133
1339	MSTRG.2463	Ca_21847	Ca1	5.675	0.807
1340	MSTRG.13648	-	Ca5	5.726	-0.798
1341	MSTRG.562	-	Ca1	5.732	-3.834
1342	MSTRG.22141	Ca_17227	scaffold1047	5.888	-1.158
1343	MSTRG.5300	-	Ca3	5.942	-1.899
1344	MSTRG.24716	-	scaffold537	6.072	1.281
1345	MSTRG.9720	-	Ca4	6.144	-3.448
1346	MSTRG.22332	Ca_22947	scaffold118	6.181	1.004
1347	MSTRG.19670	-	Ca7	6.292	-0.480
1348	MSTRG.6297	Ca_08196	Ca3	6.364	1.834
1349	MSTRG.21738	Ca_20106	Ca8	6.408	0.475
1350	MSTRG.22289	Ca_25662	scaffold1131	6.487	-2.369
1351	MSTRG.11148	-	Ca5	6.700	-3.734
1352	MSTRG.25012	Ca_20156	scaffold674	6.909	1.046
1353	MSTRG.6544	-	Ca3	7.098	1.177
1354	MSTRG.4730	Ca_10186	Ca2	7.154	2.826
1355	MSTRG.201	-	Ca1	7.215	-1.496
1356	MSTRG.22292	Ca_25666	scaffold1131	7.297	-2.017
1357	MSTRG.10327	Ca_13055	Ca4	7.356	0.630
1358	MSTRG.6	-	C11048020	7.539	-0.407
1359	MSTRG.11110	-	Ca5	7.703	-3.892
1360	MSTRG.4070	-	Ca2	8.757	-3.794
1361	MSTRG.7	-	C11047824	8.864	-0.992
1362	MSTRG.23801	-	scaffold2850	9.000	-0.848
1363	MSTRG.21024	-	Ca8	9.122	0.003
1364	MSTRG.10328	Ca_13054	Ca4	10.080	1.215